

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 13:01:28 ; Search time 3582 Seconds  
(without alignments)  
16064.488 Million cell updates/sec

Title: US-10-696-261-19

Perfect score: 4683  
Sequence: 1 ttggccactccctctcttcgcg.....cgcataagagggagtgcccaa 4683

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	4683	100.0	4683	US-10-696-261-19	Sequence 19, Appli
2	4683	100.0	4683	US-10-696-262-19	Sequence 19, Appli
3	4683	100.0	4683	US-10-696-900-19	Sequence 19, Appli
4	4663.8	99.6	4683	US-10-427-129-6	Sequence 6, Appli
5	4663.8	99.6	4683	US-10-959-017-2	Sequence 2, Appli
6	4663.8	99.6	4683	US-11-145-035-25	Sequence 25, Appli
7	4253.2	90.8	4718	US-10-291-583-6	Sequence 6, Appli
8	4253.2	90.8	4718	US-10-696-261-1	Sequence 1, Appli
9	4253.2	90.8	4718	US-10-696-282-1	Sequence 1, Appli
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13	4253.2	90.8	4718	US-11-145-035-19	Sequence 19, Appli
14	3678.4	78.5	4721	US-10-291-583-1	Sequence 1, Appli
15	3678.4	78.5	4721	US-11-145-035-37	Sequence 37, Appli
16	3604.8	77.0	13804	US-10-427-129-11	Sequence 11, Appli
17	3441.6	73.5	4382	US-10-496-799-1	Sequence 1, Appli

18	3404.6	72.7	4385	7	US-10-291-583-5	Sequence 5, Appli
19	3370.4	72.0	4393	7	US-10-291-583-4	Sequence 4, Appli
20	3370.4	72.0	4393	7	US-10-423-704A-1	Sequence 1, Appli
21	3370.4	72.0	4393	15	US-11-145-035-39	Sequence 19, Appli
22	3296.2	70.4	4679	3	US-09-804-898-1	Sequence 10, Appli
23	3296.2	70.4	4679	3	US-09-945-681-10	Sequence 12, Appli
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28	3293	70.3	4679	15	US-11-184-380-25	Sequence 25, Appli
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45	3182.8	68.0	4722	15	US-11-145-035-21	Sequence 21, Appli

## ALIGNMENTS

RESULT 1  
US-10-696-261-19  
; Sequence 19, Application US/10696261  
; Publication No. US20040057931A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, James M.  
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,  
; TITLE OF INVENTION: Vectors and Host Cells Containing Same  
; FILE REFERENCE: GNPVN.031USA  
; CURRENT APPLICATION NUMBER: US/10/696,261  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: US/09/807,802A  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: US 60/107,114  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/25694  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 4683  
; TYPE: DNA  
; ORGANISM: AAV-6  
US-10-696-261-19  
Query Match 100.0%; Score 4683; DB 8; Length 4683;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 4081 CGGATGACACTTTTCAACCCGCTCTCTCATAGGGCGGCTTTGGAATTAAGACCCGCTC 4140  
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|  
|  
Db 4081 CGGATGACACTTTTCAACCCGCTCTCTCATAGGGCGGCTTTGGAATTAAGACCCGCTC 4140  
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|  
|  
QY 4141 CTCAGATCTCATCAAAAAACAGCCTGTCTGCGAATCTCCGCGACAGATTTTCGCTA 4200  
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|  
|  
Db 4141 CTCAGATCTCATCAAAAAACAGCCTGTCTGCGAATCTCCGCGACAGATTTTCGCTA 4200  
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QY 4201 CAAAGTTTCTTCAATTCATCCAGATTTCCAGAGCAAGTACGCTGAGATTTGAT 4260  
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|  
|  
Db 4201 CAAAGTTTCTTCAATTCATCCAGATTTCCAGAGCAAGTACGCTGAGATTTGAT 4260  
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|  
|  
QY 4261 GGGAGCTGCAAGAAAGAAACAGCAAGCGTGGAAATCCGGAAGTCAAGTATCATCTTACT 4320  
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|  
|  
Db 4261 GGGAGCTGCAAGAAAGAAACAGCAAGCGTGGAAATCCGGAAGTCAAGTATCATCTTACT 4320  
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QY 4321 ATGCAAAATCTGCCAAGTGTATTTCACTGTGGAACAACATGAGCTTTATCTAGAGCTC 4380  
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|  
Db 4321 ATGCAAAATCTGCCAAGTGTATTTCACTGTGGAACAACATGAGCTTTATCTAGAGCTC 4380  
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|  
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QY 4381 GCCCATTTGGACCCGTTTACTCTACCCGCTGCTGTAATGTGTATTAATTAATAACCG 4440  
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Db 4381 GCCCATTTGGACCCGTTTACTCTACCCGCTGCTGTAATGTGTATTAATTAATAACCG 4440  
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QY 4441 GTTAATTTGTGATGATTAATTTGTGCTCATGTCTTATTTATTTATCTGTGATCAATA 4500  
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|  
Db 4441 GTTAATTTGTGATGATTAATTTGTGCTCATGTCTTATTTATTTATCTGTGATCAATA 4500  
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|  
QY 4501 GCAACGGTTCACATTAATGCTTAAAGTGGCTTCGGAATACCCCTAGATGAGATT 4560  
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|  
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Dh 4501 GCAACGGTACACATTAAGTCTTGGCTTCGGGAATACCCCTAATGATGAGATT 4560  
Qy 4561 GCCACATCCCTCTATAGCGCGCTCGCTCGTGGGGCCGAGAGAGAGCTTCGCG 4620  
Db 4661 GCCACATCCCTCTATAGCGCGCTCGCTCGTGGGGCCGAGAGAGAGCTTCGCG 4620  
Qy 4621 TCTGCGGACCTTTGGTCCGACGAGCCCAACGAGCGAGCGGCGCATAGAGGAGTGGC 4680  
Db 4621 TCTGCGGACCTTTGGTCCGACGAGCCCAACGAGCGAGCGGCGCATAGAGGAGTGGC 4680  
Qy 4681 CAA 4683  
Db 4681 CAA 4683

## RESULT 2

US-10-696-282-19  
; Sequence 19, Application US/10696282  
; Publication No. US20040057932A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, James M.  
; APPLICANT: Xiao, Weidong  
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,  
; TITLE OF INVENTION: Vectors and Host Cells Containing Same  
; FILE REFERENCE: GNPVN.031USA  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 4683  
; TYPE: DNA  
; ORGANISM: AAV-6  
US-10-696-282-19

Query Match 100.0%; Score 4683; DB 8; Length 4683;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCACTCCCTCTCTGCGGCTCGCTCACTGAGCGCGGCGCAAAAGTCCG 60  
Db 1 TTGGCACTCCCTCTCTGCGGCTCGCTCACTGAGCGCGGCGCAAAAGTCCG 60  
Qy 61 CGACGCGCGGCTTTGCGCGGCGGCTCACTGAGCGAGCGCGGCGAGAGGAGTG 120  
Db 61 CGACGCGCGGCTTTGCGCGGCGGCTCACTGAGCGAGCGCGGCGAGAGGAGTG 120  
Qy 121 GCCAATCTCATCTAGAGGCTTCGAGAGGCGTGAAGTCTGAATGATCTGATAG 180  
Db 121 GCCAATCTCATCTAGAGGCTTCGAGAGGCGTGAAGTCTGAATGATCTGATAG 180  
Qy 121 GCTTGGAGAGGCTCTGATTAAGAGTCACTGAGGCTTTGCGACATTTGCGACCAT 240  
Db 121 GCTTGGAGAGGCTCTGATTAAGAGTCACTGAGGCTTTGCGACATTTGCGACCAT 240  
Qy 181 GCTTGGAGAGGCTCTGATTAAGAGTCACTGAGGCTTTGCGACATTTGCGACCAT 240  
Db 181 GCTTGGAGAGGCTCTGATTAAGAGTCACTGAGGCTTTGCGACATTTGCGACCAT 240  
Qy 241 GTGTCACGCTGGATTTAAAGCCGAGTGAAGCGAGGCTTCATTTGAAGCGGGA 300  
Db 241 GTGTCACGCTGGATTTAAAGCCGAGTGAAGCGAGGCTTCATTTGAAGCGGGA 300  
Qy 301 GGTGTAAGCGGAGCGCATGCGGGGTTTAAAGATTGATTAAGTCCGAGCGA 360  
Db 301 GGTGTAAGCGGAGCGCATGCGGGGTTTAAAGATTGATTAAGTCCGAGCGA 360  
Qy 361 CTTGACGAGCATGCGCGGATTTTGAAGCTTTGAGAGCTTTGAGAACTGGGCGGAGAAAGA 420  
Db 361 CTTGACGAGCATGCGCGGATTTTGAAGCTTTGAGAGCTTTGAGAACTGGGCGGAGAAAGA 420

Qy 421 ATGGAGATTCGCGCAGATTTCTGACATGATCTGAATCTGATTTAGAGAGGACCCCTGAC 480  
Db 421 ATGGAGATTCGCGCAGATTTCTGACATGATCTGAATCTGATTTAGAGAGGACCCCTGAC 480  
Qy 481 GGTGGCGGAGAGCTGCGAGCGGCTTCTGCTGCTCACTGGCGCGCGGTAGTAAAGGCCC 540  
Db 481 GGTGGCGGAGAGCTGCGAGCGGCTTCTGCTGCTCACTGGCGCGCGGTAGTAAAGGCCC 540  
Qy 541 GAGAGCCCTCTCTTTGTTGAGTTCGAGAGGCGAGTCTCACTTCCACCTCCATATTCT 600  
Db 541 GAGAGCCCTCTCTTTGTTGAGTTCGAGAGGCGAGTCTCACTTCCACCTCCATATTCT 600  
Qy 601 GGTGAGACCAAGGGGCTCAATTCATGATGCTGAGGCGGCTTCTGATGATTAAGCGA 660  
Db 601 GGTGAGACCAAGGGGCTCAATTCATGATGCTGAGGCGGCTTCTGATGATTAAGCGA 660  
Qy 661 CAAGCTGTGACAGCATTTACCGCGGGATTCGAGCCGACCTTCCCACTGGTTCCGGGT 720  
Db 661 CAAGCTGTGACAGCATTTACCGCGGGATTCGAGCCGACCTTCCCACTGGTTCCGGGT 720  
Qy 721 GACCAAGACGCTAATGCGCGGAGGGGAAAGAGGTGTGAGAGAGTGTACATCC 780  
Db 721 GACCAAGACGCTAATGCGCGGAGGGGAAAGAGGTGTGAGAGAGTGTACATCC 780  
Qy 781 CAATCACTCTCTGCGCAAGCTGAGCCGAGCTGAGTGGGCGTGAATTAATGAGGA 840  
Db 781 CAATCACTCTCTGCGCAAGCTGAGCCGAGCTGAGTGGGCGTGAATTAATGAGGA 840  
Qy 841 GTATATAGGCGGCTTTTAACTGTGCGGAGCGCAACGCGCTGTGGCGGACGACCTGAC 900  
Db 841 GTATATAGGCGGCTTTTAACTGTGCGGAGCGCAACGCGCTGTGGCGGACGACCTGAC 900  
Qy 901 CCAAGTCAAGCAAGCCAGAGAGCAAGAGAGAACTGAAACCCCAATTTCTGACGGCG 960  
Db 901 CCAAGTCAAGCAAGCCAGAGAGCAAGAGAGAACTGAAACCCCAATTTCTGACGGCG 960  
Qy 961 TGTATCCGCTCAAAAACCTTCGCAAGCTGATCATGAGCTGTGGTGTGAGACG 1020  
Db 961 TGTATCCGCTCAAAAACCTTCGCAAGCTGATCATGAGCTGTGGTGTGAGACG 1020  
Qy 1021 GGGATCACTCTCGAGAGAGAGTGAATCCAGAGAGACCAAGGCTTCGATCTCTTCAA 1080  
Db 1021 GGGATCACTCTCGAGAGAGAGTGAATCCAGAGAGACCAAGGCTTCGATCTCTTCAA 1080  
Qy 1081 GCGGCTCTCAACTCGCGGCTTCAGATCAAGCGGCTGTGAATGCGGCAAGATCAT 1140  
Db 1081 GCGGCTCTCAACTCGCGGCTTCAGATCAAGCGGCTGTGAATGCGGCAAGATCAT 1140  
Qy 1141 GCGGCTGACCAATTCGCGGCTTCGATCTGATGAGGCTTCGCGCGCGCAATTAA 1200  
Db 1141 GCGGCTGACCAATTCGCGGCTTCGATCTGATGAGGCTTCGCGCGCGCAATTAA 1200  
Qy 1201 AACCAACCGATTTACCGCATCTCTGAGCTGAAGCGGTAGACCTTCGATCCCGGCTC 1260  
Db 1201 AACCAACCGATTTACCGCATCTCTGAGCTGAAGCGGTAGACCTTCGATCCCGGCTC 1260  
Qy 1261 GGTCTTCTCGGCTGGCGCGGAGAAAGGTTGCGAAAAACGAAACCATCTGGCTTTGG 1320  
Db 1261 GGTCTTCTCGGCTGGCGCGGAGAAAGGTTGCGAAAAACGAAACCATCTGGCTTTGG 1320  
Qy 1321 GCGGCGCAAGCGGCAAGCAATGCGGAGAGGATGCGGCGCGCTGCTTCTA 1380  
Db 1321 GCGGCGCAAGCGGCAAGCAATGCGGAGAGGATGCGGCGCGCTGCTTCTA 1380  
Qy 1381 GCGGCTGCTCACTGAGCAATGAGAACTTCTCTTCAAGATTTGCTGCAAGAGTGT 1440  
Db 1381 GCGGCTGCTCACTGAGCAATGAGAACTTCTCTTCAAGATTTGCTGCAAGAGTGT 1440  
Qy 1441 GATCTGTTGAGAGAGGCAAGATGACGCGCAAGGTGTGAGGTGCGGCAAGGCAATTTCT 1500  
Db 1441 GATCTGTTGAGAGAGGCAAGATGACGCGCAAGGTGTGAGGTGCGGCAAGGCAATTTCT 1500  
Qy 1501 CCGCGGAGCAAGGTGCGGCTGAGCAAAAAGTGAAGTCTGCGCGCAATGATCCAC 1560



Db	1501	CGGCGGAGCAAGGTGCGGTGGACCAAAAGTGCAAGTGTCCGCCAGATGATCCAC	1560
Qy	1561	CCCCGTGATTCGTCACTCCACACCAACATGTGCCCGGTGATTGACGGGAACAGACCAAC	1620
Db	1561	CCCCGTGATTCGTCACTCCACACCAACATGTGCCCGGTGATTGACGGGAACAGACCAAC	1620
Qy	1621	CTTGCAGACCAAGCAGCGGTTGACGAGCCGATGTTCAAAATTGAACTCACCGCGGTCT	1680
Db	1621	CTTGCAGACCAAGCAGCGGTTGACGAGCCGATGTTCAAAATTGAACTCACCGCGGTCT	1680
Qy	1681	GGAGCATGACTTTGGCAAGTGACAAAGCAGAGATCAAAAGATTCTTCCGTGGCGCA	1740
Db	1681	GGAGCATGACTTTGGCAAGTGACAAAGCAGAGATCAAAAGATTCTTCCGTGGCGCA	1740
Qy	1741	GGATACAGTGACCGAGGTGGCGCATGAGTTCTACGTCAAGAAAGGTGAGCCACACACAG	1800
Db	1741	GGATACAGTGACCGAGGTGGCGCATGAGTTCTACGTCAAGAAAGGTGAGCCACACACAG	1800
Qy	1801	ACCCGCCCCCGATGACGGGGATAAAGGAGCCCAAGGGGGCGTGCCTCCAGTGGCGGA	1860
Db	1801	ACCCGCCCCCGATGACGGGGATAAAGGAGCCCAAGGGGGCGTGCCTCCAGTGGCGGA	1860
Qy	1861	TCCATCGACGTTCAGACGGCGAAGAGCTCCGGTGGACTTTGGCGACAGGTACCAAAACA	1920
Db	1861	TCCATCGACGTTCAGACGGCGAAGAGCTCCGGTGGACTTTGGCGACAGGTACCAAAACA	1920
Qy	1921	ATGTTCTGTGACCGCGGGGATGCTTCAAGTGTCTTTCCCTGCAAAACATGCGAGAGAT	1980
Db	1921	ATGTTCTGTGACCGCGGGGATGCTTCAAGTGTCTTTCCCTGCAAAACATGCGAGAGAT	1980
Qy	1981	GAATCAGAAATTTCAACATTTGCTTACCGACGGGACCAAGACCTGTTGAAATGTTTCC	2040
Db	1981	GAATCAGAAATTTCAACATTTGCTTACCGACGGGACCAAGACCTGTTGAAATGTTTCC	2040
Qy	2041	CGGCGTGTCAAGATCTCAACCGGTGTGTGAGAAAGAGACGTATCCGAAACTCTGGCCAT	2100
Db	2041	CGGCGTGTCAAGATCTCAACCGGTGTGTGAGAAAGAGACGTATCCGAAACTCTGGCCAT	2100
Qy	2101	TCATCATCTGCTGGGGCGGGCTCCCGAAGATTGCTTCCGTCCGATCTGTGTCACAGT	2160
Db	2101	TCATCATCTGCTGGGGCGGGCTCCCGAAGATTGCTTCCGTCCGATCTGTGTCACAGT	2160
Qy	2161	GGATCTGAGTACGTGTGTTCTGAGCAATTAATGACTTAACCAAGTATGCTGCGCATG	2220
Db	2161	GGATCTGAGTACGTGTGTTCTGAGCAATTAATGACTTAACCAAGTATGCTGCGCATG	2220
Qy	2221	GTTATCTTTCAGATTGCTCGAGGACAACTCTGAGGGCATTTGCGCATGTGTGGACT	2280
Db	2221	GTTATCTTTCAGATTGCTCGAGGACAACTCTGAGGGCATTTGCGCATGTGTGGACT	2280
Qy	2281	TGAAAACCTGAGAGCCCGAAACCCAAAGCCAAACAGCAAAAGCAGAGCAGCGCGGGTCT	2340
Db	2281	TGAAAACCTGAGAGCCCGAAACCCAAAGCCAAACAGCAAAAGCAGAGCAGCGCGGGTCT	2340
Qy	2341	TGGTGCTTCCAGGCTACAGATACCTCCGGAACCTTCAACGGAAGTGGAGAGGGGAGCCCG	2400
Db	2341	TGGTGCTTCCAGGCTACAGATACCTCCGGAACCTTCAACGGAAGTGGAGAGGGGAGCCCG	2400
Qy	2401	TCAAACGCGGCGAGATGACAGCGGCGCTTCGAGCAGCAAGAGGCTTACGACCAAGAGCTCA	2460
Db	2401	TCAAACGCGGCGAGATGACAGCGGCGCTTCGAGCAGCAAGAGGCTTACGACCAAGAGCTCA	2460
Qy	2461	CGGCTGACATTCCTGATCTGCGGTATTAACACGCCGACCGCGAGTTTACGAGAGGTCTGC	2520
Db	2461	CGGCTGACATTCCTGATCTGCGGTATTAACACGCCGACCGCGAGTTTACGAGAGGTCTGC	2520
Qy	2521	AAGAAGATACGTCTTTTGGGGCAACCTCGAGCGAGAGTCTTCCAGGCGCAAGAAAGAGG	2580
Db	2521	AAGAAGATACGTCTTTTGGGGCAACCTCGAGCGAGAGTCTTCCAGGCGCAAGAAAGAGG	2580
Qy	2581	TTCTCGAACTTTTGTGTGTTGAGGAAGGTGCTAAGACGGCTCTTGAAAGAAACGTC	2640
Db	2581	TTCTCGAACTTTTGTGTGTTGAGGAAGGTGCTAAGACGGCTCTTGAAAGAAACGTC	2640
Db	2581	TTCTCGAACTTTTGTGTGTTGAGGAAGGTGCTAAGACGGCTCTTGAAAGAAACGTC	2640
Qy	2641	CGGTAGACAGTTCGCAACAAAGCCAGACTCTCTCTCGGGGATTTGGCAAGACAGGCCAGC	2700
Db	2641	CGGTAGACAGTTCGCAACAAAGCCAGACTCTCTCTCGGGGATTTGGCAAGACAGGCCAGC	2700
Qy	2701	AGCCGCTTAAAAAGAGACTCAATTTTGGTTCAGACTGGGAGCTCAGAGTCAAGTCCCGGAC	2760
Db	2701	AGCCGCTTAAAAAGAGACTCAATTTTGGTTCAGACTGGGAGCTCAGAGTCAAGTCCCGGAC	2760
Qy	2761	CACAACTCTCGAGAACTTCAGCAACCCCGCTGTGTGGAGCTTACATAGGCTT	2820
Db	2761	CACAACTCTCGAGAACTTCAGCAACCCCGCTGTGTGGAGCTTACATAGGCTT	2820
Qy	2821	CAGCGGTGGCGCACCAATGGCAACATTAAGAAAGCGCCGACGGAGTGGGTATGCT	2880
Db	2821	CAGCGGTGGCGCACCAATGGCAACATTAAGAAAGCGCCGACGGAGTGGGTATGCT	2880
Qy	2881	CAGGAAATTTGCGATTGCGATTCCACATGCTGGGGGACAGAGTCAACACAGACCC	2940
Db	2881	CAGGAAATTTGCGATTGCGATTCCACATGCTGGGGGACAGAGTCAACACAGACCC	2940
Qy	2941	GAACATGGGCTTGCCCACTATTAACAACCACTCTTCAACAGCAAAATCTCAAGTCTTCA	3000
Db	2941	GAACATGGGCTTGCCCACTATTAACAACCACTCTTCAACAGCAAAATCTCAAGTCTTCA	3000
Qy	3001	CGGGGGCCAGCAAGACCACTACTTCCGCTACAGACCCCTGGGGGATTTTGTGAT	3060
Db	3001	CGGGGGCCAGCAAGACCACTACTTCCGCTACAGACCCCTGGGGGATTTTGTGAT	3060
Qy	3061	TCACAGATTCACATGCGCATTTTCCACACGCTGACGTCGACGACTCATCAACAACAAT	3120
Db	3061	TCACAGATTCACATGCGCATTTTCCACACGCTGACGTCGACGACTCATCAACAACAAT	3120
Qy	3121	GGGATTTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCAAGTCAAGAGGTCA	3180
Db	3121	GGGATTTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCAAGTCAAGAGGTCA	3180
Qy	3181	CGAGATGATGAGGTGTACAGCACTCGCTAATACTTTACAGACAGGTTAAAGTCTTGT	3240
Db	3181	CGAGATGATGAGGTGTACAGCACTCGCTAATACTTTACAGACAGGTTAAAGTCTTGT	3240
Qy	3241	CGGACTCGGAGTACAGTTCCTGAGAGTCCGCTGAGGCTGAGCAACAGGCTGCTCTC	3300
Db	3241	CGGACTCGGAGTACAGTTCCTGAGAGTCCGCTGAGGCTGAGCAACAGGCTGCTCTC	3300
Qy	3301	CGTTCCGGCGGAGCTGTTCATGATTCGCGAGTACCGGCTACCTAACGCTCAACAATGGCA	3360
Db	3301	CGTTCCGGCGGAGCTGTTCATGATTCGCGAGTACCGGCTACCTAACGCTCAACAATGGCA	3360
Qy	3361	GCCAGGCAATGGAGCGCTCATCTTTTAACTGCTGGAATATTTCCATCCGAGTGTCTGA	3420
Db	3361	GCCAGGCAATGGAGCGCTCATCTTTTAACTGCTGGAATATTTCCATCCGAGTGTCTGA	3420
Qy	3421	GAACGGGCAATTAATTTTAACTTACCTGAGTACACCTTGAAGGAGCGTCTTCCAGAGAGCT	3480
Db	3421	GAACGGGCAATTAATTTTAACTTACCTGAGTACACCTTGAAGGAGCGTCTTCCAGAGAGCT	3480
Qy	3481	ACGCGCACAGCCAGAGCTGAGCCGGCTGATGATTCCTTCATGACCAAGTACCTGATAT	3540
Db	3481	ACGCGCACAGCCAGAGCTGAGCCGGCTGATGATTCCTTCATGACCAAGTACCTGATAT	3540
Qy	3541	ACCTGAAACAGAACTCAACATCAATGCTCGGAAAGTGGCCCAAAACAGAGACTTGTGTTAGCC	3600
Db	3541	ACCTGAAACAGAACTCAACATCAATGCTCGGAAAGTGGCCCAAAACAGAGACTTGTGTTAGCC	3600
Qy	3601	GTCGGTCTCCAGCTGAGCATGCTGTTGAGCCCAAAATAGGCTTACCTGACCTGTTAAC	3660
Db	3601	GTCGGTCTCCAGCTGAGCATGCTGTTGAGCCCAAAATAGGCTTACCTGACCTGTTAAC	3660
Qy	3661	GGCAGACAGCGGCTTTCTTAAACAAACAAAGCAACCAACAGCACTTTACTGAGCTG	3720
Db	3661	GGCAGACAGCGGCTTTCTTAAACAAACAAAGCAACCAACAGCACTTTACTGAGCTG	3720

Qy	3721	ATGCGTCAAAATATPAACCTTAAATGGCGGTAAATCATATAATCAACCTGGCACTGTAAAG	3780
Dp	3721	GTGCTTCAAAATATPAACCTTAAATGGCGGTAAATCATATAATCAACCTGGCACTGTAAAG	3780
Qy	3781	CCTCACAAAGACGACAAAGACAAGTCTTCTTCCATAGCGGTGCATGATTTTGGAA	3840
Dp	3781	CCTCACAAAGACGACAAAGACAAGTCTTCTTCCATAGCGGTGCATGATTTTGGAA	3840
Qy	3841	AGGAGAGGCGCGGAGCTTCAAAACATGATTTGGACAAATGTATGATCAACACGAAGG	3900
Dp	3841	AGGAGAGGCGCGGAGCTTCAAAACATGATTTGGACAAATGTATGATCAACACGAAGG	3900
Qy	3901	AAATCAAAAGCATTACCCCGTGGCCAACGAAAGATTTGGAGACTGTGACATCTCC	3960
Dp	3901	AAATCAAAAGCATTACCCCGTGGCCAACGAAAGATTTGGAGACTGTGACATCTCC	3960
Qy	3961	AGAGCAGCAGACACAGACCCCTGCGACCCGAGATGTGATGTTATGAGACCTTACCTGAA	4020
Dp	3961	AGAGCAGCAGACACAGACCCCTGCGACCCGAGATGTGATGTTATGAGACCTTACCTGAA	4020
Qy	4021	TGTGTGTGGCAAGACAGAACGTATPCTTGACAGGTCCTATTTGGGCCAAATTTCTCACA	4080
Dp	4021	TGTGTGTGGCAAGACAGAACGTATPCTTGACAGGTCCTATTTGGGCCAAATTTCTCACA	4080
Qy	4081	CGGATGAGACATTTCACCCGTCCTCTCATAGGGCGGCTTTGSACTTAAAGCACCGCCTC	4140
Dp	4081	CGGATGAGACATTTCACCCGTCCTCTCATAGGGCGGCTTTGSACTTAAAGCACCGCCTC	4140
Qy	4141	CTCAGATCTCATCAAAAACAGCGCTGTTCTTGCGAATCTTCGCGACAGTTTGGGCTA	4200
Dp	4141	CTCAGATCTCATCAAAAACAGCGCTGTTCTTGCGAATCTTCGCGACAGTTTGGGCTA	4200
Qy	4201	CAAAGTTGCTTCATTATCAACCCAGTATTCACAGGACAAGTAGCGGTGAGATGAT	4260
Dp	4201	CAAAGTTGCTTCATTATCAACCCAGTATTCACAGGACAAGTAGCGGTGAGATGAT	4260
Qy	4261	GGGAGCTCAGAAAAGAAAACAGCAAAACGCTGGAATCCGAAAGTCAGTATCATCTAACT	4320
Dp	4261	GGGAGCTCAGAAAAGAAAACAGCAAAACGCTGGAATCCGAAAGTCAGTATCATCTAACT	4320
Qy	4321	ATGCAAAATTCGCCAAGCTTGAATTTCACTGTGGACAAACAATGACCTTATATAGACCTC	4380
Dp	4321	ATGCAAAATTCGCCAAGCTTGAATTTCACTGTGGACAAACAATGACCTTATATAGACCTC	4380
Qy	4381	GCCCCATTGGGACCCGTTACCTCACCCGTCCTGTAAATGTGTATATCAATPAACCG	4440
Dp	4381	GCCCCATTGGGACCCGTTACCTCACCCGTCCTGTAAATGTGTATATCAATPAACCG	4440
Qy	4441	GTTAATTCGTCAAGTGAACCTTTGGTCTCATATGCTTATATATCTGATCAACATA	4500
Dp	4441	GTTAATTCGTCAAGTGAACCTTTGGTCTCATATGCTTATATATCTGATCAACATA	4500
Qy	4501	GCAACCGGTTACACTTAACGTCTTAAGTTGGCGCTTCGGAAATACCCCTAAGATGAGACTT	4560
Dp	4501	GCAACCGGTTACACTTAACGTCTTAAGTTGGCGCTTCGGAAATACCCCTAAGATGAGACTT	4560
Qy	4561	GCCCACTCCCTATAGCGCGCTCGCTCGCTTGGTGGGCGCGACAGACAGACTTCGCG	4620
Dp	4561	GCCCACTCCCTATAGCGCGCTCGCTCGCTTGGTGGGCGCGACAGACAGACTTCGCG	4620
Qy	4621	TCTGGGACCTTTGGTTCGACAGGCCCAACGAGACGAGACCGCATAGAGGAGTGGC	4680
Dp	4621	TCTGGGACCTTTGGTTCGACAGGCCCAACGAGACGAGACCGCATAGAGGAGTGGC	4680
Qy	4681	CNA 4683	
Dp	4681	CNA 4683	

RESULT 3  
US-10-696-900-19  
; Sequence 19, Application US/10696900

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; Publication No. US20040057933A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNPV, 031USA
; CURRENT APPLICATION NUMBER: US/10/696, 900
; PRIOR APPLICATION NUMBER: US/09/807, 802A
; PRIOR FILING DATE: 2002-10-30
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107, 114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: AAV-6
; US-10-696-900-19

Query Match          100.0%; Score 4683; DB 8; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGCACTCCCTCTGCGCGCTGCTCGCTCACTGAGCCGGGCGAACCAGAGTGGCC 60
DB      1 TTGGCACTCCCTCTGCGCGCTGCTCGCTCACTGAGCCGGGCGAACCAGAGTGGCC 60

QY      61 CGACGCCCGGGCTTTGCCCGGGGGGCTCTCATGTAGCGAGCGGCGCAGAGGGAGTG 120
DB      61 CGACGCCCGGGCTTTGCCCGGGGGCTCTCATGTAGCGAGCGGCGCAGAGGGAGTG 120

QY      121 GCCAATCCCATCATCTAGAGGGTCCCTGGAGGGGGTGGAGTGGTGAAGTGAATTAAGTCATAG 180
DB      121 GCCAATCCCATCATCTAGAGGGTCCCTGGAGGGGGTGGAGTGGTGAAGTGAATTAAGTCATAG 180

QY      181 GGTAGGGAGAGTCCCTGATTTAGAGGTACGTGAGTGTTTTGGACATTTTGGACACCAT 240
DB      181 GGTAGGGAGAGTCCCTGATTTAGAGGTACGTGAGTGTTTTGGACATTTTGGACACCAT 240

QY      241 GTGTGTCACGCTGGGTATTTAAGCCCGAGTGAAGCAGCAGGGTCTCCATTTTGAAGCGGGA 300
DB      241 GTGTGTCACGCTGGGTATTTAAGCCCGAGTGAAGCAGCAGGGTCTCCATTTTGAAGCGGGA 300

QY      301 GGTTTGAACGGCGACGGCCCATGCCGGGGTTTACGAGATTGTGATTAAGTCCCGACGCA 360
DB      301 GGTTTGAACGGCGACGGCCCATGCCGGGGTTTACGAGATTGTGATTAAGTCCCGACGCA 360

QY      361 CCTTGAAGAGCATCTGCCCGGCAATTTTGTGACAGCTTTGTGAACGTGGGTGGCCGAGGAAGA 420
DB      361 CCTTGAAGAGCATCTGCCCGGCAATTTTGTGACAGCTTTGTGAACGTGGGTGGCCGAGGAAGA 420

QY      421 ATGGAGATTGGCCCGCAGATTTCTGACATGATCTTGAATCTGATTGAGCAGGCAACCTCTGAC 480
DB      421 ATGGAGATTGGCCCGCAGATTTCTGACATGATCTTGAATCTGATTGAGCAGGCAACCTCTGAC 480

QY      481 CGTGGCCGAGAGGTGTGACGGCCGACTTCTGTGTTCATCTGGCGCGCGGTGAGTAAAGCCCC 540
DB      481 CGTGGCCGAGAGGTGTGACGGCCGACTTCTGTGTTCATCTGGCGCGCGGTGAGTAAAGCCCC 540

QY      541 GGAGGACCTCTCTTTGTTCAGTTTCGAGAGAGGCGAGTCTCACTTCCACCTCCATATCT 600
DB      541 GGAGGACCTCTCTTTGTTCAGTTTCGAGAGAGGCGAGTCTCACTTCCACCTCCATATCT 600

QY      601 GGTGAGACCAACGGGGGTCAAAATTCATGATGTGTGGCCGCTTCTGTGATCAGATTAGCGA 660
DB      601 GGTGAGACCAACGGGGGTCAAAATTCATGATGTGTGGCCGCTTCTGTGATCAGATTAGCGA 660

QY      661 CAACTGTGTGACACATCTACCGCGGGATGAGCCGACCTGTGCCAATGTGTTGGGGT 720
DB      661 CAACTGTGTGACACATCTACCGCGGGATGAGCCGACCTGTGCCAATGTGTTGGGGT 720

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Db 721 GACCAAGACGGCTAATGGGCGGAGGGGGAAACAAGTGTGTGACGAGTGTACATCCC 780  
Qy 781 CAACTACCTCTGCCCAAGACTCAGCCGAGCTGCAGTGGGCGTGAATTAAATGAGAGA 840  
Db 781 CAACTACCTCTGCCCAAGACTCAGCCGAGCTGCAGTGGGCGTGAATTAAATGAGAGA 840  
Qy 841 GTATATAAGCGGTTTAAACCTTGCGAGCGCAACCGGCTGTGGCGCACGACCTGAC 900  
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Qy 901 CCACTTCAGCCGAGACCCGAGAGCAAGAGAACTGAAACCCCAATTCTGAGCGCGC 960  
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Qy 1201 AACCAACCGCATTTTACCGCATCTTGAGCTGAACGGCTACGACCTTGCTACGCGGCTC 1260  
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Qy 1321 GCCGCGCAACAGGCGGCAAGAACCAATCGCGGAGCAATCGGCCAGCGCGTCCCTTCTA 1380  
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Qy 1441 GATCTGTGGGAGAGGAGGCAAGATGACGGGCCAAGTCTGTGAGTCCGCGCAAGGCTATTCT 1500  
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Qy 1681 GGAGCATGACTTTTGGCAAGTGAACAAGGAGGATCTTCCGCTGGGCGCA 1740  
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Qy 1741 GGATCATGCTGACCGAGGTGGCGCATGAGTTTCACTGAGAAAGGTTGAGCCCAACAG 1800  
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Qy 1801 ACCGCGCCCGATGACGGGGAATAAAGGAGCCCAAGGGGCTGCCCCCTGAGTGGCGGA 1860  
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Qy 2701 AGCCCGCTAATAAAGACTCAATTTTGTGAGACTGAGAGTCAAGAGTCAAGTCCCGAC 2760  
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Db 2821 CAGCGGTGGCGCAACCAATGCGCAATTAACGAAGCGCGCGACGAGTGGGTAAATGCT 2880

QY	2881	AAGGAATTTGGATTGGCATTTCCAAATGGCTGGGGAAGAAGTATCATCAACAGCACCC	2940
Db	2881	CAGGAATTTGGATTGGCATTTCCAAATGGCTGGGGAAGAAGTATCATCAACAGCACCC	2940
QY	2941	GAACATGGGGCTTGGCCCACTTATACAACAACAACCTTCAAAACAAATCTCCAGTCTTCAA	3000
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QY	3001	CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCAACCCCTGGGGGTAATTTGATT	3060
Db	3001	CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCAACCCCTGGGGGTAATTTGATT	3060
QY	3061	TCAACAGATTCACATCGCATTTTCTCACCACGGTACGTGGCAGGACATCATCAACAATTT	3120
Db	3061	TCAACAGATTCACATCGCATTTTCTCACCACGGTACGTGGCAGGACATCATCAACAATTT	3120
QY	3121	GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAATCCAAGAGTCA	3180
Db	3121	GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAATCCAAGAGTCA	3180
QY	3181	CGACGAATGATAGGGGCTCAAGCAACATCGCTAATACCTTACACAGACGGTTCAAGTCTGT	3240
Db	3181	CGACGAATGATAGGGGCTCAAGCAACATCGCTAATACCTTACACAGACGGTTCAAGTCTGT	3240
QY	3241	CGGACTCGGAAGTACCAAGTTCCCGTACGTCCTCGGCTCTGCGACACAGGGCTGCTCCCTC	3300
Db	3241	CGGACTCGGAAGTACCAAGTTCCCGTACGTCCTCGGCTCTGCGACACAGGGCTGCTCCCTC	3300
QY	3301	CGTTCCCGGGCGGACGCTGTTCAATGATTCGGCAGTACGGTACTCAACGTTCAACATGGCA	3360
Db	3301	CGTTCCCGGGCGGACGCTGTTCAATGATTCGGCAGTACGGTACTCAACGTTCAACATGGCA	3360
QY	3361	GCCAGGCAGTGGGAGCGTCACTCTTTTACTGCTGGAAATATTTCCATCGCAGATGTGCGA	3420
Db	3361	GCCAGGCAGTGGGAGCGTCACTCTTTTACTGCTGGAAATATTTCCATCGCAGATGTGCGA	3420
QY	3421	GAACGGGCAATTAATCTTTACCTTACGCTACCTTTGAGAGAGTGGCTTTTCAACAGCACT	3480
Db	3421	GAACGGGCAATTAATCTTTACCTTACGCTACCTTTGAGAGAGTGGCTTTTCAACAGCACT	3480
QY	3481	AACGSCACAGCCAGAGCCTGGACCGGGCTGATGAATCCTCTCATGACACAGTACCTGTAAT	3540
Db	3481	AACGSCACAGCCAGAGCCTGGACCGGGCTGATGAATCCTCTCATGACACAGTACCTGTAAT	3540
QY	3541	ACCTGAACAGAACTCAACATCATGCTCGGAAAGTCCCAAAACAAGGACTTGCTGTTTAGCC	3600
Db	3541	ACCTGAACAGAACTCAACATCATGCTCGGAAAGTCCCAAAACAAGGACTTGCTGTTTAGCC	3600
QY	3601	GTGGGTCTCCAGCTGGCAATGTCTGTTCAGCCCAAAAATGGCTACCTGGACCCCTGTAAC	3660
Db	3601	GTGGGTCTCCAGCTGGCAATGTCTGTTCAGCCCAAAAATGGCTACCTGGACCCCTGTAAC	3660
QY	3661	GGCAGCAGACGGCTTTCTAAAACAAAAAACAACAACAACAGCAACTTTTACTGGACTG	3720
Db	3661	GGCAGCAGACGGCTTTCTAAAACAAAAAACAACAACAACAGCAACTTTTACTGGACTG	3720
QY	3721	GTGCTTCAAAATATTAACCTTAATGGGGGTGAATCTATTAATCAACCTTGGCACTGTAATGG	3780
Db	3721	GTGCTTCAAAATATTAACCTTAATGGGGGTGAATCTATTAATCAACCTTGGCACTGTAATGG	3780
QY	3781	CCTCACAACAAAGACGACAACAAACAAGTCTTTTCCATAGCGGGTCTCATGATTTTGGAA	3840
Db	3781	CCTCACAACAAAGACGACAACAAACAAGTCTTTTCCATAGCGGGTCTCATGATTTTGGAA	3840
QY	3841	AGAGAGCGCCGGAGCTTCAAAACATGCAATTGGACATGTCAATGATCAAGACGAAAGG	3900
Db	3841	AGAGAGCGCCGGAGCTTCAAAACATGCAATTGGACATGTCAATGATCAAGACGAAAGG	3900
QY	3901	AAATCAAAAGCACTAACCCCGGGGCAACGAAAGATTTGGGACTGTGGCACTCAATCTCC	3960
Db	3901	AAATCAAAAGCACTAACCCCGGGGCAACGAAAGATTTGGGACTGTGGCACTCAATCTCC	3960
QY	3961	AGAGCAGCAGCACAGACCCCTGGACCGGAGATGTGCATGTTATGGGACCTTACCTGGAA	4020

Db	3961	AGAGCAGCAGACAGAGACCGTATACCTGACGGGTCTTATTTGGGCCAAAATTCCTACA	4020
Qy	4021	TGTGTGGCAAGACAGAGACCGTATACCTGACGGGTCTTATTTGGGCCAAAATTCCTACA	4080
Db	4021	TGTGTGGCAAGACAGAGACCGTATACCTGACGGGTCTTATTTGGGCCAAAATTCCTACA	4080
Qy	4081	CGGATGACATTTTCAACCCGCTCTCTCATATGGGCGGCTTTTGACTTAAGCACCCTC	4140
Db	4081	CGGATGACATTTTCAACCCGCTCTCTCATATGGGCGGCTTTTGACTTAAGCACCCTC	4140
Qy	4141	CTCAGATCTCATGAAAAACAAGCGCTGTCTCTGGAAATCTCTCGGCAGAGTTTTCGCTA	4200
Db	4141	CTCAGATCTCATGAAAAACAAGCGCTGTCTCTGGAAATCTCTCGGCAGAGTTTTCGCTA	4200
Qy	4201	CAAGTTTGTCTTCAATTCATCCAGATATTCACAGACAAAGTGAAGGTGGAATTTGAAT	4260
Db	4201	CAAGTTTGTCTTCAATTCATCCAGATATTCACAGACAAAGTGAAGGTGGAATTTGAAT	4260
Qy	4261	GGAGAGCTCAGAAAAGAAAAACAGCAAAAGCTGGAATCCCGAAGTGCAGTATACATCTACT	4320
Db	4261	GGAGAGCTCAGAAAAGAAAAACAGCAAAAGCTGGAATCCCGAAGTGCAGTATACATCTACT	4320
Qy	4321	ATGCAAAATCTGCCAAGCTTGATTTCACTGTGCAACAATGCACTTTATATGAGCTTC	4380
Db	4321	ATGCAAAATCTGCCAAGCTTGATTTCACTGTGCAACAATGCACTTTATATGAGCTTC	4380
Qy	4381	GCCCCATTTGGACCCGTTACTCAACCCGTCCTCGTAAATTTGTGTTAATCAATTAACCG	4440
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Qy	4441	GTTAATTCGTCAAGTTGAACCTTGTGTCAATGCTTAAATCTTATATCTTATCTGTCACATA	4500
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Qy	4501	GCAACCGGTTACACATTTAATCTGTTAGTGGGCTTGGGGAATACCCCTAGTGAAGATT	4560
Db	4501	GCAACCGGTTACACATTTAATCTGTTAGTGGGCTTGGGGAATACCCCTAGTGAAGATT	4560
Qy	4561	GCCCACTCTCTTATGCGCGCTCGCTCGCTCGTGGTGGGGCGCGAGACAGCTCTGCGG	4620
Db	4561	GCCCACTCTCTTATGCGCGCTCGCTCGCTCGCTCGTGGTGGGGCGCGAGACAGCTCTGCGG	4620
Qy	4621	TCTGGGACCTTTTGGTCCGACAGGCCCAACGAGGACGAGCGGCTATAGGAGATGGC	4680
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Qy	4681	CAA 4683	
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RESULT 4			
US-10-427-129-6			
Sequence 6, Application US/10427129			
Publication No. US20040101514A1			
GENERAL INFORMATION:			
APPLICANT: Liu, Yunhong			
APPLICANT: Luo, Jia			
APPLICANT: During, Matthew			
TITLE OF INVENTION: High Transgene Expression of A Pseudotyped Adeno-Associated Virus			
FILE REFERENCE: 102182-24			
CURRENT APPLICATION NUMBER: US/10/427, 129			
CURRENT FILING DATE: 2003-05-01			
PRIOR APPLICATION NUMBER: 09/804, 898			
PRIOR FILING DATE: 2001-03-13			
PRIOR APPLICATION NUMBER: 60/189, 110			
PRIOR FILING DATE: 2000-03-14			
NUMBER OF SEQ ID NOS: 15			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 6			
LENGTH: 4683			
TYPE: DNA			

ORGANISM: adeno-associated virus 2  
US-10-427-129-6

Query Match 99.6%; Score 4663.8; DB 8; Length 4683;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 181 GGTAGGAGGTCCTGTATTAGAGTCACTGAGTGTGTCGACATTTTGGACACCAT 240
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QY 2701 AGCCGCTAAAGAGACTCAATTTTGTGCTGAGCTGGGAGCTCAGAGTCAATGCCAGC 2760  
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Db 2761 CACAACCTCTGGAGAACCTTCAGCAACCCCGCTGTGTGGAGCTAATGAGCTT 2820  
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Db 2821 CAGGCGGTGGGCAACCAATGGCAAGCAATTAAGAGGCGCGAGCGAGTGGGTATGCT 2880  
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Db	4261	GGGAGCTCAGAAAGAAAAACAGCAACGCTGGAAATCCGAAAGTCAGTATCACTTAAC	4320
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Db	4321	ATGCAAAATCTGCCACCGTGAATTTCACTGTGACAAACAATGSACTTATATCTAGCCTC	4380
Qy	4381	GCCCCATTGGACCCCGTTACCTCACCCGTCCTCCCTGTAAATGTGTATCAATAAACCG	4440
Db	4381	GCCCCATTGGACCCCGTTACCTCACCCGTCCTCCCTGTAAATGTGTATCAATAAACCG	4440
Qy	4441	GTTAATTTGTGTCACTTGAACCTTGTGTCATGTCTTATATCTTATCTGTACCAATA	4500
Db	4441	GTTAATTTGTGTCACTTGAACCTTGTGTCATGTCTTATATCTTATCTGTACCAATA	4500
Qy	4501	GCAACCGGTTACACATTAACGTCTAGTTGGGCTTGGGAATACCCCTAGTAGTGGAACTT	4560
Db	4501	GCAACCGGTTACACATTAACGTCTAGTTGGGCTTGGGAATACCCCTAGTAGTGGAACTT	4560
Qy	4561	GCCCACTCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTTGGCG	4620
Db	4561	GCCCACTCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTTGGCG	4620
Qy	4621	TCTGGGACCTTTGTGTCGCGAGGCCCAACGAGCGAGGAGCGGCATATAGAGGAGTGGC	4680
Db	4621	TCTGGGACCTTTGTGTCGCGAGGCCCAACGAGCGAGGAGCGGCATATAGAGGAGTGGC	4680
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Db	4681	CAAA 4683	

RESULT 5  
US-10-959-017-2

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Sequence 2 Application US/10959017
Publication No. US20050106125A1
GENERAL INFORMATION:
APPLICANT: FALCK-PEDERSEN, ERIK S
APPLICANT: PHILIPPOT, NICOLA
TITLE OF INVENTION: USE OF AA V INTEGRATION EFFICIENCY ELEMENT FOR MEDIATING
TITLE OF INVENTION: SITE-SPECIFIC INTEGRATION OF A TRANSCRIPTION UNIT
FILE REFERENCE: 230526
CURRENT APPLICATION NUMBER: US/10/959,017
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: PCT/US03/11191
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/371,044
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 4683
TYPE: DNA
ORGANISM: adeno-associated virus serotype 6
US-10-959-017-2

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Query Match	99.6%	Score 4663.8;	DB 10;	Length 4683;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 4671; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

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Db		1	TTGGCCTACTCCCTCTCTCGGCGCTCGCTCGGTCACTGAGGCGGGGCGACCAAAGGTGGCC	60
QY		61	CGACGCCCGGGCTTTCGCCGGGCGGCTCACTGAGCGAGCGCGCAGAGAGGAATG	120
Db		61	CGACGCCCGGGCTTTCGCCGGGCGGCTCACTGAGCGAGCGCGCAGAGAGGAATG	120
QY		121	GCCAACTCCACACTAGGGGGTTCTCGAGGGGTGAGATCTGTAATTACGTCAAG	180
Db		121	GCCAACTCCACACTAGGGGGTTCTCGAGGGGTGAGATCTGTAATTACGTCAAG	180
QY		181	GGTAGGAGAGTCTGTATTAGAGGTACCGTAGAGTGTTTTCGACATTTTCGCACCACCAT	240
Dy		181	GGTAGGAGAGTCTGTATTAGAGGTACCGTAGAGTGTTTTCGACATTTTCGCACCACCAT	240

Db	181	GGTTAAGGAGGATCTGTATTTAGAGTCAAGTAAAGTGTTCGACATTTTCGACACAT	240
OY	241	GTGGTCAAGCTGGGATATTTAAGCCGAGTGAAGCAGCAGGGTCTTCATTTTGAAGCGGGA	300
Db	241	GTGGTCAAGCTGGGATATTTAAGCCGAGTGAAGCAGGAGGTCTTCATTTTGAAGCGGGA	300
OY	301	GGTTTGAACGCGCAGCGCATGCGGGGTTTTACGAGATGTGATTAAGTCCCGACGA	360
Db	301	GGTTTGAACGCGCAGCGCATGCGGGGTTTTACGAGATGTGATTAAGTCCCGACGA	360
OY	361	CCTTGAAGAGATCTGCCCGGCAATTTCTGACAGCTTTTGAACCTGAGTGGCCGAGAAAGA	420
Db	361	CCTTGAAGAGATCTGCCCGGCAATTTCTGACAGCTTTTGAACCTGAGTGGCCGAGAAAGA	420
OY	421	ATGGAGATGGCCGCGCAGATTCTGACATGGAATCTGAATGTGATTTAGCAGGCAACCCCTAC	480
Db	421	ATGGAGATGGCCGCGCAGATTCTGACATGGAATCTGAATGTGATTTAGCAGGCAACCCCTAC	480
OY	481	CGTGGCCGAGAAGGTGCAGCGCGCATTCCTGGTCCACTGCGCGCGCGGTGAGTAAAGGCC	540
Db	481	CGTGGCCGAGAAGGTGCAGCGCGCATTCCTGGTCCACTGCGCGCGCGGTGAGTAAAGGCC	540
OY	541	GGAGGCCCTCTTCTTTGTTCACTTCGAGAAAGGGGAGTCTTAATTTCCACTTCATATCT	600
Db	541	GGAGGCCCTCTTCTTTGTTCACTTCGAGAAAGGGGAGTCTTAATTTCCACTTCATATCT	600
OY	601	GGTGAAGACACGGGGGGTCAATCCATGATGTCCTGGGCGGCTTCCTGAGTCAAGTAAAGGA	660
Db	601	GGTGAAGACACGGGGGGTCAATCCATGATGTCCTGGGCGGCTTCCTGAGTCAAGTAAAGGA	660
OY	661	CAAGCTGGTGACAGCCATCTACCCGCGGATGAGACCGCACCTTCGCCAATGTTTGCAGGT	720
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OY	721	GACCAAGACGCGTAAATGAGCGCCGAGAGGGGGGAAACAAGTGTGTGACGAGTGTCTACATCC	780
Db	721	GACCAAGACGCGTAAATGAGCGCCGAGAGGGGGGAAACAAGTGTGTGACGAGTGTCTACATCC	780
OY	781	CAACTACTCTCTGCGCCCAAGACTCAAGCCCGAGCTCAAGTGGCCGAGTAAATGAGAGGA	840
Db	781	CAACTACTCTCTGCGCCCAAGACTCAAGCCCGAGCTCAAGTGGCCGAGTAAATGAGAGGA	840
OY	841	GTATATAAGCGCGTGTAACTTGAGCCGAGCAGAAACGCTCGTGGCGCAGCACTTAC	900
Db	841	GTATATAAGCGCGTGTAACTTGAGCCGAGCAGAAACGCTCGTGGCGCAGCACTTAC	900
OY	901	CCACGTACGCCAGCCAGAGAGCAGAAACAAGGAATCTGAACCCCAATTTCTGACGCGC	960
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Db	1021	GGGATCAACCTCCGAGAAGCAGTGGATTCAGAGAGAACCAAGGCTCGTACATCTCCTTCAA	1080
OY	1081	CGCCGCTCCAACTCGCGGTCTCCAGATCAAGGCGCTCTGGACATGCGCGCAAGATCAT	1140
Db	1081	CGCCGCTCCAACTCGCGGTCTCCAGATCAAGGCGCTCTGGACATGCGCGCAAGATCAT	1140
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Db	1201	AACCAACCGCATTTTACCGCATCTGAGACTGAAAGGCTTACGACCTTCGCTACGCGGCTC	1260
OY	1261	CGTCTTCTCGGCTGGGCCAGAAAAGTTTCGAAAAACGAAACACATCTTGACTTTTGG	1320



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Db 1861 TCCATCGACGTGACGCGGAGGAGCTCGGTGGACTTTGGCGACAGGTACCAAAACAA 1920  
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QY 4681 CAA 4683  
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Db 4681 CAA 4683  
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RESULT 6  
US-11-145-035-25  
; Sequence 25, Application US/11145035  
; Publication No. US20050287122A1  
; GENERAL INFORMATION:  
; APPLICANT: Bartlett et al.  
; TITLE OF INVENTION: AAV VECTORS AND METHODS  
; FILE REFERENCE: 2835/4135  
; CURRENT APPLICATION NUMBER: US/11/145,035  
; PRIOR FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US 10/038,972  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/260,124  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 25  
; LENGTH: 4683  
; TYPE: DNA  
; ORGANISM: Adeno-associate virus 6  
US-11-145-035-25  
Query Match 99.6%; Score 4663.8; DB 15; Length 4683;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
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QY 181 GGTGAAGAGGTCCTGATTAAGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240  
| | | | |  
Db 181 GGTGAAGAGGTCCTGATTAAGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240  
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QY 481 CGTGGCGAAGAGCTGACGCGCACTTCTGATTCATGCGCGCGCTGAAGTGAAGGCGCC 540  
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Qy 4681 CAA 4683  
Db 4681 CAA 4683

RESULT 7  
US-10-291-583-6  
; Sequence 6, Application US/10291583  
; Publication No. US20030138772A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Guangping  
; APPLICANT: Wilson, James M.  
; APPLICANT: Alviria, Mauricio  
; TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Virus (AAV) Sequences and Isolating No. US20030138772A1 Sequences Identifi

FILE REFERENCE: UPN-02735USA  
CURRENT APPLICATION NUMBER: US/10/291,583  
CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: US 60/350,607  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/341,117  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: US 60/377,066  
PRIOR FILING DATE: 2002-05-01  
PRIOR APPLICATION NUMBER: US 60/386,675  
PRIOR FILING DATE: 2002-06-05  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 6  
LENGTH: 4718  
TYPE: DNA  
ORGANISM: adeno-associated virus serotype 1  
US-10-291-583-6

Query Match 90.8%; Score 4253.2; DB 7; Length 4718;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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RESULT 8
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; Sequence 1, Application US/10696261
; Publication No. US20040057931A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GANPN.031USA
; CURRENT FILING DATE: US/10/696, 261
; PRIOR APPLICATION NUMBER: 2003-10-29
; PRIOR FILING DATE: US/09/807, 802A
; PRIOR APPLICATION NUMBER: 2002-02-21
; PRIOR FILING DATE: US 60/107, 114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 4718
; TYPE: DNA
; ORGANISM: AAV-1
; FEATURE:
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Query Match	90.8%	Score 4253.2	DB 8	Length 4718
Best Local Similarity	94.7%	Pred. No. 0		
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Db 2998 AAATCTCAAGTCTTCAACGGGGGCGAGCAACCAACCACTAATTGGCTACAGCAACCC 3057  
Qy 3043 CCTGGGGTATTTGATTTTCAACAGATTCACACTGCGATTTCTCAACAGTGAAGTGGAGC 3102

Db 3058 CCTGGGGGATTTGATTTCACAGATTCCATGCGCACTTTTTCACACGATGAGCG 3117  
Qy 3103 GACTCATCAACAATTTGGGATTTCCGGCCCAAGAGCTCACTTCAAGCTTTCAACA 3162  
Db 3118 GACTCATCAACAATTTGGGATTTCCGGCCCAAGAGCTCACTTCAAGCTTTCAACA 3177  
Qy 3163 TCCAGTCAAGAGGATGACGAGATGATGAGCTGACAGACATGCTTAATTAACCTTACA 3222  
Db 3178 TCCAGTCAAGAGGATGACGAGATGATGAGCTGACAGACATGCTTAATTAACCTTACA 3237  
Qy 3223 GCACGGTTCAAGCTTTGTCGAGCTCGAGTACCAAGTCCCGTACGCTCTGCGC 3282  
Db 3238 GCACGGTTCAAGCTTTGTCGAGCTCGAGTACCAAGTCCCGTACGCTCTGCGC 3297  
Qy 3283 ACCAGGGGTCGCTCCCTCCGTTCCCGGGGAGCGTTGATGATTCGAGATACGGCTAC 3342  
Db 3298 ACCAGGGGTCGCTCCCTCCGTTCCCGGGGAGCGTTGATGATTCGAGATACGGCTAC 3357  
Qy 3343 TAAAGCTCAACAATGAGCAGCAGGAGCGTACGCTACCTTTTACTGCTGGAATATT 3402  
Db 3358 TGAAGCTCAACAATGAGCAGCAGCAGGAGCGTACGCTACCTTTTACTGCTGGAATATT 3417  
Qy 3403 TCCCATGCGAGATGCTGAGAACGGGCAATTAATTACTTCAAGCTACCTTCAAGACG 3462  
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Qy 3463 TGCCTTTCACAGAGCTAGCGGACAGCAGAGCTGAGACGGGTGATGATCCTCTCA 3522  
Db 3478 TGCCTTTCACAGAGCTAGCGGACAGCAGAGCTGAGACGGGTGATGATCCTCTCA 3537  
Qy 3523 TCGACCAATACCTGATTAATCTGAAACAGAACTCAACAATCACTCGGAGTGCCTCA 3582  
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Qy 3583 AGGACTTCTGTTTACGCTGAGTCTCAAGCTGAGTCTGTTTCAAGCTTCAAGCTGAG 3642  
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Qy 3643 TACCTGAGCCCTGTTTACCGGAGCAGCGGCTTTCAAAACAAAACAGACAAACAACA 3702  
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Qy 3763 ACCCTGAGCTGCTTACGCTTCAACAAGACAGACAAAGCAAGTCTTCCCATGAGCG 3822  
Db 3778 ACCCTGAGCTGCTTACGCTTCAACAAGACAGACAAAGCAAGTCTTCCCATGAGCG 3837  
Qy 3823 GTGTCATGATTTTGGAAAGAGAGCGCGGAGCTTCAAAACATGCTTGGACAATGCA 3882  
Db 3838 GTGTCATGATTTTGGAAAGAGAGCGCGGAGCTTCAAAACATGCTTGGACAATGCA 3897  
Qy 3883 TGATACACAGAGAGAGAAATCAAAAGCACTAACCCCGTGGCCACCGAAAGATTGGGA 3942  
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Qy 3943 CTGTGGCAGTCAATTTCCAGAGCAGACACAGACCTTGGCAACCGAGATGCTGATTA 4002  
Db 3958 CTGTGGCAGTCAATTTCCAGAGCAGACACAGACCTTGGCAACCGAGATGCTGATTA 4017  
Qy 4003 TGGGAGCTTACCTGGAATGTTGGGCAAGACAGAGATGATACCTGAGGGTCTTATTT 4062  
Db 4018 TGGGAGCTTACCTGGAATGTTGGGCAAGATGAGATGATGATGAGGGTCTTATTT 4077  
Qy 4063 GGGCCAAAATTTCTTCAACGAGATGAGCACTTCAACCCCTCTCTCTCAATGGCGGCTTTG 4122  
Db 4078 GGGCCAAAATTTCTTCAACGAGATGAGCACTTCAACCCCTCTCTCTTANVGCGGCTTTG 4137  
Qy 4123 GACTTAAAGCACCGGCTCTCTCAGATCTCATCAAAAACAGCGCTTCTCTGGAATCTTC 4182  
Db 4138 GACTTAAAGCACCGGCTCTCTCAGATCTCATCAAAAACAGCGCTTCTCTGGAATCTTC 4197

Qy 4183 CGGAGAGTTTTGCGGTACAAAGTTTGTTCATTCATCACCCAGTATTCACAGACAAG 4242  
Db 4198 CGGCGAGTTTTGAGCTACAAAGTTTGTTCATTCATCACCCAGTATTCACAGACAAG 4257  
Qy 4243 TGAAGCTGAGATTTGAATGGGAGCTGAGAAAGAAAACAGCAACGCTGGAATCCGAG 4302  
Db 4258 TGAAGTGAAGATTTGAATGGGAGCTGAGAAAGAAAACAGCAACGCTGGAATCCGAG 4317  
Qy 4303 TGAAGTGAAGATTTGAATGGGAGCTGAGAAAGAAAACAGCAACGCTGGAATCCGAG 4362  
Db 4318 TGAAGTGAAGATTTGAATGGGAGCTGAGAAAGAAAACAGCAACGCTGGAATCCGAG 4377  
Qy 4363 GACTTATTAAGCTTACGCTGCGCCCAATGGACAGCAGCTTACCTACCCGCTGGAATTTG 4422  
Db 4378 GACTTATTAAGCTTACGCTGCGCCCAATGGACAGCAGCTTACCTACCCGCTGGAATTTG 4437  
Qy 4423 GTGTTAATCAATTAACCGGTTAATGCTGTCAGTTGAATCTTGGTCTCATGCTTATTA 4482  
Db 4438 GTGTTAATCAATTAACCGGTTAATGCTGTCAGTTGAATCTTGGTCTCATGCTTATTA 4497  
Qy 4483 TCTTATCTGTCACCATAGCAACCGGTTAATGCTGTCAGTTGAATCTTGGTCTCATGCTTATTA 4540  
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Qy 4582 TCGCTGCTGCTGAGTGGGCGCGGAGAGCAAGCTTCTGCTGCTGAGACCTTTGCTGCA 4641  
Db 4617 TCGCTGCTGCTGAGTGGGCGCGGAGAGCAAGCTTCTGCTGCTGAGACCTTTGCTGCA 4676  
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RESULT 9  
US-10-696-282-1  
Sequence 1, Application US/10696282  
Publication No. US20040057932A1  
GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
APPLICANT: Xiao, Weidong  
TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,  
FILE REFERENCE: GNPVN.031USA  
CURRENT FILING DATE: US/10/696,282  
PRIOR APPLICATION NUMBER: US/09/807,802A  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/107,114  
PRIOR FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: PCT/US99/25694  
PRIOR FILING DATE: 1999-11-02  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 4718  
TYPE: DNA  
ORGANISM: AAV-1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (335)..(2206)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2223)..(4430)  
OTHER INFORMATION:  
US-10-696-282-1

Query Match 90.8%; Score 4253.2; DB 8; Length 4718;

Best Local Similarity 94.7%; Pred. No. 0;									
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;									
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Db	1	TTGGCCACTCCCTCTCTGCGGCTGCTGCTGCTCACTGAGCCGGGCGCAAGAGTGGCC	60						
Qy	61	CGAGCCCGGGCTTTGCGCGGCGCTCAGTGAAGCGAGCGCGCGAGAGGAGATG	120						
Db	61	AGACGGCAGAGCTCTGCTCTGCGGCGCCACCGAGCGAGCGCGAGAGGAGATG	120						
Qy	121	GCCAACTCCATCACTAGGGGT-----TCCTGAGGGGTGAGTCTGTA	163						
Db	121	GCGAACTCATCACTAGGGGTATATGCGAAGCGCTCCACGCTGCCCGCTCAGGCTGA	180						
Qy	164	CTGAAATTACGTATAGGGTTAGAGAGTCTGTATTAGAGTCACTGAGTG-TTTTGC	222						
Db	181	CGTAAATTACGTATAGGG---GAGTGGTCCGTATAGTGTCTCACTGAGTGGCTTTGC	237						
Qy	223	GACATTTTGGACACCATGTGTCACTGCTGGGTATTTAAGCCCGAGTGAAGCAGAGGT	282						
Db	238	GACATTTTGGACACCATGTGTCACTGCTGGGTATTTAAGCCCGAGTGAAGCAGAGGT	297						
Qy	283	CTCCATTTTGAAGCGGAGTTTGAACGCGACGCGCATGCGGGGTTTTCAGAGATTGT	342						
Db	298	CTCCATTTTGAACCGGAAATTGAAACGAGCAGCAGCCATGCGGGCTTCTACGAGATGT	357						
Qy	343	GATTAAAGTCCCGACGACCTTGAACGAGCATCTGCCGACATTTTCTGACAGCTTTGTAA	402						
Db	358	GATCAAGGTGCGGACGACCTGAGCAGACCATGCGGGCATTTTCTGACTGTTTGTAG	417						
Qy	403	CTGGGTGCGCGAGAGGAAATGGAGTTGCCCGCAGATTCTGACATGATCTGAATCTGAT	462						
Db	418	CTGGGTGCGCGAGAGGAAATGGAGTGTGCCCCGATTTCTGACATGATCTGAATCTGAT	477						
Qy	463	TGACAGGCAACCCCTGACCGTGCAGAGAACTGCAAGCCATTCTGATCCAATGCGG	522						
Db	478	TGACAGGCAACCCCTGACCGTGCAGAGAACTGCAAGCCATTCTGATCCAATGCGG	537						
Qy	523	CCGCGTGAATGAGGCCCGGAGGCCCTCTTCTTTGTCAGTTTCAGAAAGGCGAGTCTTA	582						
Db	538	CCGCGTGAATGAGGCCCGGAGGCCCTCTTCTTTGTCAGTTTCAGAAAGGCGAGTCTTA	597						
Qy	583	CTTCACTCCATATTTCTGTGAGAGCAACGGGGGTCAATCCATGTCGTGGGCGCGTT	642						
Db	598	CTTCACTCCATATTTCTGTGAGAGCAACGGGGGTCAATCCATGTCGTGGGCGCGTT	657						
Qy	643	CTTGAATCAGATTAGCGACAGCTGTGTCAGACCATCAACCGGGATCGAGCCGACT	702						
Db	658	CTTGAATCAGATTAGCGACAGCTGTGTCAGACCATCAACCGGGATCGAGCCGACT	717						
Qy	703	GCCCAACTGTTTCCGCGTGACCAAGACGCGTAATGCGCGGAGGGGGAACAAGTGT	762						
Db	718	GCCCAACTGTTTCCGCGTGACCAAGACGCGTAATGCGCGGAGGGGGAACAAGTGT	777						
Qy	763	GGAAGATGCTACATCCCACTAATCTCTGTCGCAAGCTACAGCCCGAGCTGAGTGGC	822						
Db	778	GGAAGATGCTACATCCCACTAATCTCTGTCGCAAGCTACAGCCCGAGCTGAGTGGC	837						
Qy	823	GTGACTAACATGAGAGATATATTAAGCGCTGTTTAACTGTGCCGAGCAACGGCT	882						
Db	838	GTGACTAACATGAGAGATATATTAAGCGCTGTTTAACTGTGCCGAGCAACGGCT	897						
Qy	883	CTGTGGCGACGACTGACCCAGCTGACGACGCCAGAGCAGAAACAAGGAATCTGAA	942						
Db	898	CTGTGGCGACGACTGACCCAGCTGACGACGCCAGAGCAGAAACAAGGAATCTGAA	957						
Qy	943	CCCCAATTCTGACGGGCTGTCACTCCGCTCAAAAACTCCGCAAGCTATAGAGCTGGT	1002						
Db	958	CCCCAATTCTGACGGGCTGTCACTCCGCTCAAAAACTCCGCGGCTATAGAGCTGGT	1017						
Qy	1003	CGGGTGGCTGTGACCGGGGCACTCACTCCGAGAGCAGTGAATCCAGAGGACAGGC	1062						

Db	1018	CGGGTGGCTGTGACCGGGGCACTCACTCCGAGAGCAGTGAATCCAGAGGACAGGC	1077						
Qy	1063	CTCGTACATCTCTTTCAACCGCGCTCTCAATCTCGCGTCTCCAGATCAAGCGCTGGA	1122						
Db	1078	CTCGTACATCTCTTTCAACCGCGCTCTCAATCTCGCGTCTCCAGATCAAGCGCTGGA	1137						
Qy	1123	CAATGCGGCAAGATCAATGGCGTGAACCAAAATCCGCGCGGAGTACTGATAGGCCCCG	1182						
Db	1138	CAATGCGGCAAGATCAATGGCGTGAACCAAAATCCGCGCGGAGTACTGATAGGCCCCG	1197						
Qy	1183	TCGCGCGCGACATTAACCAACGCAATTTTACCGATCTCTGAGCTGAACGCTACGA	1242						
Db	1198	TCGCGCGCGACATTAACCAACGCAATTTTACCGATCTCTGAGCTGAACGCTACGA	1257						
Qy	1243	CCCTGCTACGCGCGCTCGTCTTTCTGCGCTGGGCCAGAAAAGTTTGGAAAACGCA	1302						
Db	1258	ACCTGCTACGCGCGCTCGTCTTTCTGCGCTGGGCCAGAAAAGTTTGGAAAACGCA	1317						
Qy	1303	CACCATGCGCTGTTTGGGCGGACACAGGGGCAAGCAACATCGCGAAGCATGCG	1362						
Db	1318	CACCATGCGCTGTTTGGGCGGACACAGGGGCAAGCAACATCGCGAAGCATGCG	1377						
Qy	1363	CCACGCGTGCCTTTCTACGCGCTCGTCACTGACCAATGAGAACTTTCCTTCAACGA	1422						
Db	1378	CCACGCGTGCCTTTCTACGCGCTCGTCACTGACCAATGAGAACTTTCCTTCAATGA	1437						
Qy	1423	TTGCGTGAACAAGTGTGATCTGCTGGAGAGAGGCAAGTGAACGCGCAAGTCTGGA	1482						
Db	1438	TTGCGTGAACAAGTGTGATCTGCTGGAGAGAGGCAAGTGAACGCGCAAGTCTGGA	1497						
Qy	1483	GTCGCGCAAGGCAATTCGCGCGGACAGAGGTGCGGTGAGCAAAAAGTCAAGTGTG	1542						
Db	1498	GTCGCGCAAGGCAATTCGCGCGGACAGAGGTGCGGTGAGCAAAAAGTCAAGTGTG	1557						
Qy	1543	CGCCAGATCGATCCACCCCGGTGATGTCACCTTCCAAACCAACATGTGCGCGTAT	1602						
Db	1558	CGCCAGATCGATCCACCCCGGTGATGTCACCTTCCAAACCAACATGTGCGCGTAT	1617						
Qy	1603	TGACGGGAACAGCACACCTTTCAGACACAGACCGTTGAGAGACGGGATGTTCAATT	1662						
Db	1618	TGACGGGAACAGCACACCTTTCAGACACAGACCGTTGAGAGACGGGATGTTCAATT	1677						
Qy	1663	TGAATCAACCGCGGTGAGAGTGAATTTGGCAAGGTGCAAAAGCAGAAAGTCAAGA	1722						
Db	1678	TGAATCAACCGCGGTGAGAGTGAATTTGGCAAGGTGCAAAAGCAGAAAGTCAAGA	1737						
Qy	1723	GTTCTTCCGCTGGCGAGATCACTGACCGAGTGGCGCATGATTAAGTCAAGTCAAAA	1782						
Db	1738	GTTCTTCCGCTGGCGAGATCACTGACCGAGTGGCGCATGATTAAGTCAAGTCAAAA	1797						
Qy	1783	GGGTGAGCCAAACAAGACCCCGGATGACCGCGATTAAGCGAGCCCAAGCGGGC	1842						
Db	1798	GGGTGAGCCAAACAAGACCCCGGATGACCGCGATTAAGCGAGCCCAAGCGGGC	1857						
Qy	1843	CTGCCCCCTAGTGGCGGATCATGAGTCAAGCGGGAAGGAACTCGGTGCACTTTGC	1902						
Db	1858	CTGCCCCCTAGTGGCGGATCATGAGTCAAGCGGGAAGGAACTCGGTGCACTTTGC	1917						
Qy	1903	CGACAGGTACCAAAACAATGTTCTCGTCAACGCGGAGATGTTTCAATGCTTTCCCTG	1962						
Db	1918	CGACAGGTACCAAAACAATGTTCTCGTCAACGCGGAGATGTTTCAATGCTTTCCCTG	1977						
Qy	1963	CAAAAATGCGAGAGAAATGAATCAGAATTTTCAACATTTGCTTTCAGCGACGGGACAGAGA	2022						
Db	1978	CAAAAATGCGAGAGAAATGAATCAGAATTTTCAACATTTGCTTTCAGCGACGGGACAGAGA	2037						
Qy	2023	CTGTTCAAGATGTTTCCCGCGGTGTGAGATCTCAACCGGTGCTCGAAGAAAGAGAGTA	2082						
Db	2038	CTGTTCAAGATGTTTCCCGCGGTGTGAGATCTCAACCGGTGCTCGAAGAAAGAGAGTA	2097						
Qy	2083	TCGGAAACTCTGTGCAATTCATCATCTGCTGGGCGGGCTTCCGAGATTGCTTGTGCGC	2142						
Db	2098	TCGGAAACTCTGTGCAATTCATCATCTGCTGGGCGGGCTTCCGAGATTGCTTGTGCGC	2157						

Oy 2143 CTGGGATCTGGTCAACGATGGAATTGGATGACGTGTTTCTGAGCAATTAATGACTTAAAC 2202  
Db 2158 CTGGGATCTGGTCAACGATGGAACCTGGATGACGTGTTTCTGAGCAATTAATGACTTAAAC 2217  
Oy 2203 CAGGATATGGCTGCGGATGGTTATCTTCCAGATTGGCTCGAGGACAAACCTCTCTGAGGCA 2262  
Db 2218 CAGGATATGGCTGCGGATGGTTATCTTCCAGATTGGCTCGAGGACAAACCTCTCTGAGGCA 2277  
Oy 2263 TTCCGCAATGGTGGGACTTGGAACTTGAGACCCCGAAACCCAAAGCCCAACGACAAAAGC 2322  
Db 2278 TTCCGCAATGGTGGGACTTGGAACTTGAGACCCCGAAACCCAAAGCCCAACGACAAAAGC 2337  
Oy 2323 AGGACGACGCGCGGGGTCTGGTCTTCTGGCTACAAATACCTCGGACCTTTCACGAGAC 2382  
Db 2338 AGGACGACGCGCGGGGTCTGGTCTTCTGGCTACAAATACCTCGGACCTTTCACGAGAC 2397  
Oy 2383 TCACCAAGGGGAGCCGCTCAACCGGCGGATGACGCGGCCCTTCGAGCAGCAAGGCT 2442  
Db 2398 TCACCAAGGGGAGCCGCTCAACCGGCGGAGCGAGCGGCCCTTCGAGCAGCAAGGCT 2457  
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Db 2458 ACGACCAAGCTCAAAAGCGGGTGAATCCGTACTTCGGTTTAACTACCGCCGACGCGC 2517  
Oy 2503 AGTTTCAGGACCGTCTGCAAGAAAGATAGTCTTTTGGGGGCAACCTCGGGGAGAGTCT 2562  
Db 2518 AGTTTCAGGACCGTCTGCAAGAAAGATAGTCTTTTGGGGGCAACCTCGGGGAGAGTCT 2577  
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Oy 2743 CAGAGTCAGTCCCGGACCCCAACCTCTCGAGAACTTCACGAAACCCCGCTGTGTG 2802  
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Oy 2803 GACCTACTACATGAGCTTCAAGCGGTGGCGACCAATGGCAGAACTTAACGAAGCGCGC 2862  
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Oy 2863 ACGGAGTGGTAAATGCTCAGAGAAATTGGCAATTGGATTTCACATGCTGGGCGACAG 2922  
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Oy 2983 AAATCTCAGTGTCTCAACGGGGGCGACAGCAACCACTTAATGGCTCAAGCAAC 3042  
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Oy 3043 CTTGGGGGTATTTGATTTCAACAGATTCACTGCAATTTCTCAACGATGAGCGAC 3102  
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Db 3178 TCCAAGTCAAGAGGTCAAGCAATGATGGGTCAAGCAATGCTTAATACCTTACCA 3237

Oy 3223 GCAAGTTCAAGTCTTGTCCGACTCGGAGTACAGATTCCCGTACGTCTCGGCTCGGC 3282  
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Oy 3283 ACCAGGCTGCTCTCTCCGTTCCGGCGGACGTTTCAATGATTCGCGAGTACGGCTAAC 3342  
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Oy 3883 TGATCAGACGAGAGAGAAATCAAGCACTAAACCCGTTGGCCACGGAAGATTTGGGA 3942  
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Oy 3943 CTGTGGAGTCAATCTTCAAGACGACGACAGACCTCTGACCGGAGATGTGCATGTA 4002  
Db 3958 CTGTGGAGTCAATCTTCAAGACGACGACAGACCTCTGACCGGAGATGTGCATGTA 4017  
Oy 4003 TGGGAGCTTAACTTGGAAATGTGTGGCAAGACAGACCTTAATCTGCAAGGCTTATTT 4062  
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Oy 4063 GGGGCAAAATTTCTCAACAGGATGACATTTTACCCGTTCTCTCATGAGGCGGCTTTG 4122  
Db 4078 GGGGCAAAATTTCTCAACAGGATGACATTTTACCCGTTCTCTCATGAGGCGGCTTTG 4137  
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Oy 4183 CGGCAAGTTTTCGGCTTACAAAGTTTGGCTTCAATCAACCCAGATTTCCAGAGAAAG 4242  
Db 4198 CGGCAAGTTTTCAGCTTCAAAAGTTTGGCTTCAATCAACCCAGATTTCCAGAGAAAG 4257  
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Db 4258 TGAGCTGAGATTTGAAATGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGGAAG 4317  
Oy 4303 TGAGTATACATTAATCTATGCAAAATCTGCAACGTTGATTTCACTGTGGAACAATG 4362



OY	1183	TTCCGCCCGCGACATTAAAAACCAACCGCATTTACCGCATCTCTGGAGCTGAAACGGCTAAGCA	1242
Db	1198	TTCCGCCCGCGGACATTAAAAACCAACCGCATCTACCGCATCTCTGGAGCTGAAACGGCTAAGCA	1257
OY	1243	CCCTTCCTACGCGCGGCTCCGTCCTTCTCGGCTGGGCGCCAGAAAAGGTTTCGAAAAACGCA	1302
Db	1258	AOCITGCTACGCGCGGCTCCGTCCTTCTCGGCTGGGCGCCAGAAAAGGTTTCGAAAAACGCA	1317
OY	1303	CACCATCTGGCTGTTTGGGCGGGCCACAACGGGCAAGACCAACATCGCGAAAGCCATGCG	1362
Db	1318	CACCATCTGGCTGTTTGGGCGGGCCACAACGGGCAAGACCAACATCGCGAAAGCCATGCG	1377
OY	1363	CCAGCGCGGCGCCCTTCTACGGCTGGTCAACCTGGACCAATGAGAACTTTCCTTCAACGA	1422
Db	1378	CCAGCGCGGCGCCCTTCTACGGCTGGTCAACCTGGACCAATGAGAACTTTCCTTCAATGA	1437
OY	1423	TTGCGTCGACAAGATGATCTGGTGGAGAGAGGGCAAGATGACGGCCAAAGTCTGTGA	1482
Db	1438	TTGCGTCGACAAGATGATCTGGTGGAGAGAGGGCAAGATGACGGCCAAAGTCTGTGA	1497
OY	1483	GTCCGCCAAGCGCATTTCTCCGCGGGAGCAAGGTGTGGGTGACCAAAAGTCAAGTCTGC	1542
Db	1498	GTCCGCCAAGCGCATTTCTCCGCGGGAGCAAGGTGTGGGTGACCAAAAGTCAAGTCTGC	1557
OY	1543	CGCCGAGATCGATCCCAACCCCGTGATGTCACCTCCAAACAACAATGTCGCGCGTGAT	1602
Db	1558	CGCCGAGATCGATCCCAACCCCGTGATGTCACCTCCAAACAACAATGTCGCGCGTGAT	1617
OY	1603	TGACGGGGAACAGCACACCTCTGAGACACAGCACCGCTTGCAGGACCGGATGTTCAATT	1662
Db	1618	TGACGGGGAACAGCACACCTCTGAGACACAGCACCGCTTGCAGGACCGGATGTTCAAAAT	1677
OY	1663	TGAATCTACCCGCGCTGTGGAGCATGACTTTGGCAAGGTGACAAGAGCGAAGTCAAAAG	1722
Db	1678	TGAATCTACCCGCGCTGTGGAGCATGACTTTGGCAAGGTGACAAGAGCGAAGTCAAAAG	1737
OY	1723	GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGCGCATGAGTTCTACGTACAAA	1782
Db	1738	GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGCGCATGAGTTCTACGTACAAA	1797
OY	1783	GGGTGGAGCCAAACACACACCGCGCCCGGATGACGGGATTTAAAGCGAGCCCAAGCGGGC	1842
Db	1798	GGGTGGAGCCAAACACACACCGCGCCCGGATGACGGGATTTAAAGCGAGCCCAAGCGGGC	1857
OY	1843	CTGCCCTCAGTCCGGGATTCATCGACGTCACACCGGAGAGAGTCCGGATGAATTGTC	1902
Db	1858	CTGCCCTCAGTCCGGGATTCATCGACGTCACACCGGAGAGAGTCCGGATGAATTGTC	1917
OY	1903	CGACAGGTACCAAAAACAATGTTCTGCTCAACCGGGCATGCTTCAGATGCTGTTCCCTG	1962
Db	1918	CGACAGGTACCAAAAACAATGTTCTGCTCAACCGGGCATGCTTCAGATGCTGTTCCCTG	1977
OY	1963	CAAAAATGCGAGAAATGAATACAAATTTCAACTTTGCTTCAACGACCGGACACAGAGA	2022
Db	1978	CAAGACATGCGAGAAATGAATACAAATTTCAACTTTGCTTCAACGACCGGACACAGAGA	2037
OY	2023	CTGTTTCAGAATGTTTTCCCGGCGTGTCAGAATCTCAACCGGTCTGAGAAAGAGACGTA	2082
Db	2038	CTGTTTCAGAATGTTTTCCCGGCGTGTCAGAATCTCAACCGGTCTGAGAAAGAGACGTA	2097
OY	2083	TCGGAAAATCTGTGCTCATTCATCTGTGGGAGGAGGCTCCCGAGATTTGCTGTGGC	2142
Db	2098	TCGGAAAATCTGTGCTCATTCATCTGTGGGAGGAGGCTCCCGAGATTTGCTGTGGC	2157
OY	2143	CTGCGATCTGGTCAACGTGATCTTGATGACTGTGTTTCTGAGCAATAAATGACTTTAAAC	2202
Db	2158	CTGCGATCTGGTCAACGTGATCTTGATGACTGTGTTTCTGAGCAATAAATGACTTTAAAC	2217
OY	2203	CAGGTATGCTGGCGGATGTTACTTTCAAGATGGCTGAGAGCAAACTCTCTGAGGGCA	2262
Db	2218	CAGGTATGCTGGCGGATGTTACTTTCAAGATGGCTGAGAGCAAACTCTCTGAGGGCA	2277
OY	2263	TTCCGCCATGTGGGACTTTGAACCTGTGAGCCCGCAAAACCAAAAGCCCAACGACGAAAGC	2322

Db	2278	TTCCGAGTGGTGGGACTTGAACCTTGAGCCCGGAAGCCCAAGCCACCAAGCAAAAGC	2337
Qy	2323	AGGAGCAGCGCCGGGGCTTGGTGCTTCCCTGGCTACAAGTACCTTGGACCCCTTCAACGAC	2382
Db	2338	AGGAGCAGCGCCGGGGCTTGGTGCTTCCCTGGCTACAAGTACCTTGGACCCCTTCAACGAC	2397
Qy	2353	TCGACAAAGGGGAGCCCGTCAACCGCGCGGATGAGAGCGCCCTGAGACGACAAAGGCT	2442
Db	2358	TCGACAAAGGGGAGCCCGTCAACCGCGGGAGCGAGCGGCCCTGAGACGACAAAGGCT	2457
Qy	2443	ACGACACAGCAGCTCAAAAGCGGGTACATCCGTACTGCGGTATATACACGCGACGCG	2502
Db	2458	ACGACACAGCAGCTCAAAAGCGGGTACATCCGTACTGCGGTATATACACGCGACGCG	2517
Qy	2503	AGTTTCAGGAGCGTCTGCAAGAAATACGTTTTCGGGGGCAACCTGGGGGAGCAGTCT	2562
Db	2518	AGTTTCAGGAGCGTCTGCAAGAAATACGTTTTCGGGGGCAACCTGGGGGAGCAGTCT	2577
Qy	2563	TCGAGGCGCAAGAGGGGTCTCGAACCTTTTGGCTGTGTTGAGAAAGTCTTAAGCG	2622
Db	2578	TCGAGGCGCAAGAGGGGTCTCTCGAACCTCTCGGTCTGTGTTGAGAAAGGCGCTTAAGCG	2637
Qy	2623	CTCCTGAAAGAAAAGTCGCGGTAGAGAGTGCACAAAGCCAGACTCTCTCGGGCA	2682
Db	2638	CTCCTGAAAGAAAAGTCCGCGGTAGAGAGTGCACAAAGCCAGACTCTCTCGGGCA	2697
Qy	2663	TTGGCAACACAGGCGCAGAGCCCGCTAAAAAGACATCAATTTTGGTCAGCTGGGCACT	2742
Db	2698	TCGGCAACACAGGCGCAGAGCCCGCTAAAAAGACATCAATTTTGGTCAGCTGGGCACT	2757
Qy	2743	CAGAGTCAGTCCCGGACCCGACCAACCTCTCGGAGAACTCCAGCAACCCCGCTGTGG	2802
Db	2758	CAGAGTCAGTCCCGGATCCGATCCACAACTCTCGGAGAACTCCAGCAACCCCGCTGTGG	2817
Qy	2803	GACCTACTCAATATGGCTTCAGGCGGTGGCGGACCAATATGCGAGAAATTAAGAAAGCCCG	2862
Db	2818	GACCTACTCAATATGGCTTCAGGCGGTGGCGGACCAATATGCGAGAAATTAAGAAAGCCCG	2877
Qy	2863	ACGAGTGGGTAAATGCTCAGAAATTTGGCATTTCCACATGGCTGGGCGACAGAG	2922
Db	2878	ACGAGTGGGTAAATGCTCAGAAATTTGGCATTTCCACATGGCTGGGCGACAGAG	2937
Qy	2923	TCATCACCAACAGCAACCCGAACATGGGCTTGGCCACCTATATACACCACTCTTACAGC	2962
Db	2938	TCATCACCAACAGCAACCCGAACATGGGCTTGGCCACCTATATATACCACTCTTACAGC	2997
Qy	2983	AAATTCAGAGCTTCAACGGGGGCGAGCAACGACACTTCTGGGCTACAGCACCC	3042
Db	2998	AAATTCAGAGCTTCAACGGGGGCGAGCAACGACACTTCTGGGCTACAGCACCC	3057
Qy	3043	CTGGGGGATATTTGATTTCAACAGATTTCCACTGCCATTTCTCAACAAGTACGTGGAGC	3102
Db	3058	CTGGGGGATATTTGATTTCAACAGATTTCCACTGCCATTTCTCAACAAGTACGTGGAGC	3117
Qy	3103	GACTCATTAACAATTTGGGGAATTCGGGCCCAAGATCTCAATTGAAGTCTTCAACA	3162
Db	3118	GACTCATTAACAATTTGGGGAATTCGGGCCCAAGATCTCAATTGAAGTCTTCAACA	3177
Qy	3163	TCGAAGTCAAGAGGTCAAGCAGATGTGCGTCAAGACCATGCTAATTAACCTTACCA	3222
Db	3178	TCGAAGTCAAGAGGTCAAGCAGATGTGCGTCAAGACCATGCTAATTAACCTTACCA	3237
Qy	3223	GCAGGCTTCAAGTCTTGTGGACTCGGAGTACCAAGTTCCGTAAGTCTCGGCTCTGGC	3282
Db	3238	GCAGGCTTCAAGTCTTGTGGACTCGGAGTACCAAGTTCCGTAAGTCTCGGCTCTGGC	3297
Qy	3283	ACGAGGGTGGCTCCCTCCGTTCCCGGGGAGCGATTCAATTCGCGAGTACGAGTACC	3342
Db	3298	ACGAGGGTGGCTCCCTCCGTTCCCGGGGAGCGATTCAATTCGCGAGTACGAGTACC	3357
Qy	3343	TAACGCTCAACATGGACCGCAGTGGAGCGCTATCTTTTACCTGCTGGAAATTT	3402



Dp	3358	TGAGCGCTCAACAATGGCAGCCAAAGCCGGGAGCGTTATCCTTTTACTGCGTGGAAATTT	3417
Qy	3403	TCCCATCGCAGATGCTGTGGAACGGGCAATPAACCTTACCTTCACTACCTTGCAGAGCG	3462
Dp	3418	TCCCTTCTCAGATGCTGTGGAACGGGCAACAATTACCTTCACTACCTTGCAGAGCG	3477
Qy	3463	TGCCTTTCACAGCAGCGTACCGGCGACACCGAGCGCTGGACCGGCTGATGTAATCCTCTCA	3522
Dp	3478	TGCCCTTTCACAGCAGCGTACCGGCGACACCGAGCGCTGGACCGGCTGATGTAATCCTCTCA	3537
Qy	3523	TGCACAGTACCTGTATTAACCTGAAACAACAATCTCAATCACTGCTCGGAAAGTCCCAAAACA	3582
Dp	3538	TGCACAGTACCTGTATTAACCTGAAACAACAATCTCAATCACTGCTCGGAAAGTCCCAAAACA	3597
Qy	3583	AGGACTTCTGTTTAGCCGTGGGCTCTCAGCTGCGATGCTGTTCAAGCCCAAAACTGGC	3642
Dp	3598	AGGACTTCTGTTTAGCCGTGGGCTCTCAGCTGCGATGCTGTTCAAGCCCAAAACTGGC	3657
Qy	3643	TACCTGGACCTGTGTAACCGGCGACGAGCGCGTTTCTAAAAACAACAACAACAACA	3702
Dp	3658	TACCTGGACCTGTGTAATGGGACGAGCGCGTTTCTAAAAACAACAACAACAACAACA	3717
Qy	3703	GCAACTTACCTGGACGTGTGCTTCAAAATPAACCTTAAATGGGGGTGAATCTTATATCA	3762
Dp	3718	GCAATTTTACTGGACGTGTGCTTCAAAATPAACCTTAAATGGGGGTGAATCTATCA	3777
Qy	3763	ACCCTGGACCTGTATGGCCTCAACAACAACAACAACAACAAGTCTTTTCCATGAGCG	3822
Dp	3778	ACCCTGGACCTGTATGGCCTCAACAACAACAACAACAACAAGTCTTTTCCATGAGCG	3837
Qy	3823	GTCATATATTTTGGAAAAGGAGAGCGCCGAGCTTCAACAATGTCATTTGACATGTCA	3882
Dp	3838	GTCATATATTTTGGAAAAGGAGAGCGCCGAGCTTCAACAATGTCATTTGACATGTCA	3897
Qy	3883	TGATCAAGAGAAAGGAGAAATCAAAAGCACTAACCCCGTGGCCACCGAAAGATTTGGGA	3942
Dp	3898	TGATTTACAGAGAAAGGAGAAATTAAGCAGCTAACCCGTGGCCACCGAAAGATTTGGGA	3957
Qy	3943	CTGTGGCAGTCAATCTCCAGAGCAGCAGCAGACAGACCTTGCCAGACCGGAGATGTGATTTA	4002
Dp	3958	CCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACAGACCTTGCCAGACCGGAGATGTGATTTA	4017
Qy	4003	TGGAGCCTTACCTTGGAAATGCTGTGGCAAGACAGACGTAATACCTGACGGGTCTTATTT	4062
Dp	4018	TGGAGCCTTACCTTGGCAATGCTGTGGCAAGACAGACGTAATACCTGACGGGTCTTATTT	4077
Qy	4063	GGGCGCAAAATTCCTCAACAACGATGGACACTTTACCCGTCCTCTCTCATAGGCGCGCTTGG	4122
Dp	4078	GGGCGCAAAATTCCTCAACAACGATGGACACTTTACCCGTCCTCTCTCATAGGCGCGCTTGG	4137
Qy	4123	GACTTAAAGCACCCGCGCTCTCAGATTCCTCATCAAAACAAGCGCTGTTCTGTGCGAATCCTC	4182
Dp	4138	GACTTAAAGCACCCGCGCTCTCAGATTCCTCATCAAAACAAGCGCTGTTCTGTGCGAATCCTC	4197
Qy	4183	CGGCAAGATTTTGGGCTTCAAAAGTTTGGCTTCATTATCAACCCAGTATTTCAACAAGCAAG	4242
Dp	4198	CGGCGAGATTTTCAAGCTTCAAAAGTTTGGCTTCATTATCAACCCAGTATTTCAACAAGCAAG	4257
Qy	4243	TGAGCGTGGAGATTGATGGAGCTGCAAGAAAGAAAACAGCAACGCTGGAATCCGAG	4302
Dp	4258	TGAATGTGGAAATTTGAATGGAGCGCTGCAAGAAAGAAAACAGCAACGCTGGAATCCGAG	4317
Qy	4303	TGCAGTATACACTTAATCTATGCAAAATCTGCAACGTTGATTTCACTGTGGACAAACATG	4362
Dp	4318	TGCAGTATACACTTAATCTATGCAAAATCTGCAACGTTGATTTCACTGTGGACAAACATG	4377
Qy	4363	GACTTATATCTAGACCTTGCCCAATTTGGCACCCGTTACCTCAACCCGTCCTGTAAATGT	4422
Dp	4378	GACTTATATCTAGACCTTGCCCAATTTGGCACCCGTTACCTCAACCCGTCCTGTAAATAC	4437
Qy	4423	GTCATTAATCAATAACCGGTTAATTCGTGTCAAGTTGAACCTTGGTCTCATGTCTTATTA	4482
Dp	4438	GTCATTAATCAATAACCGGTTGATTCGTGTCAAGTTGAACCTTGGTCTCTCTCTCTTATTA	4497

QY	4483	CTTATCGGTGACCAATAGCAACCGGTTTACATTTAACTGTATGTGGCGTTCGCA--	454
DB	4498	TTCTATTC-GGTTACCAATGTTATATGCTTACATTTAACTGTTGTGGCTTCGCAATA	4556
QY	4541	-----ATACCCTAGTATGATGAGTTGGCCACTCCCTTATGCGCGC	4581
DB	4557	AAAGACTTAGCTATCGGGTTTACCCCTTAGATGATGAGATTGGCCACTCCCTCTCTGGCGC	4616
QY	4582	TTCGCTCGTCCGTGGGGCCCGGCAAGACAGACTCTGCCCTCTGTGGACCTTTGGTCCGCA	4641
DB	4617	TTCGCTCGCTCGTGGGGCGCTGCGGACCAAAAGTCCGAGACGCGAGAGCTTCTGCTTGGC	4676
QY	4642	GGCCCCACCGAGCGAGCGGCGCATTAAGAGGAGTGAGCCAA	4683
DB	4677	GGCCCCACGAGCGAGCGAGCGCCAGAGAGAGGTGGGCA	4718
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; APPLICANT: Luo, Jia			
; APPLICANT: During, Matthew			
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; NUMBER OF SEQ ID NOS: 15			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 1			
; LENGTH: 4718			
; TYPE: DNA			
; ORGANISM: adeno-associated virus 2			
US-10-427-129-1			
Query Match 90.8%; Score 4253.2; DB 8; Length 4718;			
Best Local Similarity 94.7%; Pred. No. 0;			
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;			
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DB	1	TTGGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCTGCGGACCAAAAGTCCGC	60
QY	61	CGAGCGCCCGGGCTTGGCCCGGGCGGCTCTAGTAGCGAGCGACCGCGCANAAGGAGTG	120
DB	61	AGAGGGAGAGCTGTGCTTGGCGGGCCCGACGAGCGAGGACCGCGCANAAGGAGTG	120
QY	121	GCCAACTCCATCACTAAGGGT-----TCCTGAGAGGGGTGAGTCTGTGA	163
DB	121	GGCAACTCCATCACTAAGGGTAATCGGAGAGCGCCCTCCACGCTGCCCGCTCAGCGCTGA	180
QY	164	CGTAATAATTAAGCTATAGGTTAAGGAGTCTGTATTTAAGATTCACGTGAGTG-TTTTGC	222
DB	181	CGTAATAATTAAGCTATAAGG---GAGTGTCTGTGATTTAGCTGTCACGTAGTCTTTTGC	237
QY	223	GACATTTTGGACACCATGTGTGTACAGCTGTGGTATTTTAAGCCGAGTGAAGACGACGAGGT	282
DB	238	GACATTTTGGACACCATGTGTGTGTATATATGCGCGAGTGAAGACGACGAGAT	297
QY	283	CTCCATTTTGAAGCGGAGGTTTGAACGCGACAGCCGATGCGGGGTTTTCAGAGATTGT	342
DB	298	CTCCATTTTGAACCGCGAAATTTTGAACGAGAGACGACATGCGGGCTTCTAGAGATTCGT	357
QY	343	GATTAAAGTCCCAAGCACTTATGACAGACTTGGCCCGGCAATTTTGAACAGCTTTGTGA	402
DB	358	GATCAAGGTCCGAGCGACCTTGAACGACACTGTGCGGGGCAATTTTGAACCTGTTGTGAG	417



403 CTGGGTGGCCGAGAGGAATGGAGTTGGCCGCAGATTCTGACATGATGATCTGAATCTGAT 462  
418 CTGGGTGGCCGAGAGGAATGGAGTTGGCCGCAGATTCTGACATGATGATCTGAATCTGAT 477  
463 TGAAGAGGCAACCCCTGACCGTGGCCGAGAAAGCTGACGCGCACTTCTCTGATCCAATGGCG 522  
478 TGAGAGGCAACCCCTGACCGTGGCCGAGAAAGCTGACGCGCACTTCTCTGATCCAATGGCG 537  
523 CCGGTGTGATGAAGGCCCCCGGAGGCCCTCTTCTTTGTAGTTCCAGAAAGGCGAGTCTTA 582  
538 CCGGTGTGATGAAGGCCCCCGGAGGCCCTCTTCTTTGTAGTTCCAGAAAGGCGAGTCTTA 597  
583 CTTCCACCTCCATATTTCTGTGTGAGAACCGAGGGGTTCAATTCATGATGATGATGATGATGAT 642  
598 CTTCCACCTCCATATTTCTGTGTGAGAACCGAGGGGTTCAATTCATGATGATGATGATGATGAT 657  
643 CTTGAT 702  
658 CTTGAT 717  
703 GCCCAACTGTGTTCCGGGTGACCAAGACGCTGATGATGATGATGATGATGATGATGATGATGAT 762  
718 GCCCAACTGTGTTCCGGGTGACCAAGACGCTGATGATGATGATGATGATGATGATGATGATGAT 777  
763 GGAAGAGTGTACATCCCACTACCTCTGCGCCCAAGACTCAGCCGAGCTGACAGTGGGC 822  
778 GGAAGAGTGTACATCCCACTACCTCTGCGCCCAAGACTCAGCCGAGCTGACAGTGGGC 837  
823 GTGATCATACATGAGAGATATATAGCGCGTGTATTAACCTGACGAGCGCAACGCGCT 882  
838 GTGATCATACATGAGAGATATATAGCGCGTGTATTAACCTGACGAGCGCAACGCGCT 897  
883 GTGATCATACATGAGAGATATATAGCGCGTGTATTAACCTGACGAGCGCAACGCGCT 942  
898 GTGATCATACATGAGAGATATATAGCGCGTGTATTAACCTGACGAGCGCAACGCGCT 957  
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958 CCCCATTCTGACGCGCTGTGATCCGGTCAAAAACTCCGCGCGCTGATGATGATGATGATGATGAT 1017  
1003 CCGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062  
1018 CCGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077  
1063 CTTGATCATACATGAGAGATATATAGCGCGTGTATTAACCTGACGAGCGCAACGCGCT 1122  
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1258 ACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317  
1303 CACCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362  
1318 CACCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377  
1363 CCAAGCGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422  
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1483 GTCCGCAAGGCAATTTCTCGGCGGCAAGAGTGGCGGTGACCAAAAGTGAAGTGTGTC 1542  
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1543 CGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1602  
1558 CGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1617  
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1678 TGAATCAACCGCGCTGTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737  
1723 GTTCTTCCGCTGGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1782  
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1783 GGTGTGAGCAAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1842  
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1918 CGAAGGATCAAGCAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1977  
1963 CAAGAATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2022  
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2023 CTGTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2082  
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2323 AGAAGCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2382  
2338 AGAAGCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2397  
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2503 AGTTTCAAGAGCGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2562  
2518 AGTTTCAAGAGCGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2577  
2563 TCGAAGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2622

Db	2578	TCGAGGCCAAGAGCGGGTCTCGAACCCTCGGCTGTGAGGAAGCCCTAAGACGG	2637
Qy	2623	CTCCGGAAGAAAGCGTCGGGTAGAGCAGTCGCCACAAGAGCCAGACTCTCTCGGCA	2682
Db	2638	CTCCGGAAGAAAGCGTCGGGTAGAGCAGTCGCCACAAGAGCCAGACTCTCTCGGCA	2697
Qy	2683	TTGGCAGACAGGCCAGACGCCCGCTAATAAAGAGACTCAATTTTGGTCAGACTGGCACT	2742
Db	2698	TCGGCAAGACAGGCCAGACGCCCGCTAATAAAGAGACTCAATTTTGGTCAGACTGGCACT	2757
Qy	2743	CAGACTCAGTCCCGGACCCCAACACTCTCGAGAACTCTCGAGCAACCCCGCTGCTGG	2802
Db	2758	CAGACTCAGTCCCGGATCCCAACACTCTCGAGAACTCTCGAGCAACCCCGCTGCTGG	2817
Qy	2803	GACCTACACATGCTTCAGGCGGTGGCGCACCATAGGACAGACAATTAAGAGGCGCG	2862
Db	2818	GACCTACACATGCTTCAGGCGGTGGCGCACCATAGGACAGACAATTAAGAGGCGCG	2877
Qy	2863	ACGAGTGGGTAAATGCTCAGGAAATTGGCAATTGGATTCCATAGCTGGGCGACAG	2922
Db	2878	ACGAGTGGGTAAATGCTCAGGAAATTGGCAATTGGATTCCATAGCTGGGCGACAG	2937
Qy	2923	TCATACACACCGACCCGAACTGGGCTTGGCCACTATTAACCACTCTTAACAGC	2982
Db	2938	TCATACACACCGACCCGCACTGGGCTTGGCCCACTTAACCACTCTTAACAGC	2997
Qy	2983	AAATCTCAGTGCCTCAACGGGGGGCAGACAACACACATACTTGGGCTACAGCACCC	3042
Db	2998	AAATCTCAGTGCCTCAACGGGGGGCAGACACACACATACTTGGGCTACAGCACCC	3057
Qy	3043	CCTGGGGGTATTTGATTTCAACAGATTCACTGCCATTTCTCAACAGTACCTGGCAGC	3102
Db	3058	CCTGGGGGTATTTGATTTCAACAGATTCACTGCCATTTCTCAACAGTACCTGGCAGC	3117
Qy	3103	GACTCATTAACAACAATTGGGGATTCCGGCCCAAGACTCACTTCAAGCTTTCAACA	3162
Db	3118	GACTCATTAACAACAATTGGGGATTCCGGCCCAAGACTCACTTCAAGCTTTCAACA	3177
Qy	3163	TCCAAGTCAAGAGGTCACGAAATGATGAGTCAACATGAGCTTAATTAACCTTAACA	3222
Db	3178	TCCAAGTCAAGAGGTCACGAAATGATGAGTCAACATGAGCTTAATTAACCTTAACA	3237
Qy	3223	GCAAGGTTCAAGTCTTGTTCGGAATTCGAGTACCAAGTTCCCGTACGCTCCGCGCTCGGC	3282
Db	3238	GCAAGGTTCAAGTCTTGTTCGGAATTCGGAATTCGAGTACCAAGTTCGCGCTCGGC	3297
Qy	3283	ACCAAGGCTGCTCCCTCCGTTCCCGGCGGACGTGTTATGATTCGAGTACGGCTAAC	3342
Db	3298	ACCAAGGCTGCTCCCTCCGTTCCCGGCGGACGTGTTATGATTCGAGTACGGCTAAC	3357
Qy	3343	TAAAGCTCAACAATGGCGACGACGAGTGGGACGCTACCTCTTTAATCGCTGGAAATTT	3402
Db	3358	TAAAGCTCAACAATGGCGACGACGAGTGGGACGCTACCTCTTTAATCGCTGGAAATTT	3417
Qy	3403	TCCCATCGCAATGCTGAGAAAGGGCAATTAATTACCTTAGCTACACTTCGAGACG	3462
Db	3418	TCCCATCGCAATGCTGAGAAAGGGCAATTAATTACCTTAGCTACACTTCGAGACG	3477
Qy	3463	TGCCTTTCACAGCAGCTACCGGCAACGCTGAGACCTGAGCCGGGTGATCTCTCA	3522
Db	3478	TGCCTTTCACAGCAGCTACCGGCAACGCTGAGACCTGAGCCGGGTGATCTCTCA	3537
Qy	3523	TCGACCAATACCTGATTAACCTGGAACAATCAACAACTCCGGAAGTCCCAAAACA	3582
Db	3538	TCGACCAATACCTGATTAACCTGGAACAATCAACAACTCCGGAAGTCCCAAAACA	3597
Qy	3583	AGGACTTGTGTTAGCCGTGGGTTCCAGCTGCGATCTGTTACGCCAAAAACTGGC	3642
Db	3598	AGGACTTGTGTTAGCCGTGGGTTCCAGCTGCGATCTGTTACGCCAAAAACTGGC	3657
Qy	3643	TACCTGAGCCCTGTTACCGGCAAGCGCGTTTCTAATAAACAACAACAACAACA	3702

Db	3658	TACCTGGACCCCTGTTATGCGACGACGCGCTTTCTAAAAAGAAAAAGACAACAACA	3717
Qy	3703	GCAACTTTTACCTGGACCTGGTGCCTTCAAAATAATAACTTTAATGGCGCTGAATCTATAATCA	3762
Db	3718	GCAATTTTACCTGGACCTGGTGCCTTCAAAATAATAACTTAATGGCGGTGAATCATCATCA	3777
Qy	3733	ACCCTGGACCTGCTATGGCTCTCACAAAGACGACAAAGACAAAGTCTTTTCCCATGAGCG	3822
Db	3778	ACCCTGGACCTGCTATGGCTCTCACAAAGACGACAAAGTCTTTTCCCATGAGCG	3837
Qy	3823	GTGTCAATGATTTTGGAAAAGAGAGCGCGGAGCTTCAAACTGTCATTTGACATGTCA	3882
Db	3838	GTGTCAATGATTTTGGAAAAGAGAGCGCGGAGCTTCAAACTGTCATTTGACATGTCA	3897
Qy	3883	TGATTCACAGACGAAGAGAAATCAAAAGCACTAACCCCGTGGCAACGAAAGATTTGGGA	3942
Db	3898	TGATTTACAGACGAAGAGAAATTTAAAGCACTAACCCGTGGCAACGAAAGATTTGGGA	3957
Qy	3913	CTGTGGCAGTCAATCTCCAGACGACGACACAGACCTTGGCAACGGAGATGTGATGTTA	4002
Db	3958	CCGTGGCAGTCAATTTCCAGACGACGACACAGACCTTGGCAACGGAGATGTGATGTTA	4017
Qy	4003	TGGAGCCTTACCTGCGAAATGGTGTGGCAAGACAGACGATTAACCTGAGGGTCTTATTT	4062
Db	4018	TGGAGCAGTAACTGGCGATGGTGTGGCAAGATAGAGAGTGTACTGAGGGTCCCATTT	4077
Qy	4053	GGGCGAAATTCCTCACACGAGATGGACACTTTCACCCGCTCTCTCTACATGGGCGGCTTGG	4122
Db	4078	GGGCGAAATTCCTCACACGATGGACACTTTCACCCGCTCTCTCTTAATGGGCGGCTTGG	4137
Qy	4123	GACTTAAGCACCCGCGCTCTCAGATCTCTCATCAAAAAACAGCGCTGTTCTTGGCAATCCTC	4182
Db	4138	GACTCAAGAACCCGCGCTCTCAGATCTCTCATCAAAAAACAGCGCTGTTCTTGGCAATCCTC	4197
Qy	4183	CGGCGAGATTTTCCGCTACAAAGTTTGGTTCATTCATACCAGATTTCCACAGACAG	4242
Db	4198	CGGCGAGATTTTCAAGCTACAAAGTTTGGTTCATTCATCCCAATCTCACAGAGACAG	4257
Qy	4243	TGAGCGTGGAAATGGAATGGAGGCTGCAGAAAGAAAAACAGCAACGCTGGAATCCGAG	4302
Db	4258	TGAGGTGGAAATTGAAATGGAGGCTGCAGAAAGAAAAACAGACGCTGGAATCCGAG	4317
Qy	4303	TGCAGTATACATCTAATCTATGCAAAATCTGCGAACGTTGATTTCACTGTGACAACAATG	4352
Db	4318	TGCAGTACACATCAATTAATGCAAAATCTGCGAACGTTGATTTCACTGTGACAACAATG	4377
Qy	4353	GACTTTATACCTGAGGCTTCGCCCCATTGGCACCCGTTACTACACCCGTCCTGTAAATGT	4422
Db	4378	GACTTTATACCTGAGGCTTCGCCCCATTGGCACCCGTTACTACACCCGTCCTGTAAATTA	4437
Qy	4423	GTGTTAATCAATTAACCGGTTAATTGCGTCACTGTGAACCTTGGTCTCATGTCTTATTA	4482
Db	4438	GTGTTAATCAATTAACCGGTTAATTGCGTCACTGTGAACCTTGGTCTCATGTCTTATTA	4497
Qy	4483	TCTTATCTGATCACCATAGCAACCGGTTACACATTAACCTGTAGTTGCGCTTCGCA--	4540
Db	4498	TCTTATC--GGTTACATGTTATATGCTTACATTAACCTGTGTGCGCTTCGCGATA	4555
Qy	4541	-----ATACCCCTTAATGATGGAATTTGCCCACTCCCTTATAGCGCGC	4581
Db	4557	AAAGACTTAACGTCATCGGGTTAACCCCTTAATGATGGAATTTGCCCACTCCCTTACGCGGC	4616
Qy	4582	TGCGTCCGCTGGTGGGCGCGGACAGACGACGTCCTGCGGCTGTGGGACCTTTGGTCCGCA	4641
Db	4617	TGCGTCCGCTGGTGGGCGCTGCGACCAAAGCTCCGACGACGAGACGCTGTCTGTGCC	4676
Qy	4642	GGCCCCACGACGACGACGCGCATAGAGAGTGGCCAA	4683
Db	4677	GGCCCCACGACGACGACGCGCATAGAGAGTGGCCAA	4718

RESULT 12  
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Qy 1783 GGGTGAAGCCAAACAAGACCCGCCGATGACGGATATAAAGCGAGCCCAAGCGGCG 1842  
Db 1798 GGGTGAAGCCAAACAAGACCCGCCGATGACGGATATAAAGCGAGCCCAAGCGGCG 1857  
Qy 1843 CTGCCCCCTCAGTCGGGAGTCCATCGAGCTGACGCGGAAAGAGCTCCGGTGAATTGCG 1902  
Db 1858 CTGCCCCCTCAGTCGGGAGTCCATCGAGCTGACGCGGAAAGAGCTCCGGTGAATTGCG 1917  
Qy 1903 CGACAGGTAACCAAAATGTTCTGTCACGCGGCGATGCTTCAGATGCTGTTCCCGG 1962  
Db 1918 CGACAGGTAACCAAAATGTTCTGTCACGCGGCGATGCTTCAGATGCTGTTCCCGG 1977  
Qy 1963 CAAAAATGCGAGAGATGATCAGATTTCAACTTTGCTTCAGCGACGGAGCCAGAGA 2022  
Db 1978 CAAAGCATGCGAGAGATGATCAGATTTCAACTTTGCTTCAGCGACGGAGCCAGAGA 2037  
Qy 2023 CTGTTCAAGATGTTTCCCGGCGGTGTCAGAAATCTCAACCGGTCGTCAAGAAAGAGACGTA 2082  
Db 2038 CTGTTCAAGATGTTTCCCGGCGGTGTCAGAAATCTCAACCGGTCGTCAAGAAAGAGACGTA 2097  
Qy 2083 TCGGAAATCTGTGTCATTCATCATCTGTGGGGCGGGCTCCCGAGATTTGCTGTGGC 2142  
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Qy 2143 CTGCGATCTGGTCAACGTGATCTGGATGACTGTGTTCTGAGCAATAATGACTTTAAAC 2202  
Db 2158 CTGCGATCTGGTCAACGTGATCTGGATGACTGTGTTCTGAGCAATAATGACTTTAAAC 2217  
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Qy 2323 AGGACGACGGCGGGGTCTGTGCTTCTGTGCTTCAAGTACTCGGACCCCTTCAACGAGC 2382  
Db 2338 AGGACGACGGCGGGGTCTGTGCTTCTGTGCTTCAAGTACTCGGACCCCTTCAACGAGC 2397  
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Qy 2443 AGGACGACGACTCAAAACGGGTGACATCCGTAACCTGCGGTATTAACAACGCCAGCGCG 2502  
Db 2458 AGGACGACGACTCAAAACGGGTGACATCCGTAACCTGCGGTATTAACAACGCCAGCGCG 2517  
Qy 2503 AGTTTCAGAGCGTCTGCAAGAAAGATAGTCTTTTGGGGGCAACTCGGGGAGAGTCT 2562  
Db 2518 AGTTTCAGAGCGTCTGCAAGAAAGATAGTCTTTTGGGGGCAACTCGGGGAGAGTCT 2577  
Qy 2563 TCCAGGCCAAGAAGGGTCTCGAACCTTTTGTGCTGTGAGGAAAGTCTTAAGACG 2622  
Db 2578 TCCAGGCCAAGAAGGGTCTCGAACCTTTGCTGTGAGGAAAGGGCTTAAGACG 2637  
Qy 2623 CTCTCTGAAAAGAAAGTCCGGTAAAGAGCTGCGCAAGAGCCAGACTCTCTCTGGGCA 2682  
Db 2638 CTCTCTGAAAAGAAAGTCCGGTAAAGAGCTGCGCAAGAGCCAGACTCTCTCTGGGCA 2697  
Qy 2683 TTGCGAAGACAGGCGCGGCTTAAGAAAGACTCAATTTTGGTCAAGCTGGGCACT 2742  
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Qy 2803 GACCTACATCAATGGCTTCAAGCGGTGGCGCAACAAATGGCAATTAACGAAGCGCGG 2862  
Db 2818 GACCTACATCAATGGCTTCAAGCGGTGGCGCAACAAATGGCAATTAACGAAGCGCGG 2877  
Qy 2863 ACGGATGGGTAAATGCTCAGGAAATTGGCAATTGCGATTCACATGCTGGGCGCAAG 2922

Db 2878 ACGGATGGGTAAATGCTCAGGAAATTGGCAATTGGATTCACATGCTGGGCGCAAG 2937  
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Db 2938 TCATACCAACAGACACCCGAACATGGGCTTTGCCACTTATTAACAACCTTACAGC 2997  
Qy 2983 AAATCTCAGTCTTCAACGGGGGCGACAGACGAAACCACTACTTGGCTACAGACCC 3042  
Db 2998 AAATCTCAGTCTTCAACGGGGGCGACAGACGAAACCACTACTTGGCTACAGACCC 3057  
Qy 3043 CCTGGGGTATTTGATTTCAACAGATTCACATGCAATTTCTACACAGTGAAGTGGACG 3102  
Db 3058 CCTGGGGTATTTGATTTCAACAGATTCACATGCAATTTCTACACAGTGAAGTGGACG 3117  
Qy 3103 GACTCATCAACAACATTTGGGGAATTCGGGCCAAGAGACTCAACTTCAAGCTTTCAACA 3162  
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Qy 3283 ACCAGGGCTGCTTCCCTGCTTCCCGGCGACGTTGTCATGATTCGAGTACGGCTAAC 3342  
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Qy 3523 TCGAACGATACCTGTATTTAATTCAAGAACTCAATTCAGTCCGGAAAGTCCCAAAACA 3582  
Db 3538 TCGAACGATACCTGTATTTAATTCAAGAACTCAATTCAGTCCGGAAAGTCCCAAAACA 3597  
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Qy 3643 TACCTGAACTGTTTACCGGACGAGCGGCTTTCTAAACCAAAACAGACAAACAACA 3702  
Db 3658 TACCTGAACTGTTTATTCGACGAGCGGCTTTCTAAACCAAAACAGACAAACAACA 3717  
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Db 3718 GCAACTTTACTGTGACCTGTGCTTCAAAATTAACCTTAATGGGCGTGAATCTTAATCA 3777  
Qy 3763 ACCCTGGCACTGATATGGCTCAACAAGAGAGCAAAAGCAATTTCTTTCCATGAGCG 3822  
Db 3778 ACCCTGGCACTGATATGGCTCAACAAGAGAGCAAAAGCAATTTCTTTCCATGAGCG 3837  
Qy 3823 GTGTCAATGATTTTGGAAAGAGCGCCGAGCTTCAAACTGTCAATTGCAATGTCA 3882  
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Qy 3943 CTGTGGAGTCAATCTCAGAGCAGACAGACCTGTGACCCGAGATGTGATGTTA 4002



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Db 1078 CTCGTACATCTCTTCAACGCCGCTTCAACTCGCGGTCTCCAGATCAAGCGCGCTTGGAA 1137  
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Db 1918 CGACAGGTACCAAAACAATGTTCTGTCACGCGGGAGTCTTCAATGATGTTCCCTG 1977  
Qy 1963 CAATAATGCAGAGAAATGAATCAGAAATTTCAACATTTGCTTACGCAACGGGACAGAGA 2022  
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Db 2158 CTGCGATTTGGTCAACGTGGACCTGGATGATCTGTGTTTCTGACCAATTAATGACTTAAC 2217  
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Db 2398 TCGAACAGGGGAGCCGCTCAACCGCGGATGTCAGAGCGGCTCTGAGACGACAAAGGCT 2457  
Qy 2443 ACGACAGCACTCAAAAGCGGATGACAAATCCGTAACCTGCGTATTAACCAACGCGACG 2502  
Db 2458 ACGACAGCACTCAAAAGCGGATGACAAATCCGTAACCTGCGGATTAACCAACGCGACG 2517  
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Qy 2563 TCCAGGCCCAAGAAAGGTTCTGAACCTTTGGCTGTGATGAGAAAGGTTCTAAGACG 2622  
Db 2578 TCCAGGCCCAAGAAAGGTTCTGAACCTTTGGCTGTGATGAGAAAGGTTCTAAGACG 2637  
Qy 2623 CTCTGGAAGAAAGCGTCCGCTAGAGAGTGCACCAAGAGCCAGACTCTCTCGGCA 2682  
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Db 2698 TTGGCAAGACAGGCCAGACGCCGCTTAAGAAAGATCTCAATTTGTGTCAGCTGGCACT 2757  
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Qy 4003 TGGAGAGCTTACCTGGAGATGTGTGGAGAGCAGAGAGATGCTGAGAGGTCCTAATTT 4062
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Db 4258 TGAGGTGAGATGGAATGGAGCTGAGAAAGAAACAGCAAAAGCTGGATCCCGAG 4317

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Db 4438 GTGTATATCAATTAACCGGTTAAATGCTGCAAGTGAATCTTGGTCAATGCTTATTA 4497
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Db 4498 TCTTATC-GGTTACATGATTAATGCTTACATTAATCTGTTAGTTGGCTTGGCAATA 4556
Qy 4541 -----ATACCCCTAGATGAGAGTTGCCCACTCCCTATNGGCGC 4581
Db 4557 AAAGACTTACGTATCGGTTTACCCCTAGATGAGAGTTGCCCACTCCCTCTCGCGCGC 4616
Qy 4582 TCGCTCGCTCGGTGGGCGCGGAGAGAGAGCTCTGCGCTGTCGAGACTTTGGTCCGCA 4641
Db 4617 TCGCTCGCTCGGTGGGCGCGGAGAGAGAGCTCTGCGCTGTCGAGACTTTGGTCCGCA 4676
Qy 4642 GGCCCAACGAGCGAGCGGAGCGGCAATGAGGAGTGCCCA 4683
Db 4677 GGCCCAACGAGCGAGCGGAGCGGCAATGAGGAGTGCGCA 4718

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RESULT 14
US-10-291-583-1
; Sequence 1, Application US/10291583
; Publication No. US20030138772A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; APPLICANT: Alviria, Mauricio
; TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Virus (f
; FILE REFERENCE: UBN-02735USA
; CURRENT APPLICATION NUMBER: US/10/291,583
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/350,607
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/341,117
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/377,066
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/386,675
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 4721
; TYPE: DNA
; ORGANISM: adeno-associated virus serotype 7
US-10-291-583-1

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Query Match 78.5%; Score 3678.4; DB 7; Length 4721;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 4135; Conservative 0; Mismatches 541; Indels 52; Gaps 8;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGGCGCGGAGCAACCAAGTCCG 60
Db 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCGCTCGTGGGCGCTGCGGACCAAGTCCG 60
Qy 61 CGAGCGCCGGGCTTTGGCGCGGCTCAAGTACGAGCGAGCGCGCAGAGAGGAGTG 120
Db 61 AGAGCGGAGAGCTCTGCTGCGCGGCCCAAGAGCGAGCGCGCATAGAGGAGTG 120
Qy 121 GCCAATCTCATCTAGGGTTCTCTGAGG-----GTTGAGTCTGAGC 164
Db 121 GCCAATCTCATCTAGGGTTACCGCGAGAGCGCTCCACGCTGCGGCTGAC 180

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OY	165	GTGATATTACGTCATAGGGTTAGGAGAGTCTCTGATTTAGAGGTCACTGAGTG- TTTTGGG	223
Dp	161	GTAAATCAACGTATAGGG--GAGTGGTCTGTATTATAGGTGTCACTGAGTGGTTTGGG	237
OY	224	ACATTTTCGACACACCATGTGTCA CGCTGGGATATTTAAGCCGAGAGACCCAGAGGTC	283
Dp	228	ACATTTTCGACACACCGTGGCCATTYAGAGGTATATATGGCCGAGTGAAGCCAGAGATC	297
OY	284	TCCATTTTGAAGCGGAGGTTTGAACGCGACGCCATCCCGGGGTTTACGAGATTGTG	343
Dp	298	TCCATTTTGAACCGCAAAATTTTAAACAGACGACGCCATCCGGGTTTCAACGAGATCGTG	357
OY	344	ATTAAAGTCCCCAGGACCTTGACAGACATCTGCCGGGATTTCTBACAGCTTTGGTAAAC	403
Dp	358	ATCAAGGTGCCAGAGGACCTTGACAGACATCTGCCGGGATTTCTBACGTCTTTGGTAAAC	417
OY	404	TGGGTGGCCGAGAAAGAAATGGAGTTGGCCGACAGATTCTGACATGATCTGATCTGATT	463
Dp	418	TGGGTGGCCGAGAAAGAAATGGAGTGGCCCGGATTTGACATGATCTGATCTGATCTGATC	477
OY	464	GAGCAGGCAACCCCTGACCGTGGCCGAGAAAGCTGACGCGGACTTCTTGCTTCCACTGGCCG	523
Dp	478	GAGCAGGCAACCCCTGACCGTGGCCGAGAAAGCTGACGCGGACTTCTTGCTTCCACTGGCCG	537
OY	524	CGCGTAGTAAAGGCCCGGAGGCCCTCTTCTTGTTCAGTTGAGAAAGGCGAGTCCCTAC	583
Dp	538	CGCGTAGTAAAGGCCCGGAGGCCCTCTTCTTGTTCAGTTGAGAAAGGCGAGACTAC	597
OY	584	TTCCACCTTCATATTTCTGGTGAGACCAACGGGGGTCAAAATCCATGTGCTGGGCGGCTTC	643
Dp	598	TTCCACCTTCACGTTCTGGTGAGACCAACGGGGGTCAAAATCCATGTGCTGAGCGCCCTTC	657
OY	644	CTGATCAGATTAAGGACAAAGCTGGTGACACATCTACCGGGGATTCAGGCCGACCTCG	703
Dp	658	CTGATCAGATTCGGGAGAGCTGGTCCACACCATTTACCGGGGATTCAGGCCGACCTCG	717
OY	704	CCCAACTGGTTCCGCGTGACCAAGACGCGCTAAATGGCGCCGAGGGGGGAAACAAGTGTGTG	763
Dp	718	CCCAACTGGTTCCGCGTGACCAAGACGCGCTAAATGGCGCGGGGGGAAACAAGTGTGTG	777
OY	764	GACGAGTCTACATTCGCCCACTACTCTCTGCCCAAGACTCAGCGCCGAGCTGCAGTGGGG	823
Dp	778	GACGAGTCTACATTCGCCCACTACTCTCTGCCCAAGACCCAGCCGACGTGCAGTGGGG	837
OY	824	TGCACTTAACATGAGAGAGTATATAAGCGGCTTTTAACTTGAGCCGAGCCAAACGGCTC	883
Dp	838	TGCACTTAACATGAGAGAGTATATAAGCGGCTTTTGAACCTTGAGCCGAGCCAAACGGCTC	897
OY	884	GTGGCGCACGACTTGACCCACGTCAGCCAGACCCAGAGACAGAACAAAGAAATCTGAAC	943
Dp	898	GTGGCGCACGACTTGACCCACGTCAGCCAGACCCAGAGACAAAGAAAGAAATCTGAAC	957
OY	944	CCCAATTTGACGCGCCTGTACTCCGGTCAAAAACCTCCGACGCTACATGAGAGCTGGTAC	1000
Dp	958	CCCAATTTGACGCGCCTGTACTAGGTCAAGTCAAAAACCTCCGCGGCTACATGAGAGCTGGTAC	1014
OY	1004	GAGTGGCTGTGGACCGGGGCACTCACTTCGAGAAACATGTGATCCAGAGAGACCAAGGCC	1060
Dp	1018	GAGTGGCTGTGGACCGGGGCACTCACTTCGAGAAACATGTGATCCAGAGAGACCAAGGCC	1074
OY	1064	TCGTACATCTCTTCAACGCGGCCCTTCCACTGGCGGTCCCAAGTCAAGGCCGCTCTGGAC	1120
Dp	1078	TCGTACATCTCTTCAACGCGGCCCTTCCACTGGCGGTCCCAAGTCAAGGCCGCGCTGGAC	1134
OY	1124	AATGCGGCAAGATCATGGCGCTGACCAAAATCCGCGCCCGACTACCTGTGTAGGCCCTCGCT	1180
Dp	1138	AATGCGGCAAGATCATGGCGCTGACCAAAATCCGCGCCCGACTACCTGTGTAGGCCCTCGCT	1194
OY	1184	CGCGCCCGGCAATTAAAAACAACCGCATTTACACGATCTCTGAGGTGAACGGCTACGAC	1240
Dp	1198	CTGCGCGGCAATTAAAAACAACCGCATCTACCGATCTTGAGGTGGAACGGGTACGAT	1254

QY	1244	CCCTGCTAAGCCCGGCTCCGTTCTTCTCGGCTGGGCCAAGAAAGTTCCGAAACCGAAC	1303
Db	1258	CCGTGCTTAGCCGGCTCCGTTCTTCGGCTGGGCCAAGAAAGTTCCGAAAGCCGAAC	1317
QY	1304	ACCATCTGGCTGTTTGGGCGGGCAACAAGGGAAGACCAACATTCGCGAAGCATCGCC	1363
Db	1318	ACCATCTGGCTGTTTGGGCGGGCAACAAGGGAAGACCAACATTCGCGAAGCATCGCC	1377
QY	1364	CAGCCGTGACCTTCTACGGCTGCGTCAACTGAGACCAATGAGAACTTTCCTTCACGAT	1423
Db	1378	CAGCCGTGACCTTCTACGGCTGCGTCAACTGAGACCAATGAGAACTTTCCTTCACGAT	1437
QY	1424	TGCGTGCACAAATGATGATCTGTGTGGGAGAGAGGCAAGTGAACGGCCAAAGTGTGGAG	1483
Db	1438	TGCGTGCACAAATGATGATCTGTGTGGGAGAGAGGCAAGTGAACGGCCAAAGTGTGGAG	1497
QY	1484	TCGCGCAAGGCCATTCGCGCGGCGCAAGGTGGCGGTGGACCAAAAGTGCAGTGGTCC	1543
Db	1498	TCGCGCAAGGCCATTCGCGCGGCGCAAGGTGGCGGTGGACCAAAAGTGCAGTGGTCC	1557
QY	1544	GCCGAGATGATCCCAACCCCGCTGATCGTCACTTCAACACCAACATGTGCGCGTGATT	1603
Db	1558	GCCGAGATGATCCCAACCCCGCTGATCGTCACTTCAACACCAACATGTGCGCGTGATT	1617
QY	1604	GACGGGAACAGCACCACTTTCAGACACAGACGCGTTCGAGGACCGGATGTTCAAAATTT	1663
Db	1618	GACGGGAACAGCACCACTTTCAGACACAGACGCGTTCGAGGACCGGATGTTCAAAATTT	1677
QY	1664	GAACTCACCCCGCTGTGAGATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAAAG	1723
Db	1678	GAACTCACCCCGCTGTGAGATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAAAG	1737
QY	1724	TTCTTCCGCTGGGCGCAGGATCACGAGCCGAGGTGGCCATAGTGTCTACGCAGAAAG	1783
Db	1738	TTCTTCCGCTGGGCGCAGGATCACGAGCCGAGGTGGCCATAGTGTCTACGCAGAAAG	1797
QY	1784	GGTGAGCCCAACACAGACCCGCCCGCGATGACGCGGATAAAAAGCAAGCCCAAGCGGGCC	1843
Db	1798	GGTGAGCCCAACACAGACCCGCCCGCGATGACGCGGATAAAAAGCAAGCCCAAGCGGGCC	1857
QY	1844	TGCCCCCTCAGTGGCGGATTCATTCAGAGTCAGACGCGGAAAGAGACTCCGGTGGACTTTGGC	1903
Db	1858	TGCCCCCTCAGTGGCGGATTCATTCAGAGTCAGACGCGGAAAGAGACTCCGGTGGACTTTGGC	1917
QY	1904	GACAGGTACCAAAACAAATGTTCTGTGTCAGCGGGGATGTTAGATGCTTTCCTGTC	1963
Db	1918	GACAGGTACCAAAACAAATGTTCTGTGTCAGCGGGGATGTTAGATGCTTTCCTGTC	1977
QY	1964	AAAAATGCGAGAGATGATCAGAAATTTCAACTTTGCTTCAACGCAAGGACCAAGAC	2023
Db	1978	AAAAATGCGAGAGATGATCAGAAATTTCAACTTTGCTTCAACGCGGATCAAGAC	2037
QY	2024	TGTTCAAGATGTTTCCCGGCGGTGCAGATCTCAACCGGTGCTCAAGAAAGAGACGTAT	2083
Db	2038	TGTTTAGAGTGTTCCTCCGCGCGTGCAGATCTCAACCGGTGCTCAAGAAAGAGACGTAT	2097
QY	2084	CGGAACCTGTGCAATTCATCATCTGCTGGGGCGGGCTCCGAGATGTTGTTCTCGGCC	2143
Db	2098	CGGAACCTGTGCAATTCATCATCTGCTGGGGCGGGCTCCGAGATGTTGTTCTCGGCC	2157
QY	2144	TGCGACTGTGTCAAGGTGATCTGAGTGACTGTGTTTTCAGAGCAATAATGACTTAAACC	2203
Db	2158	TGCGACTGTGTCAAGGTGATCTGAGTGACTGTGTTTTCAGAGCAATAATGACTTAAACC	2217
QY	2204	AGGATAGCTGCGCATGTTATCTTTCAGATTTGGCTTCAGAGACACTCTCTGAGGGCAT	2263
Db	2218	AGGATAGCTGCGCATGTTATCTTTCAGATTTGGCTTCAGAGACACTCTCTGAGGGCAT	2277
QY	2264	TCGGCAGGTGTGGGACTTGAACCTGGAGCCCGCAAAACCAAAAGCACAACAGCAAAAGCA	2323
Db	2278	TCGGCAGGTGTGGGACTTGAACCTGGAGCCCGCAAAACCAAAAGCACAACAGCAAAAGCA	2337
QY	2324	GGACACACGGCCGGGGCTGTGTTCTTCTGGCTTCAAGTACTTCGACCTTTCACAGGACT	2383

Db	2338	GGACACAGGCGCGGGGCTCTGGTGCTTCTCTGGCTACAGTACCTCGAGCCCTTCAACGAGCT	2397
Qy	2384	CGACAGGGGGAGCCCGTCAACCGCGCGAGATGCAAGCGGCGCTCGAGCACGAACAGCCTA	2443
Db	2398	CGACAGGGGGAGCCCGTCAACCGCGCGAGCGAGCGGCGCTCGAGCACGAACAGCCTA	2457
Qy	2444	CGACCAAGAGCTCAAGCGGGGTGACATCCGTACTCTGGGTAATACACGCGGACGCCGA	2503
Db	2458	CGACCAAGAGCTCAAGCGGGGTGACATCCGTACTCTGGGTAATACACGCGGACGCCGA	2517
Qy	2504	GTTTCAGAGCGTCTGCAAGAAAGATAGTCTTTTGGGGGCAACCTCGGGCGAGAGTCTT	2563
Db	2518	GTTTCAGAGCGGTCTGCAAGAAAGATAGTCAATTGGGGGCAACCTCGGGCGAGAGTCTT	2577
Qy	2564	CCAGGCCAAGAAAGAGGTTCTCGAACCTTTTGGTCTGGTTGAGAAAGGTGTGAAGCGGC	2623
Db	2578	CCAGGCCAAGAAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGAAAGCGCTTAAGACGCG	2637
Qy	2624	TCCTGGAAAGAAAGCTCCGGTAAGAGCACTCGCACA--AAGCCAGACTCTCTCGGG	2680
Db	2638	TCCTGGCAAGAAAGAACCGGTAAGAGCCTCACCTCAGGTTCCCGCGACTCTTCAACGGG	2697
Qy	2681	CATTGGCAAGACAGGCGCGAGCGCCGCTAAAGAAAGACTCAATTTTGGTTCAGCTGGCGA	2740
Db	2688	CATCGGCAGAAAGGCGCGAGCGCCGCGAAGAAAGACTCAATTTCCGTCAAGCTGGCGA	2757
Qy	2741	CTCAGAGTCAGTCCCGGACCCGACCAACCTCTCGAGAACCTTCACAGAACCCCGCGTGT	2800
Db	2758	CTCAGAGTCAAGTCCCGGACCCGACCAACCTCTCGAGAACCTTCACAGAGCGCTCTAAGGT	2817
Qy	2801	GGGACCTTACTACATGCTGTTCAAGCGGGTGGCGCACCAATGCGACAAATACGAAGCGC	2860
Db	2818	GGGATCTGGTACAGTGGCTGCGAGGGGGGCGGACCAATGCGACAAATACGAAGGTGC	2877
Qy	2861	CGAGGAGTGGGGTATGCTCTGAGAAATTTGGCATTTGCAATTCGATGGCTGGGCGACAG	2920
Db	2878	CGAGGAGTGGGGTATGCTCTGAGAAATTTGGCATTTGCAATTCGATGGCTGGGCGACAG	2937
Qy	2921	AGTCATCAACCAAGACCCGGAACATGCGGCTTGGCCACTATATACCAACCACTCTACAA	2980
Db	2938	AGTCATTAACCAAGACCCGGAACCTGGGCCCTGCGCACTTACCAACCAACCACTCTACAA	2997
Qy	2981	GCAAAATCTCCAGTCTTCACAGGCGGGCGAGACGACCAACCACTATTGGGCTTACAGCAC	3040
Db	2998	GCAAAATCTCCAGTAAACCTGACAGGTAGTACCAACCAACCACTATTGGGCTTACAGCAC	3057
Qy	3041	CCCGTGGGGGTAATTTGATTTTCAACAGATTCACATGCAATTTTTCACCAAGTACTGGCA	3100
Db	3058	CCCGTGGGGGTAATTTTGAATTTTCAAGATTCACATGCAATTTTTCACCAAGTACTGGCA	3117
Qy	3101	GCGACTCATCAACCAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAGTCTTCA	3160
Db	3118	GCGACTCATCAACCAACTGGGGATTCGGGCCCAAGAGAGTGGGGTTCAAGTCTTCA	3177
Qy	3161	CATCCAAAGTCAAGAGTCAAGACGAAATGATGGCGTCAAGCAATTCGTAAATTAACCTTAC	3220
Db	3178	CATCCAAAGTCAAGAGGATCAAGACGAAATGACGGCGTTACGACCAATTCGTAAATTAACCTTAC	3237
Qy	3221	CAGACCGTTTAAAGTCTTGTGGACTCGGAATCAAGTCCCGTAAGTCTCTGGCTCTGC	3280
Db	3238	CAGACCGATTAAGGATTTCTGGACTCGGAATCAAGTCCCGTAAGTCTCTGGCTCTGC	3297
Qy	3281	GCACCAAGGGCTGCGCTCCCTCGGTTCCGGCGGACGATGTTCAATGATTCGCGAGTACGGCTA	3340
Db	3298	GCACCAAGGGCTGCGCTCCCTCGGTTCCGGCGGAGGATCTTCAATGATTTCTCAATACGGCTA	3357
Qy	3341	CTTAACGCTCAACATGGCACGACGACGAGTGGAGCGTCACTCTTTTATCTGCTCGATATA	3400
Db	3358	CTGAAGTCTCAACATGGCAATGCAAGTCTGTGGAGGTTCCCTTTTCAATCTGCTCGAGTA	3417
Qy	3401	TTTCCCATCGAGATGCTGAGAACGGGCAATTAATTTTACCTTTCAGCTTACACTTTGAGGA	3460

Db	3418	CTTCCCTCTCAAGTGTGAGAACGGGCAACAACCTTGTAGTTCACTACAGCTTCGAGGA	3477
Qy	3461	CGTGCCTTTTCACAGCAAGCTACGCGACAGCAAGCAAGCTTGACCGGCTGATGTAATCTCT	3520
Db	3478	CGTGCCTTTTCACAGCAAGCTACGCGACAGCAAGCAAGCTTGACCGGCTGATGTAATCTCT	3537
Qy	3531	CATGACCACTTACTGTATTACTGTAACGAATCTCAATCAATCAATCCGGA---AGTCCCA	3577
Db	3538	CATGACCACTTACTGTATTACTGTAACGAATCTCAATCAATCAATCCGGAAGCGACAGCTGG	3597
Qy	3578	AAACAAGACTTGTCTGTTTACCGGTGGTCTCAGCTGACATGTCTGTTACGCCCAAAA	3637
Db	3598	CAATCGGGAAGCTGAGTTTACCGAGGGGGGCTTCAATATATGCGCAACAAGCAAGAA	3657
Qy	3638	CTGGCTACCTGGAACCGTGTATCCGGACAGACGGCGTTTCTAAACAAAAACAGACAA	3697
Db	3658	TTGGTTACTGGAACCTTGTCTCGGCAACAAAGAGTCTCAAAACGCTGATCAAAACAA	3717
Qy	3698	CAACAGAACTTTTAACTCTGGACTGTGTCTTCAAAATTTAACTTATGTGGCGTGAATCAT	3757
Db	3718	CAACAGCAATTTTGTCTTGGACTGTGTGTCCACAAATATCACTGGAACGGCAAGAACTGTT	3777
Qy	3758	AATCAACCTTGGGCACTGATGGAATGGCTCCACACAAGACGACAAAGCAAGTTCTTCCAT	3817
Db	3778	GGTTATATCCCGGGCTGGCCATGCGCACTACAGAAGACAGACGGCTTTTCCATC	3837
Qy	3818	GAGCGGTGTGATGATTTTGTGAAAGAGAGCGCGAGCTTCAAACTGTGATTTGACAA	3877
Db	3838	CAGCGGAGTCTGTGATTTTGTGAA---AATCTGAGAGCACTAACAAATCTACATTTGAAA	3894
Qy	3878	TGTATATATCAACAGAGAGAGAAATCAAAAGCACTAACCCCGTGGCACCGAAAGTT	3937
Db	3895	TGTGTATATACAAATGAAAGAAATTTGTCTCTATCTGTAGGCAAGGAAATTA	3954
Qy	3938	TGGGACTGTGGCAATCTCCAGAGCAGACAGACCCCTGGACCGGAGATGTCA	3997
Db	3955	CGGATATGTAGACAGCACTTACAGCGGCTAATTCTGACGCCAGACACAAGTTGTCA	4014
Qy	3998	TGTTATGGAGCCTTACTTGATATGTGTGGCAAGACAGAGCTATCTTGACAGGGTCC	4057
Db	4015	CAACAGAGGAGCCTTACTGTGATGTGTGGCAAGACCGGAGCGTATCTGTGAGGGTCC	4074
Qy	4058	TATTTGGGCCAAATTTCTCAACGAGATGACAATTCAACCCGTCTCTCATAGGGCGG	4117
Db	4075	CATCTGGGCCAAATTTCTCAACGAGATGACAATTCAACCCGTCTCTTGTATGGGCGG	4134
Qy	4118	CTTTGACCTTAACGACCGCGCTCTCAGATCTCATCAAAACAGCGCTGTTCCGCGAA	4177
Db	4135	CTTTGACCTTAACGACCGCGCTCTCAGATCTCTCAATCAAAACATCTCCGTTCCGCTAA	4194
Qy	4178	TCTCCGGGCAAGTTTTCGGCTTAAAGTTTGCTTCAATTCACCCAGTATTCACAGG	4237
Db	4195	TCTCCGGGAGTGTATTACTCTCTGCGCAAGTTTGCTTCTTCAATCAACAGTACAGACCGG	4254
Qy	4238	ACAAGTAGCGGTGAGATTGAAATGGAGCTGCAGAAAGAAAACAGCAAAACGCTGGAATCC	4297
Db	4255	ACAAGTACGAGTGAATGAGAGGGAGCTGCAGAAAGAAAACAGCAAAACGCTGGAATCC	4314
Qy	4298	CGAAGTCACTATACATCTTATATGCAAAATCTGCCAACGTGATTTCACTGTGAGCAA	4357
Db	4315	GGAGATTCACTATACCTTCAACTTTGAAAGAGAGCTGGTGTGACTTTGCGCTTGACAG	4374
Qy	4358	CAATGACCTTTTAACTAGAGCTGCGCCCATTTGGACCGGTTACCTCAACCGCTCCCTGTA	4417
Db	4375	CCAGGGTGTACTCTGAGCTTCCCTTATTTGGCACTGTATCTCAACCCGTAATCTGTA	4434
Qy	4418	ATTGTGTATTAATCAATTAACCGGTTAATTGTGTCACTGAACTTTGTGTCAATGCTCT	4477
Db	4435	ATTGACGTTTAATCAATTAACCGGTTGATTTGTTCAAGTGAACCTTGTGTCTCCGTGCT	4494
Qy	4478	TATTTATCTTATCTGTGACCAATGACACCGGTTACATTAATCTGTTAGTTGGCGTTGG	4537
Db	4495	TCTTATCTTATCTGTTTCCATATGCAACGTTGTAACATTAATCTGTTGGGTGGCGTTCA	4553

OY	453 8	CGA-----	ATACCCCTAGTATGGAGTTGCCCATCTCCCTCAT	457 5
Db	455 4	CGAATAGAAAC	CTGACGTCAACCCGCGTACCCCTATGTATGAGATTGGCACATCCCTCAT	461 3
OY	457 6	GCGCGCTGCTCGCTCGGTGGGGGCGGAGAGAGCTCTGCGGTGCGGACCTTTGG		463 5
Db	461 4	GCGGCTGCTGCTCGGTGGGGGCTTGCGGACCAAAAGGTCCGACAGCGAGAGCTTGC		467 3
OY	463 6	TCCGACGAGCCCA	CCGAGCGAGCGCGCATAGAGGAGTGGCCAA	468 3
Db	467 4	TTCTGCGGCCCCA	CCGAGCGAGCGAGCGCGCATAGAGGAGTGGCCAA	472 1

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RESULT 15
US-11-145-035-37
; Sequence 37, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 4721
; TYPE: DNA
; ORGANISM: Adeno-associated virus 7
US-11-145-035-37

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Query Match	78.5%	Score 3678.4	DB 15	Length 4721
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Matches 4135; Conservative 0; Mismatches 541; Indels 52; Gaps 8;

QY	1	TTGGGACATCCCTCTCTGGGGGCGTGGTGGTCACTGAGAGCGGGGAGACCAAGGTCGCC	60
Db	1	TTGGGACATCCCTCTATATGCGGCGCTCGCTGCTGGTGGGGGCGCTGGGACCAAGGTCGCC	60
QY	61	CGAGCGCCCGGCGCTTGGCCCGGGCGGCGCTCAGTGAGCGAGCGGCGGAGAGGAGTG	120
Db	61	AGAGCGGAGAGCTCTGCTCTGGCGGGCCCAAGGAGCGAGCGGCGGAGTGAAGGAGTG	120
QY	121	GGCAACTCCATCTACCTAAGGGGTTCCTGGAGG-----GGTGAAGTCGTGAC	164
Db	121	GGCAACTCCATCTACTAAGGGGTACCGGAGGCGCTCCACGCTGGCGGCTGACGCTGGAC	180
QY	165	GTGAATTACGTCATAGGGGTTAAGGAGGTCCTGTATTAGAAGTCAAGTGAAGTGTG--TTTGGG	223
Db	181	GTAATACAGTCATAGGGG---GAGTGTCTGTATTAGCTGTACAGTGAAGTGTCTTTGGG	237
QY	224	ACATTTTGGACACCATATGTGTCAAGCTGGGTATTTAAGCCGAGTGAAGCAGGAGGTC	283
Db	238	ACATTTTGGACACCCACGCGGCATTGAGGTATATATGCGGAGTGAAGGAGCAGAGATC	297
QY	284	TCCATTTTGAAGCGGAGGTTTGAAGCGCGAGGCGCATCGGGGGTTTACAGAGATTGTG	343
Db	298	TCCATTTTGAACCGGCAAAATTTAACAGAGACAGCCATGCGGGTTTCTACAGATCTGTC	357
QY	344	ATTAAAGTCCCGACGACCTTGACGAGCATCTGCGCGGATTTCTGACAGCTTTGTGAAC	403
Db	358	ATCAAGGTGCGGAGCGACTTGACGAGCACCTGCGGGGATTTCTGACTCGTTGTGAAC	417
QY	404	TGGGTGGCGGAGAAAGTAATGGAGTTGGCCGCGAGATTTGACATCGGATCTGAATCTGAAT	463
Db	418	TGGGTGGCGGAGAAAGTAATGGAGCTGCCCCCGGATTTCTGACATGGAATCTGAATCTGAAT	477
QY	464	GAGCAGGACCCCTGACCGGTGGCGAGAAAGCTGACGCGGACTTCTGTGTCACTGGGCG	523

Db	478	GAGCAGGCA	CCCCCTAACCGTGGCCGAGAGCTGCAGCCGACTTCTTGSTCCATGCGCC	537
Qy	524	CGCGTAGTAAG	CCCCCGGAGGCCCTCTTCTTGTTCAGTTTCGAAAGGCGAGTCTTAAC	583
Db	538	CGCGTAGTAAG	CCCCCGGAGGCCCTGTGTTCTTGTTCAGTTTCGAAAGGCGAGGCTAAC	597
Qy	584	TTCCACCTTC	CAATTTCTGTGTGGAGACCAACGGGGGTTCAAACTCATGTGTGTGGCCGCTTC	643
Db	598	TTCCACCTTC	CAAGTTCGTGTGGAGACCAACGGGGGTTCAAACTCATGTGTGTAGCCGCTTC	657
Qy	644	CTGAGTCAAG	TTAAGGACAAGCTGGTGTGAGACATCTACCGCGGATGTGAGCCGACCTCG	703
Db	658	CTGAGTCAAG	ATTGGGAAGAGCTGGTCCAGACATCTACCGCGGAGTGTAGCCACGCTG	717
Qy	704	CCCAACTGG	TTCCGCGTGAACCAAGACGGGTATGTGCGCGGAGGGGGAAACAAGTGTG	763
Db	718	CCCAACTGG	TTTGGCGGTACCAAGACGGGTATGTGCGCGCGGGGGGAAACAAGTGTG	777
Qy	764	GACGAGTCT	CAATCCCACTACTCTCTGCCAAGACTCAAGCCGAGCTGCATGGGCG	823
Db	778	GACGAGTCT	CAATCCCACTACTCTCTGCCAAGACCGAGCTGCATGGGCG	837
Qy	824	TGGAATTAC	ATGAGAGATTATTAAGGCGGTTTAACTCTGGCCGACCGCAAAGGCTC	883
Db	838	TGGAATTAC	ATGAGAGATTATTAAGGCGGTTTGAACCTGGCCGAACGCAAGGCTC	897
Qy	884	GTGGCGCAG	ACCTTAACCGTACGCGAGACCCAGAGCAGAAACAAGAGATCTGAAC	943
Db	898	GTGGCGCAG	ACCTTAACCGTACGCGAGACCGAGAGCAGAACAAAGAGATTTGAAC	957
Qy	944	CCCAATTCT	GACGCGCTGTCAATCCGATCAAAAACTTCGCAACGTACATGAGCTGTG	1003
Db	958	CCCAATTCT	GACGCGCGGTGTCAAGTCAAAAACTTCGCGGCTTACATGAGCTGTG	1017
Qy	1004	GGGTGGCT	GTGTGACCCGGGGCATCACTTCCGAAAGCATGTGATTCAGAAGACCAAGCC	1066
Db	1018	GGGTGGCT	GTGTGACCCGGGGCATCACTTCCGAAAGCATGTGATTCAGAAGACCAAGCC	1077
Qy	1064	TGTCATCT	CTCTTCAACGCGCCCTCAACTCGCGGTCCCAAGTCAAGGCGCTGTGAC	1122
Db	1078	TGTCATCT	CTCTTCAACGCGCCCTCAACTCGCGGTCCCAAGTCAAGGCGCTGTGAC	1133
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Qy	1244	CTGCTTAC	GCGCGGCTCGCTCTTCTTCTGCGGCTGGGCGCAAAAAAGTTTGGAAAAACGCAAC	1303
Db	1258	CTGCTTAC	GCGCGGCTCGCTCTTCTTCTGCGGCTGGGCGCAAAAAAGTTTGGAAAAACGCAAC	1317
Qy	1304	ACCATCTGG	CTGTTTGGGCGCGGACCAACGGGGCAAGACCAATTCGCGGAAGCCATCGCC	1363
Db	1318	ACCATCTGG	CTGTTTGGGCGCGGACCAACGGGGCAAGACCAATTCGCGGAAGCCATCGCC	1377
Qy	1364	CACGCGTG	CCCTTCTACGCTGCTCACTGACCAATGAGAACTTTCCCTTCAACGAT	1422
Db	1378	CACGCGTG	CCCTTCTTACGCGCTGCTCACTGACCAATGAGAACTTTCCCTTCAACGAT	1437
Qy	1424	TGCGTCA	CAAGATGTGATCTGCTGGAGGAGGCAAGACGAGCCCAAGTGTGAG	1488
Db	1438	TGCGTCA	CAAGATGTGATCTGCTGGAGGAGGCAAGATGACGGCCCAAGTGTGAG	1497
Qy	1484	TCCGCAAG	GCATTTCTGCGCGGACCAAGGTGCGCGTGAACCAAAAGTCAAGTCTGCC	1543
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Db 1558 GCCAGATCGACCCACCCCGTATGTCATCTCAACCAACCAATGTCGCCGTATT 1617  
Qy 1604 GACGGGAACACACCACTTGTAGACACCAAGACGCCGTGTGACGACCGGATGTTCAATTT 1663  
Db 1618 GACGGGAACACACCACTTGTAGACACCAAGACGCCGTGTGACGACCGGATGTTCAATTT 1677  
Qy 1664 GAATCTACCCCGCTCTGAGACATGACTTTGGCAAGGTGACAAAGACGAAGTCAAAAG 1723  
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**THE ONE BLANK (USPTO)**



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OM nucleic - nucleic search, using sw model

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	4683	100.0	4683	US-09-807-802A-19	Sequence 19, Appli
2	4253.2	90.8	4718	US-09-807-802A-1	Sequence 1, Appli
3	3296.2	70.4	4679	US-10-038-972A-12	Sequence 12, Appli
4	3296.2	70.4	8698	US-09-770-315-2	Sequence 2, Appli
5	3293	70.3	4679	US-09-717-789C-25	Sequence 25, Appli
6	3270.8	69.8	4680	US-08-254-358-1	Sequence 1, Appli
7	3270.8	69.8	4680	US-08-475-391-1	Sequence 1, Appli
8	3270.8	69.8	4680	US-08-709-609-1	Sequence 1, Appli
9	3270.8	69.8	4680	PCT-US95-07178-1	Sequence 1, Appli
10	3267.8	69.8	4681	US-09-807-802A-18	Sequence 18, Appli
11	3244.2	69.3	4675	US-09-783-378A-1	Sequence 1, Appli
12	3244.2	69.3	4675	US-09-783-378A-2	Sequence 2, Appli
13	3244.2	69.3	4675	US-10-111-708-1	Sequence 1, Appli
14	3114.4	66.3	7557	US-09-770-315-3	Sequence 3, Appli
15	3008	64.2	8159	US-09-438-268-5	Sequence 5, Appli
16	2804.2	59.9	8151	US-09-438-268-2	Sequence 2, Appli
17	2532	54.1	4767	US-09-533-594B-1	Sequence 1, Appli
18	2504.4	53.5	7214	US-09-438-268-1	Sequence 1, Appli
19	2103.8	44.9	2211	US-09-807-802A-12	Sequence 12, Appli
20	2097.4	44.8	7447	US-10-216-870-11	Sequence 11, Appli
21	1812.8	38.7	1872	US-09-807-802A-4	Sequence 4, Appli
22	1715.2	36.6	4072	US-09-770-315-4	Sequence 4, Appli
23	1705.6	36.4	1800	US-09-807-802A-14	Sequence 14, Appli

24	1540.8	32.9	1641	US-09-807-802A-6	Sequence 6, Appli
25	1513.8	32.3	1605	US-09-807-802A-16	Sequence 16, Appli
26	1484.8	31.7	4910	US-08-331-384-2	Sequence 2, Appli
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35	1177.6	25.1	1200	US-09-807-802A-8	Sequence 8, Appli
36	1041.8	22.2	7744	US-10-216-870-14	Sequence 14, Appli
37	935.6	20.0	2208	US-09-533-594B-5	Sequence 5, Appli
38	903.6	19.3	969	US-09-807-802A-10	Sequence 10, Appli
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40	729.2	15.6	2307	US-09-533-427-7	Sequence 7, Appli
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#### ALIGNMENTS

RESULT 1  
US-09-807-802A-19  
Sequence 19, Application US/09807802A  
Patent No. 6759237

GENERAL INFORMATION:  
APPLICANT: Wilson, James M.  
TITLE OF INVENTION: Xlso, Weldong

TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,  
FILE REFERENCE: GNPVN.031USA  
CURRENT APPLICATION NUMBER: US/09/807, 802A

CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR FILING DATE: 1999-11-02  
NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19

LENGTH: 4683  
TYPE: DNA

ORGANISM: AAY-6  
US-09-807-802A-19

Query Match 100.0%; Score 4683; DB 3; Length 4683;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2221 GTTATCTTCAAGATTTGGCTGAGAGCAACTCTCTGAGGGCAATTCGCGAGTGGGAGCT 2280  
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Dh 2281 TGAACCTGAGGCGCCCAAAACCAAGACCAACAGCAAAAGCAGAGCAGCGCGGGGTC 2340  
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Dh 2341 TGGTCTTCTCGGTCAAGATGACTTGGACCTTTCAAAGGACTTGAACAGAGGAGGAGCTCG 2400  
Qy 2401 TGAAGCTTCTCGGTCAAGATGACTTGGACCTTTCAAAGGACTTGAACAGAGGAGGAGCTCG 2460  
Dh 2401 TGAAGCTTCTCGGTCAAGATGACTTGGACCTTTCAAAGGACTTGAACAGAGGAGGAGCTCG 2460

Qy 2461 CGGGTACAAATCCGTAACCTGCGGTATTAACACGCGGACGCGAGTTTCAGGAGCGTCTGC 2520  
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| | | | |  
Db 2521 AAGAAATATGCTCTTTTGGGGGCAACCTCGGCGAGCAGTCTTCCAGGCCCAAGAAAGAGG 2580  
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| | | | |  
Db 2581 TTCTCGAACTTTTGGTCTGGTGTGAGGAGGAGGCTTAACCGGCTCTCGGAAAGAAACCTC 2640  
Qy 2641 CGGTAGAGCAGTCCGCAACAAGCAGACTCTCTCGGCAATTGGCAAGACGCGCAGC 2700  
| | | | |  
Db 2641 CGGTAGAGCAGTCCGCAACAAGCAGACTCTCTCGGCAATTGGCAAGACGCGCAGC 2700  
Qy 2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAAGCTGGGCACTCAGAGTCAGTCCCGAC 2760  
| | | | |  
Db 2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAAGCTGGGCACTCAGAGTCAGTCCCGAC 2760  
Qy 2761 CACAACTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGAGCTTACATATGCTT 2820  
| | | | |  
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Qy 2821 CAGGCGGTGGGCGACCAATGGCAGCAATTAAGAAAGCGCGCAGCGAGTGGGTATGCT 2880  
| | | | |  
Db 2821 CAGGCGGTGGGCGACCAATGGCAGCAATTAAGAAAGCGCGCAGCGAGTGGGTATGCT 2880  
Qy 2881 CAGAAATTTGGCATTTGCGATTTCCACATGGCTGGGCGAGAGTATCAACAACGACCC 2940  
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Qy 2941 GAAATGGGCGCTTGGCCCACTTAAACAACAACCTTCAACAAGAAATCTCCAGTGTCTAA 3000  
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| | | | |  
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Qy 3421 GAACGGGCAATTAATCTTACCTTCAAGCTACACCTTTCGAGAGCGTCTTTTCCACAGCAGCT 3480  
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| | | | |  
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Qy 3721 GTGCTTCAAAATATTAATGAGGAGTGAATCTATTAATCAACCTGGCAGCTGTATG 3780  
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Qy 3841 AGGAGAGCGCGGAGCTTCAACACTGCATTGGAACAATGTATGATCAAGACGAGAGG 3900  
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Db 3841 AGGAGAGCGCGGAGCTTCAACACTGCATTGGAACAATGTATGATCAAGACGAGAGG 3900  
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Db 3901 AAATCAAAAGCCACTAACCCCGTGGCCACCGAAATTTGGGACTGTGGCAGTCAATCTCC 3960  
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Db 3961 AGACAGCAGCAGACGACCTTGGCAGCGGAGTGTGATGTTATGGAGACCTTACCTGAA 4020  
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Qy 4621 TCTGCGACCTTTGCTTGGTCCGAGGCCCAACGAGCAGCAGCGCATAGAGGAGTGGC 4680  
| | | | |

D	b		4621	TCTCCGACACTTTCGTCCCGAGGGCCCCACCGAGCGAAGCCGCATTAAGGAATTGGC	4680
O	y		4681	CAA 4683	
D	b		4681	CAA 4683	
RESULT 2					
US-09-807-802A-1					
; Sequence 1, Application US/09807802A					
; Patent No. 6759237					
; GENERAL INFORMATION:					
; APPLICANT: Wilson, James M.					
; APPLICANT: Xiao, Weidong					
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences					
; FILE REFERENCE: Vectors and Host Cells Containing Same					
; CURRENT APPLICATION NUMBER: US/09/807, 802A					
; PRIOR FILING DATE: 2002-02-21					
; PRIOR APPLICATION NUMBER: US 60/107,114					
; PRIOR FILING DATE: 1998-11-05					
; PRIOR APPLICATION NUMBER: PCT/US99/25694					
; NUMBER OF SEQ ID NOS: 20					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 1					
; LENGTH: 4718					
; TYPE: DNA					
; ORGANISM: AAV-1					
; FEATURE:					
; NAME/KEY: CDS					
; LOCATION: (335)..(2206)					
; OTHER INFORMATION:					
; FEATURE:					
; NAME/KEY: CDS					
; LOCATION: (2223)..(4430)					
; OTHER INFORMATION:					
US-09-807-802A-1					
Query Match                      90.8%; Score 4253.2; DB 3; Length 4718;					
Beat Local Similarity    94.7%; Pred. No. 0;					
Matches 4471; Conservative    0; Mismatches 208; Indels    43; Gaps    5;					
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D	b		1	TTGGCCAATCCCTCTCTGCGCGCTGCGTCACTGAGCGGGGCTCGGACCAAAGTCCGC	60
O	y		61	CGAGCCGCCGGGCTTGGCCCGGGCGGCTCAGTAGCGAGCGAGCGCGCAGAGAGGAGTG	120
D	b		61	AGAGCGCAGAGCTGTGCTCTCCCGGCCCAACCGACGACGAGCGCGCAGAGAGGAGTG	120
O	y		121	GCCAACTCATCTAGAGGGT-----TCCTGAGGGGTGAGTGTGA	163
D	b		121	GGAACCTCATCTAGAGGGTAAATCGAAGCGCTCCACGCTGCGCGCTCAGCGCTGA	180
O	y		164	CGTGAATTACGTCAATAGGTTAAGGAGGTCTGTATTAGAAGTACAAGTAGTG--TTTTC	222
D	b		181	CGTAATAATGCTCANAGG---GAGTGTCTGTATTAGCTGTACAAGTAGTGCTTTTTC	237
O	y		223	GACATTTTGCACACCAATGTGTACAGCTGGGTATTAAAGCCCGAGTAGACACAGAGGT	282
D	b		238	GACATTTTGCACACCAAGTGTGCACTTAGGTTAATATATGSCCGAGTAGAGCAGAGAT	297
O	y		283	CTCCATTTTGAAGCGGAGGTTTGAACGCGCAGCGCCATGCGGGGTTTTACAGATTTG	342
D	b		298	CTCCATTTTGAACCGGAATTTGAACGACGACGACCATGCGGGCTTTACAGAGATCGT	357
O	y		343	GATTAAGGTCCCACGCGCACTTTGAAGAGCATCTGACCGGCACTTTCTGACAGCTTTGGAA	402
D	b		358	GATCAAGGTGCCAGCACCTGAGCAGACACTTCCGGGCACTTTCTAATCTGTTTGTGAG	417
O	y		403	CTGGGTGGCCGAGAAGAAATGGAGTTGCGCCACGATTTCTGACATGGAATCTGAATCTGAT	462

Db	418	CTGGGTGGCGAGAAAGAAATGGAGCTGCCCCCGGATTTGACATGATCTGAATCTGAT	477
OY	463	TGAGCAGGCAACCCCTTGAACCGTGGCCCGAGAAAGCTGACAGCGGACCTTCTTGCTCCATGGCG	522
Db	478	TGAGCAGGCAACCCCTTGAACCGTGGCCCGAGAAAGCTGACAGCGGACCTTCTTGCTCCATGGCG	537
OY	523	CCGGGTAGTAAGGCCCCCGGAGGCCCTTCTTGTGTTCAAGTTCAGAGAAGGCCAGTCTTA	582
Db	538	CCGGGTAGTAAGGCCCCCGGAGGCCCTTCTTGTGTTCAAGTTCAGAGAAGGCCAGTCTTA	597
OY	583	CTTCCACCTCCATATTTCTGTGAGAGACCAACGGGGGTCAAAATCCAATGCTCTGGCCGCTT	642
Db	598	CTTCCACCTCCATATTTCTGTGAGAGACCAACGGGGGTCAAAATCCAATGCTCTGGCCGCTT	657
OY	643	CTGAGTCAGATTATAGGACAAAGCGTGGTGCAGACCATATCACCGGGGATTCGAGCGGACCT	702
Db	658	CTGAGTCAGATTATAGGACAAAGCGTGGTGCAGACCATATTCACCGGGGATTCGAGCGGACCT	717
OY	703	GCCCAACTGGTTCGGGTGACCAAGACGCGTAAATGGCGCCGAGGGGGGAAACAAGTGGT	762
Db	718	GCCCAACTGGTTCGGGTGACCAAGACGCGTAAATGGCGCCGAGGGGGGAAACAAGTGGT	777
OY	763	GGAGGATGCTACATCCCCCAATPACCTTCGCGCCACATCAAGCCGGAAGTGCAGTGGGC	822
Db	778	GGAGGATGCTACATCCCCCAATPACCTTCGCGCCACATCAAGCCGGAAGTGCAGTGGGC	837
OY	823	GTGACCTAACATGAGAGAGATATATAAGCGGTGTTTAAACTTGCCGACGAGCAACCGCT	882
Db	838	GTGACCTAACATGAGAGAGATATATAAGCGGTGTTTAAACTTGCCGACGAGCAACCGCT	897
OY	883	CGTGGCGGACGACTGACCCACGCTCAGCGAGACCAGAGACGAAACAAGGAATCTGAA	942
Db	898	CGTGGCGGACGACTGACCCACGCTCAGCGAGACCAGAGACGAAACAAGGAATCTGAA	957
OY	943	CCCCAATTCTGACGCGCGCTGTCAATCCGAGTAAAAACTCCGACGCTACATATGAGCTGCT	1002
Db	958	CCCCAATTCTGACGCGCGCTGTCAATCCGAGTAAAAACTCCGCGGCTACATGAGCTGCT	1017
OY	1003	CGGGTGGCTGTGGACCGGGGACATCACTTCGAGAGACATGATCCAAGAGACGAGGC	1062
Db	1018	CGGGTGGCTGTGGACCGGGGACATCACTTCGAGAGACATGATCCAAGAGAGACGAGGC	1077
OY	1063	CTCGTACATCCTCTTCAACGCGCGCTCAACTCGCGGATCCCAAGTCAAAAGCCGCTCGGA	1122
Db	1078	CTCGTACATCCTCTTCAACGCGCGCTCAACTCGCGGATCCCAAGTCAAAAGCCGCTCGGA	1137
OY	1123	CAATGCGGGCAAGATCAATGCGCTGACCAAAATCCGCGCCGACTTACTGTGAGGCCCGC	1182
Db	1138	CAATGCGGGCAAGATCAATGCGCTGACCAAAATCCGCGCCGACTTACTGTGAGGCCCGC	1197
OY	1183	TTCGCGCCGCGACATTAAACCAACCGGATTTACCGCATCTTGAGAGCTGAAACGGCTACGA	1242
Db	1198	TTCGCGCCGCGACATTAAACCAACCGGATTTACCGCATCTTGAGAGCTGAAACGGCTACGA	1257
OY	1243	CCCTGCGCTACGCGCGCTCCGCTCTTCTTCGCGCTGGGCGCAAGAAAAGTTTCGAAAAACGCAA	1302
Db	1258	ACCTGCTTACGCGCGGCTCCGCTCTTCTTCGCGCTGGGCGCAAGAAAAGTTTCGAAAAACGCAA	1317
OY	1303	CACCATCTGCTGTTTGGGCCGCGCACACGCGGACAGACCAACATCCCGGAAAGCATATCGC	1362
Db	1318	CACCATCTGCTGTTTGGGCCGCGCACACGCGGACAGACCAACATCCCGGAAAGCATATCGC	1377
OY	1363	CCAGCGCGTGCCTTTCATACGCGCTGCGCATCTGGACCAATGAGAACTTTCCTTCAACGA	1422
Db	1378	CCAGCGCGTGCCTTTCATACGCGCTGCGCATCTGGACCAATGAGAACTTTCCTTCAATGA	1437
OY	1423	TTTGGCTGACAAAGATGATCTTGCTGGTGGAGAGAGGCAAGATGACGCGCAAGTCTGAGA	1482
Db	1438	TTTGGCTGACAAAGATGATCTTGCTGGTGGAGAGAGGCAAGATGACGCGCAAGTCTGAGA	1497
OY	1483	GTCCGCCAAGGCCATTCTCGCGCGGACGACAGTGCCTGTGACCAAAAAGTGCAAAGTGGTC	1542
Db	1498	GTCCGCCAAGGCCATTCTCGCGCGGACGACAGTGCCTGTGACCAAAAAGTGCAAAGTGGTC	1557

QY 1543 CGCCAGATCGATCCACCCCGGTGATGTCATCTCCAAACACCAATATGTGCGGTAT 1602  
Db 1558 CGCCAGATCGATCCACCCCGGTGATGTCATCTCCAAACACCAATATGTGCGGTAT 1617  
QY 1603 TGAACGGAACAGACCACTTTCAGACACAGACCGTTTCAGACACCGATTTCAATT 1662  
Db 1618 TGACGGGAACAGACCACTTTCAGACACAGACCGTTTCAGACACCGATTTCAATT 1677  
QY 1663 TGAATCTACCCGCGCTTCGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGA 1722  
Db 1678 TGAATCTACCCGCGCTTCGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGA 1737  
QY 1723 GTTCTTCGCTGGGGGAGGATCAGGTGACGAGGTGGGCGATGATTTCTAGTCAAGA 1782  
Db 1738 GTTCTTCGCTGGGGGAGGATCAGGTGACGAGGTGGGCGATGATTTCTAGTCAAGA 1797  
QY 1783 GGGTGGAGCCAAACAAGACCCCGCGATGACCGGATTAAGCGAACCGGAGCGG 1842  
Db 1798 GGGTGGAGCCAAACAAGACCCCGCGATGACCGGATTAAGCGAACCGGAGCGG 1857  
QY 1843 CTGCCCCCTCAGTCGGGATCCATCGACGTCAAGCGGGAAGAGCTCCGGTGAATTTGC 1902  
Db 1858 CTGCCCCCTCAGTCGGGATCCATCGACGTCAAGCGGGAAGAGCTCCGGTGAATTTGC 1917  
QY 1903 CGACAGGTACCAAAACAATGTTCTGTCACGCGGGGCAATGCTTCAGATGCTTTCCCTG 1962  
Db 1918 CGACAGGTACCAAAACAATGTTCTGTCACGCGGGGCAATGCTTCAGATGCTTTCCCTG 1977  
QY 1963 CAAAACATGCGAGAAATGAATCAGAAATTTCAACATTTGCTTCACGCAACGAGACAGAGA 2022  
Db 1978 CAAAGCATGCGAGAAATGAATCAGAAATTTCAACATTTGCTTCACGCAACGAGACAGAGA 2037  
QY 2023 CTGTTTCAGAAATGTTCCCGGCGGTCTCAGAACTTCAACCGGTCTGTCAGAAAGAGAGCTA 2082  
Db 2038 CTGTTTCAGAAATGTTCCCGGCGGTCTCAGAACTTCAACCGGTCTGTCAGAAAGAGAGCTA 2097  
QY 2083 TCGGAAATCTGTGCTATTCATCATCTGTGGGGGCGGCTCCCGGATTTGCTTGTGGG 2142  
Db 2098 TCGGAAATCTGTGCTATTCATCATCTGTGGGGGCGGCTCCCGGATTTGCTTGTGGG 2157  
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QY 2203 CAGGATGCTGCGGATGCTTAATCTTCCAGATTTGCTTCAGAGCAAACTCTCTGAGGCA 2262  
Db 2218 CAGGATGCTGCGGATGCTTAATCTTCCAGATTTGCTTCAGAGCAAACTCTCTGAGGCA 2277  
QY 2263 TTTCCGAGTGGTGGGACTTGAACCTGAGACCCGAAACCCAAAGCCAAACAGAGCAAGC 2322  
Db 2278 TTTCCGAGTGGTGGGACTTGAACCTGAGACCCGAAACCCAAAGCCAAACAGAGCAAGC 2337  
QY 2323 AGACGACGCGCGGCTGTGCTTCTGTGCTACATTAATCTCGAACCTTTCACGAGC 2382  
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QY 2383 TCGACAGGGGAGCGCTCAACGCGGCGATGACGCGGCTTCGAGCAACAGGCGCT 2442  
Db 2398 TCGACAGGGGAGCGCTCAACGCGGCGATGACGCGGCTTCGAGCAACAGGCGCT 2457  
QY 2443 ACAGACAGCAGCTCAAAAGCGGCTGCAATCCGTCATCTGCGGTATTAACACCGCGAGCG 2502  
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QY 2503 AGTTTCAGAGCCTGTGCAAGAAATAGTCTTTTGGGGGCAACCTCGGGGAGAGCTCT 2562  
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QY 2563 TCCAGGCGCAAGAGAGGCTTTCGAACCTTTTGGTCTGTTGAGGAAGTGTAAAGAGC 2622  
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QY 2623 CTCTGGAAGAAAGCTCCGGTAGAGCAGTCCGCCAAGAGCAGACCTCTCTCGGCA 2682  
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QY 3103 GACTCATTAACAACAATTTGGGATTTCCGGCCCAAGAGACTCACTTCAAGCTTTCAACA 3162  
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Db 3658 TACTGGAACCTGTTTACCGGAGAGCGGCTTTTAAACAAACAAAGACAAACA 3717  
QY 3703 GCAACTTACCTGAGCTGAGTCTTCAAAATATTAACCTTAATGGGCTGAATCTATATCA 3762

Db 3718 GCAATTTTACCTGGAGCTGGTGTCTTCAAAATATACTCAATGGGGGTGAATTCATCATCA 3777  
Qy 3763 ACCCTGGACACTGCTATGGCTCTCACCAAAAGACGAACAAAGATGTTCTTCCCATGAGCG 3822  
Db 3778 ACCCTGGACACTGCTATGGCTCTCACCAAAAGACGAACAAAGATGTTCTTCCCATGAGCG 3837  
Qy 3823 GTGTCAATATTTTGGAAAGAGAGCGCGGAGCTTCAACACATGCTATGGACATGTC 3882  
Db 3838 GTGTCAATATTTTGGAAAGAGAGCGCGGAGCTTCAACACATGCTATGGACATGTC 3897  
Qy 3883 TGATCAGACGAGAGAGAAATCAAAAGCCTAAACCCCGTGGCCACCGAAAGATTGGGA 3942  
Db 3898 TGATTCACAGAGAGAGAAATTAAGCCACTAACCCGTGGCCACCGAAAGATTGGGA 3957  
Qy 3943 CTGTGGCAGTCAATCTCCAGAGCAGACAGACCCCTGGACCGGAGATGTCATGTA 4002  
Db 3958 CCGTGGCAGTCAATTTCCAGAGCAGACAGACCCCTGGACCGGAGATGTCATGTA 4017  
Qy 4003 TGGAGACCTTACCTGGAATGGTGTGGCAAGACAGAGAGTAACTGTGAGGGTCTATTT 4062  
Db 4018 TGGAGAGCTTACCTGTGAGTGTGTGGCAAGATAGAGAGTGTACCTGAGGGTCCATTT 4077  
Qy 4063 GGGCCAAAATTCCTCACAAGAGTGGACACTTTCACCCGCTCTCTCTCAATGGGCGGCTTTG 4122  
Db 4078 GGGCCAAAATTCCTCACAAGAGTGGACACTTTCACCCGCTCTCTCTCAATGGGCGGCTTTG 4137  
Qy 4123 GACTTAAGCACCCTGCTCTCAGATCCCTCATCAAAAACAGCGCTTTCTTCTCGAATCTTC 4182  
Db 4138 GACTTAAGAACCCGCTCTCTCAGATCCCTCATCAAAAACAGCGCTTTCTTCTCGAATCTTC 4197  
Qy 4183 CGGAGAGTTTTCGGCTACAAAGTTTGCTTCAATTCACCCAGTATCCACAGAGCAAG 4242  
Db 4198 CGGAGAGTTTTCAGAGTATCAAAAGTTTGCTTCAATTCACCCAGTATCCACAGAGCAAG 4257  
Qy 4243 TGAAGCTGAGATGGAATGGAGCTGCGAAGAAAGAAACAGCAACGCTGGAATCCGAG 4302  
Db 4258 TGAAGTGGAAATGGAATGGAGCTGCGAAGAAAGAAACAGCAACGCTGGAATCCGAG 4317  
Qy 4303 TGCAGTATACATCTAATCAATGCAAAATGCGCAACGTTGATTTTCACTGTGAGCAACAATG 4362  
Db 4318 TGCAGTATACATCTAATGCAAAATGCGCAACGTTGATTTTCACTGTGAGCAACAATG 4377  
Qy 4363 GACTTATATAGAGCTGCGCCCATGAGCAACCGCTTACCTCACCGCTCCCTGTAAATGT 4422  
Db 4378 GACTTATATAGAGCTGCGCCCATGAGCAACCGCTTACCTCACCGCTCCCTGTAAATGT 4437  
Qy 4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAATGGAATTTGGTCTCATGTCTTATTA 4482  
Db 4438 GTGTTAATCAATAAACCGGTTAATTCGTGTCAATGGAATTTGGTCTCATGTCTTATTA 4497  
Qy 4483 TCTTATCTGTCATCATAGCAACCGGTTAATTCATTAATGCTTGTGGTCTGGCGA - 4510  
Db 4498 TCTTATCTGTCATCATAGCAACCGGTTAATTCATTAATGCTTGTGGTCTGGCGA - 4556  
Qy 4541 -----ATAACCTAGTATGAGTGGCCACTCCCTCTATGCGCGC 4581  
Db 4557 AAAAGACTTACGTCATCGGGTTAACCTCTAGTATGAGTGGCCACTCCCTCTCTGCGCGC 4616  
Qy 4582 TCGCTCGCTCGGTGGGGCGCGGACAGAGAGCTTGCCTGCGGACCTTTGGTCCGA 4641  
Db 4617 TCGCTCGCTCGGTGGGGCGCTGCGGACAAAGGTCCGAGAGCGGAGAGCTGTGCTGCC 4676  
Qy 4642 GGGCCCAACGAGCGAGCGGAGCGCGATGAGGAGATGGCCAA 4683  
Db 4677 GGGCCCAACGAGCGAGCGGAGCGCGAGAGGAGTGGGCAA 4718

RESULT 3  
US-10-038-972A-12  
; Sequence 12, Application US/10038972A  
; Patent No. 6962815  
; GENERAL INFORMATION:

APPLICANT: J. Bartlett  
; TITLE OF INVENTION: AAV VECTORS AND METHODS  
; FILE REFERENCE: 28335/36996US  
; CURRENT APPLICATION NUMBER: US/10/038,972A  
; PRIOR APPLICATION NUMBER: US 60/260,124  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 4679  
; TYPE: DNA  
; ORGANISM: adeno-associated virus 2  
US-10-038-972A-12

Query Match 70.4%; Score 3296.2; DB 3; Length 4679;  
Best Local Similarity 82.5%; Pred. No. 0; Mismatches 803; Indels 20; Gaps 7;  
Matches 3868; Conservative 0;

Qy 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTAGAGCCGGGCGAACCAAGTCCGCC 60  
Db 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTAGAGCCGGGCGAACCAAGTCCGCC 60  
Qy 61 CGAGCGCCGGGCTTTGCGCGCGGCTCTCATGTAGCGAGCGCGCAGAGAGGAGTG 120  
Db 61 CGAGCGCCGGGCTTTGCGCGCGGCTCTCATGTAGCGAGCGCGCAGAGAGGAGTG 120  
Qy 121 GCCAATCCCATCACTAGGGGTTCTGAGAGGGGTGAGAGTGTGTAAGTATTAATGATAG 180  
Db 121 GCCAATCCCATCACTAGGGGTTCTGAGAGGGGTGAGAGTGTGTAAGTATTAATGATAG 180  
Qy 181 GGTAGGAGAGTCTGTATTAGAGTCACTGAGTGTGTCGACATTTTGCACACAT 240  
Db 181 GGTAGGAGAGTCTGTATTAGAGTCACTGAGTGTGTCGACATTTTGCACACAT 240  
Qy 241 GTGTCAAGCTGGGTATTTAAGCCCGAGTACGACCGAGGTTCCATTTTGAAGCGGGA 300  
Db 241 GTGTCAAGCTGGGTATTTAAGCCCGAGTACGACCGAGGTTCCATTTTGAAGCGGGA 300  
Qy 301 GGTTTGAACCGCGAG -CGCCATGCGGGGGTTTACAGATTTGATTAAGTCCCGCAGC 359  
Db 301 GGTTTGAACCGCGAGCGCCGATCGGGGGTTTACAGATTTGATTAAGTCCCGCAGC 360  
Qy 360 ACCTTGACGAGCATCTGCCCGGCAATTTCTGACAGCTTTGTGAACCTGGTGGCGAGAGG 419  
Db 361 ACCTTGACGAGCATCTGCCCGGCAATTTCTGACAGCTTTGTGAACCTGGTGGCGAGAGG 420  
Qy 420 AATGGAGTTGCCCGCAGATTCTGACATGATCTGAATCTGAATTTGACAGGACCCCTGA 479  
Db 421 AATGGAGTTGCCCGCAGATTCTGACATGATCTGAATCTGAATTTGACAGGACCCCTGA 480  
Qy 480 CCGTGGCGGAGAGCTGACGCGGACCTTCTGGTCCACTGGCGCGCGGTGAAGGAGCC 539  
Db 481 CCGTGGCGGAGAGCTGACGCGGACCTTCTGGTCCACTGGTCCACTGGTGAAGGAGCC 540  
Qy 540 CGAGGCGCTCTTCTTTGTTCAAGTTCAGTTCAGAGAGGCGAGTCTTCACTTCCATCATTT 599  
Db 541 CGAGGCGCTCTTCTTTGTTGTTCAAGTTCAGTTCAGAGAGGCGAGTCTTCACTTCCATCATTT 600  
Qy 600 TGTGTGAGACCAAGGGGTCAATTCATGTGCTGGGCGCTTCTGAGTCAATTAAGC 659  
Db 601 TGTGTGAGAACCAAGGGGTCAATTCATGTGCTGGGCGCTTCTGAGTCAATTAAGC 660  
Qy 660 ACAAGCTGTGACAGCATCTACCGGGGATTCGAGCGGACCCGTCGCAATGGTTCGCGG 719  
Db 661 ACAAGCTGTATCAGAGATTTTACCGGGGATTCGAGCGGACCCGTCGCAATGGTTCGCGG 720  
Qy 720 TGAACCAAGAGCGGTATGCGCGGAGAGGGGGAACAAGTGTGAGAGAGTCTACATCC 779  
Db 721 TGAACCAAGAGCGGTATGCGCGGAGAGGGGGAACAAGTGTGAGAGAGTCTACATCC 780  
Qy 780 CCAACTCTCTGCGCCCAAGACTGAGCGGAGCTGAGTGGGGTGAATTAACATGAGG 839



Dh 781 CCAATTACTTGTCCCAAAACCAGCTGAGCTCCAGTGGCGTGAATAATGGAAC 840  
Qy 840 AGTATATAAGGGGTGTTAAACCTGGCCGAGCGCAAAAGCGTCCGGGGCGACGACTGA 899  
Db 841 AGTATTTAAGCCCTGTGTTGAATCTCACGAGCGTAAACGTTGGTGGCGAGACTGGA 900  
Qy 900 CCCAGTCAGCCAGACCCAGAGACGAACAAGAGATCTGAACCCCAATTTCTGACGCG 959  
Db 901 CGCAGGTGCGAGACGAGAGCGAACAAGAAATAGAAATCCCAATTTCTGATGGCC 960  
Qy 960 CTGTATCTCGGTCAAAAACCTCCGCACTGACATGAGCTGTGCGGTGGTGTGAGCC 1019  
Db 961 CGGTATCATGATCAAAAACCTTACGCGGTAATGAGCTGGTGGGTGGTCTGTGACA 1020  
Qy 1020 GGGGATCATCTCCAGAAAGCATGGAATCCAGAGAGAACAGGCTCTGTATCTCTTCA 1079  
Db 1021 AGGGATTAACCTCGAGAAAGCATGATCAAGAGAACAGGCTCTATCATCTCTTCA 1080  
Qy 1080 AGCGCGCTCAACTCGCGGTCCAGATCAAGCGCTGTGACAATGCGGCAAGATCA 1139  
Db 1081 ATGCGGCTCCAACTCGCGGTCCCAATCAAGGCTGTCTTGAACAATGCGGAAAGATTA 1140  
Qy 1140 TGGCGCTGACCAAACTCGCGCCGACTACCTGTAGGCCCCGCTCGCCCGCGACATTA 1199  
Db 1141 TGAGCTGACTAAACCGGCCCCGACTACTGTGGGCCAGACGCCGTGGAGACATTT 1200  
Qy 1200 AAACCAACCGCATTTAACCGCATCTGTGAGCTGAACGGCTACGACCTGTGCTACGCGGCT 1259  
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Qy 1260 CCGTCTTTCTCGGCTGGGCCCCAGAAAAGGTTGCGAAAACGAAACCAATCTGGCTGTTTG 1319  
Db 1261 CCGTCTTTCTGGGATGGGCGACGAAAAGTTGGCGAAGAGAACACATCTGTGCTTTG 1320  
Qy 1320 GGGCGGCAACACGGGCAAGACCAATCGCGAAAGCAATGCGCACGCGGCTGCTTCT 1379  
Db 1321 GGGCTGCAACTCCGGGAAAGCAACATCGCGAGGCCATAGCCCACTGTGCTTCT 1380  
Qy 1380 ACGGTGGGTCACTGGAACCAATGAGAACTTCTCTTCAACGATTTGCGTCAAGATGG 1439  
Db 1391 ACGGTGGGTAACTGGAACCAATGAGAACTTCTCTTCAACGATTTGCGTCAAGATGG 1440  
Qy 1440 TGATCTGGTGGAGAGGCAAGATGACGCGCAAGGTGCTGAGTCCGCGCAAGCATTC 1499  
Db 1441 TGATCTGGTGGAGAGGCAAGATGACGCGCAAGGTGCTGAGTCCGCGCAAGCATTC 1500  
Qy 1500 TCGCGGCAACAGGTGCGCGTGAACCAAAAGTGCAGTCTGCTCCGCGCAAGTCAATCCA 1559  
Db 1501 TCGGAGGAAGCAAGGTGCGCGTGAACCAAAAGTGCAGTCTGCTCCGCGCAAGTCAATCCA 1560  
Qy 1560 CCCCCTGATCGTCACTTCCAAACCAACATGTGCGCGTGAATTAACGGAACAGACCA 1619  
Db 1561 CTCCGCTATCGTCACTTCCAAACCAACATGTGCGCGTGAATTAACGGAACCTCAACGA 1620  
Qy 1620 CTTTGAGACACAGGACGCTTGAGAGACCGGATGTTCAAAATTTGAATCTCAACGCGCTC 1679  
Db 1621 CTTTGAGACACAGGACGCGCTTGAGAGACCGGATGTTCAAAATTTGAATCTCAACGCGCTC 1680  
Qy 1680 TGGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCTTTCGCTGGGCGC 1739  
Db 1681 TGGAGCATGACTTTGGCAAGGTGACCAAGCAGAAAGTCAAAAGACTTTTTCGCGTGGGCA 1740  
Qy 1740 AGGATCAAGTGAACGAGTGGCGCATGATTTACTAGTCAAGAAAGGTGAGCGCAACACA 1799  
Db 1741 AGGATCAAGTGGTGAAGTGAAGCATGATTTCTAGTCAAAAAGGTGAGCGCAAGAAA 1800  
Qy 1800 GACCGCCCGGATGACCGGATTAAGCGAGCCCAAGCGGCTGCGCTCACTGCGCGG 1859  
Db 1801 GACCGCCCGGATGACCGAGATTAAGTGAAGCGCAAGCGGCTGCGAGTCAAGTGGCG 1860  
Qy 1860 ATTCATGAGCTGAGCGGAGAGAGCTCGGTGGAATTTGCGCGACAGATCAAAAACA 1919  
Db 1861 AGCCATTCAGCTGAGAGCGCGGA--AGCTTGATCACTACGACAGATCAAAAACA 1917

Qy 1920 AATGTTCTGTCAGCGGGGCAATGCTTCAGATGCTGTTCCCTGCAAAACATGCCGAGAA 1979  
Db 1918 AATGTTCTGTCAGCGGGGCAAGAACTGAATGCTGTTCCCTGCAAAACATGCCGAGAA 1977  
Qy 1980 TGAATCAGAAATTTCAACTTTGCTTTCAGCGACCGGACGAGACTGTTCAAGATGTTCC 2039  
Db 1978 TGAATCAGAAATTTCAAAATCTGCTTCACTCAACGACAGAAAGACTGTTAAGAGCTTTC 2037  
Qy 2040 CCGGCTGTCAAGATCTCAACCGGT--CGTCAGAAAGAGACGATTCGAAACTGTGTG 2096  
Db 2038 C---CGTTCAGAAATCTCAACCCGTTTCTGTCTGTCATAAAAAGCGGATCAAGAACTGTCT 2094  
Qy 2097 CCAATTCATCTGTGTGGGGGGGGTCCCGAGATTTGCTGCTCGGCTCGCATCTGTCTCA 2156  
Db 2095 ACATTCATCATATCATGAGAAAGGTCAGA--CGTTGCACTGCTGCGCATCTGTCTCA 2151  
Qy 2157 ACGTGAATCTGGAATGACTGTGTTCTGAGCAATAAATGACTTTAAACAGATATGGCTGCC 2216  
Db 2152 ATGTGATTTGATGATGATGATCTTGTGAACAATTAATTAATTAATGATGATGCTGCC 2211  
Qy 2217 GATGTTATCTTCCAGATTTGCTCGAGACAACTCTCTGAGGGCATTTGCGCATGTGTGG 2276  
Db 2212 GATGTTATCTTCCAGATTTGCTCGAGACAACTCTCTGAGAAATTAAGACAGTGTGG 2271  
Qy 2277 GACTTGAAACCTGAGAGCCCCGAAACCCAAAGCCAAACGACGAAAGCAGAGACGCGCG 2336  
Db 2272 AAGCTCAACCTGCGCCACCAACCAAGGCTCGAGCGGCAATTAAGAGACAGACGAG 2331  
Qy 2337 GGTCTGCTGCTTCTGCTGCTAACAATACCTCGGACCTTCAACGAGACTGACAAAGGGAG 2396  
Db 2332 GGTCTGCTGCTTCTGCTGCTAACAATACCTCGGACCTTCAACGAGACTGACAAAGGGAG 2391  
Qy 2397 CCGTCAACGCGCGGATGACAGCGGCTCTCGAGACGACAAAGGCTTACGACGAGCTC 2456  
Db 2392 CCGTCAACGAGGAGAGAGCGCGGCTCTCGAGACGACAAAGGCTTACGACGAGCTC 2451  
Qy 2457 AAAGCGGTGACATCCGCTACCTGCGATTAACAACGCGGAGCGCGAGTTTCAAGAGGCT 2516  
Db 2452 GACAGCGGAGCAACCGCTACCTCAAGTAAACAACGCGGAGCGGAGTTTCAAGAGGCT 2511  
Qy 2517 CTGCAAGAAAGATAGTCTTTTGGGGGCAACCTCGGGGAGAGAGTCTTCAAGGCCAAGAG 2576  
Db 2512 CTTAAAGAAAGATAGTCTTTTGGGGGCAACCTCGGAGAGAGTCTTCAAGGCCAAGAG 2571  
Qy 2577 AGGTTCTGAACTTTTGTGCTGTGAGGAGGTGTAAGACGCTCTGGAAGAA 2636  
Db 2572 AGGTTCTGAACTTTGAGGCTGTGAGGAACTGTTAAGACGCTCCGGAAGAAAG 2631  
Qy 2637 CGTCCGTAAGAGCTGCGCCCAAGAGACGACATCTCTTGGGCAATTTGCAACAGGC 2696  
Db 2632 AGGCGGTAAGCACTCTCTGTGAGGCAACATCTCTTGGGAAACGGAAGCGGCG 2691  
Qy 2697 CAGCAGCCCGCTAAAGAGACTCAATTTTGTGAGACTGAGACTGAGTCACTGATCCCC 2756  
Db 2692 CAGCAGCTCGAAGAAAGATTAATTTTGTGAGACTGAGAGCGAGACTGATCACT 2751  
Qy 2757 GACCCACAACTCTCGAGAACTTCAGCAACCCCGCTGCTGTGGAACCTAACAATG 2816  
Db 2752 GACCCACAACTCTCGAGAACCAACAGACCCCTCTGAGTCTGGAACCTAACAATG 2811  
Qy 2817 GCTTCAAGCGGTGCGGACCAATGAGCAATAAGAGCGCGGACGAGTGGGTAT 2876  
Db 2812 GCTACAGGCAATGCGGACCAATGAGCAATAAGAGCGCGGACGAGTGGGTAT 2871  
Qy 2877 GCTCAGGAAATTTGGCATTTGCAATGCTGAGCGGACAGAGTCAATCAACAGC 2936  
Db 2872 TCTCTGGGAAATTTGGCATTTGCAATGATGAGCGGACAGAGTCAATCAACAGC 2931  
Qy 2937 ACCGAAACATGGGCTTGGCCCACTTAACAACCACTCTAACAAGCAAAATCTCAAGTCT 2996  
Db 2932 ACCGAAACATGGGCTTGGCCCACTTAACAACCACTCTAACAAGCAAAATTTCAAGC 2991

OY	2957	TCAAAGGGGGCCAGCAACGACAAACACACTCTTGGGCTACAGACACCCCTGGGGGTAATTTT	3056
Db	2992	TCA-- -GGAGGCTCGAAGCAAACTCACTTTGGCTACAGACACCCCTGGGGGTAATTTT	3048
OY	3057	GATTTCACACAGATTTCACCTGCGATTCTTCACCACTGACGGAGCGACTCATCAACAC	3116
Db	3049	GACTTCACACAGATTTCACCTGCCACTTTTCACACGTAAGTCGGCAAAAGCTCATCAACAC	3108
OY	3117	AATTGGGGATTCCGGCCCAAGAGCTCAACTTCAAGCTCTTCAACATTCACAGTCAAGAG	3176
Db	3109	AATGGGGGATTCGAGCCCAAGAGACTCAACTTCAAGCTCTTAACTCAAGTCAAGAG	3168
OY	3177	GTCACGACGATGATGGGTCACGACCACTGGCTAATAACTTACACGACGGTTCAAGTC	3236
Db	3169	GTCACGCAAGATGACGGTACGACGACGATTCACAAATACTTACACGACGGTTCAAGTC	3228
OY	3237	TTGTGCACTCGAGAGTACGAGTCCCGGACGTCTCGGCTCTGGGCAACAGGCTGCTC	3296
Db	3229	TTTATGACTCGGAGTACCAAGCTCCCGTACGTCTCGGCTGGGGCATCAAGATGCTCTC	3288
OY	3297	CCTCGGTTCCCGGGGACGTGTTCAATGATTCGAGTACGGCTACCTAACGCTCAACAT	3356
Db	3289	CCGCGGTTCCGAGCAGACGTCTTATGATGGCACAGTATGGATACCTCAACCTGAACAC	3348
OY	3357	GGCAGCCAGGACAGTGGAGCGCTCATCTTTTACTGCTGGAAATTTTCCATGGCAATG	3416
Db	3349	GGGAGTCAGGACAGTACGAGCGCTCTTCAATTTTACTGCTGGAGTACTTCTCTTCAAGATG	3408
OY	3417	CTGAGAAAGGGGCAATTAACCTTACCTTGAGCTACACCTTCGAGGAGCGGCTTCCACAGC	3476
Db	3409	CTGCGTACCGGAAACACTTTACTTCACTTACACTTCTTGGAGACGTTCTTTTCAACAC	3468
OY	3477	AGCTACGGCACAGCCAGAGCGCTGAGCCGGCTGATGAATCTCTCATTCGACAGTACCTG	3536
Db	3469	AGCTACGCTCAAGCCAGACAGTCTGGACCGCTCTCATGAATCTCTCATTCGACAGTACCTG	3528
OY	3537	TATTTACTGAACAGACTCAATCATAGTCGGAAAGTCCCAAAACAAGACTTGTCTGTTT	3596
Db	3529	TATTACTTGAACAGAAACAACACTTCAAGTGAACCAACAGCAGTCAAGGCTTCAGTTT	3588
OY	3597	AGCGGTGGGTCTCCAGCTGGGATGTCTGTAGCCCAAAACGTGGACTACCTGGACCGGT	3656
Db	3589	TCTCAGGCGGAGCGAGTACATTCGGGACAGTCTAGAACTGGCTTCTGGACCGCTGT	3648
OY	3657	TACCGGCAGACGCGGTTCTTAAACAACAAAACAGACAAACAACAGCACTTTACTCTGG	3716
Db	3649	TACCGCCAGCAGCAGATCAAAAGACATCTGGGATTAACAACAACAGTAATCTGCTGG	3708
OY	3717	ACTGGTCTTCAAAATATTAACCTTAAATGGGCGTGAATCTAATTAACAACCTGGCACTGT	3776
Db	3709	ACTGAGCTTACCAAGTACCACTCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCGGGCC	3768
OY	3777	ATGGGCTCAACAAAGACGACAAAGCAAGTCTTCTCCACGACGGGTACATTTT	3836
Db	3769	ATGGGACCAACAAGACGATGAAGAAAGTTTCTTCTCAGACGGGGTCTCATCTTT	3828
OY	3837	GGAAAGAGAGCGCCGAGCTTCAAAACCTCATTTGACAATGTCAATGATCACAGAGAA	3896
Db	3829	GGGAAGCAAGGCTCAGAGAAAACAATGTGACATTTGAAGATCATGATTTACAGAGAA	3888
OY	3897	GAGGAATCAAAAGCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAT	3956
Db	3889	GAGGAATCAAGACAAACCAATCCGTGGCTACGGGACGATGTGTTCTGATCTAACAC	3948
OY	3957	CTTCAGACACAGACAGACACCTTGGCCGCGAATGTGCATGTTATGGAGCCTTAACT	4016
Db	3949	CTTCAGAGAGGCAACAGACAAGACAGCTACCGCAGATGTCACACACAACAGGGTCTTCCA	4008
OY	4017	GGAAATGCTGTGGCAAGACAGAGACGTAACTGACGGGTCTCTATTTGGGCAAAATTCCT	4076
Db	4009	GGCATGTGCTGGCAGACAGAGATGTGAATCTTCAAGGGGCCCATCTGGGCAAAATTTCCA	4068
OY	4077	CACACGATGACACTTTCACCCGTCTCTCTCATGGGCGGCTTTGACCTTAAGCACCCG	4136

[illegible]

QY 61 CGACGCCGGGCTTTGCCCGGGCGGCTTCAGTGAAGCAGCGCGCAGAGAGGGAGTG 120  
DB 61 CGACGCCGGGCTTTGCCCGGGCGGCTTCAGTGAAGCAGCGCGCAGAGAGGGAGTG 120  
QY 121 GCCAATCTCATCACTAGGAGGTTCTTGAGAGGGTGAAGTGTGACGTGAATTACGTCAATG 180  
DB 121 GCCAATCTCATCACTAGGAGGTTCTTGAGAGGGTGAAGTGTGACGTGAATTACGTCAATG 180  
QY 181 GGTTAGGAGAGTCTCTGTATTAGAGTCAAGTGAAGTTTGGCAATTTTGGCAACCAT 240  
DB 181 GGTTAGGAGAGTCTCTGTATTAGAGTCAAGTGAAGTTTGGCAATTTTGGCAACCAT 240  
QY 241 GTGGTCAAGTGGATTTTAAAGCCCGAGTGAAGCAGCGAGGCTCATTTTGAAGCGGGA 300  
DB 241 GTGGTCAAGTGGATTTTAAAGCCCGAGTGAAGCAGCGAGGCTCATTTTGAAGCGGGA 300  
QY 301 GGTTTGAACGGCAG - CGCATGCGGGGTTTACGAATTTGTGAATTAAAGTCCCAAG 359  
DB 301 GGTTTGAACGGCAGCGCATGCGGGGTTTACGAATTTGTGAATTAAAGTCCCAAG 360  
QY 360 ACCTTGAAGAGATCTGCCCGGCAATTTCTGACAGCTTTGTGAATGGGTGGCCGAAG 419  
DB 361 ACCTTGAAGAGATCTGCCCGGCAATTTCTGACAGCTTTGTGAATGGGTGGCCGAAG 420  
QY 420 AATGGAGTTGGCGCGCAGATTCTGACATGATCTGAATCTGATTGAGAGGCACCCTGA 479  
DB 421 AATGGAGTTGGCGCGCAGATTCTGACATGATCTGAATCTGATTGAGAGGCACCCTGA 480  
QY 480 CCGTGGCCGAGAGAGCTGACGCGCATCTTCTGTCTCACTGCGCGCGCTGAGTAAGGCC 539  
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QY 540 CGGAGGCCCTCTTCTTTGTTCAGTTTGAGAGGGCGAGTCTTAATTTCACTTCATATTC 599  
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QY 600 TGGTGAGAGCAGCGGGGGTCAAAATCCATGTCCTGGGCGGCTCTGTGATGAGATTAACG 659  
DB 601 TGGTGAGAGCAGCGGGGGTCAAAATCCATGTCCTGGGCGGCTCTGTGATGAGATTAACG 660  
QY 660 ACAAGCTGTGACAGCATCTTACCGCGGAGTGAAGCCGCTGCCAATGTTTCGGG 719  
DB 661 AAAAATGATTCAGAGATTTTACCGCGGAGTGAAGCCGCTTTCGCAATGTTTCGGG 720  
QY 720 TGACCAAGACGGGTATGCGCGCGAGGGGGAAACAAGTGTGAGCAAGTGTCTATCC 779  
DB 721 TGACCAAGACCAAAATGCGCGCGAGGGGAAACAAGTGTGAGTGTCTATCC 780  
QY 780 CCATCTACCTCTGCGCAAGCTCAGCGCGGCTGCAATGGGCGGTGAATTAACATGAGG 839  
DB 781 CCATCTACCTCTGCGCAAGCTCAGCGCGGCTGCAATGGGCGGTGAATTAACATGAGG 840  
QY 840 AGTATATAGCGCGTGTAAACCTGCGAGCGCAACGCTCGTGGCGACGACTGA 899  
DB 841 AGTATATAGCGCGTGTAAACCTGCGAGCGTGAACGCTGTGGCGACGACTGA 900  
QY 900 CCCACGTACGCAAGCCAGAGAGCAAGAGAGATCTGAACCCCAATTTCTGACGCGC 959  
DB 901 CGCAGTGTCCAGAGCGCAGAGAGCAAGAGAGATCTGAATCCCAATTTCTGATGCGC 960  
QY 960 CTGATCATCGGTCAAAAAATCCGCGAGCTCATGGAAGTGTGGGGTGTGAGAC 1019  
DB 961 CGGTGATCATCAAAATCTTCAAGCAGTACATGAGAGTGTGGGGTGTGAGAC 1020  
QY 1020 GGGGATCATCTCGAGAGAGAGTGAATCAGAGAGCAGAGCTCGTACATCTCTTCA 1079  
DB 1021 AGGGAGATTAATCTCGAGAGAGAGTGAATCAGAGAGCAGAGCTCATATCTCTTCA 1080  
QY 1080 ACGGCGCTTCAATCTCGGGTCTCCAGATCAAGGCGCTGTGACAAATCCGCAAGATCA 1139  
DB 1081 ATGGGCGCTTCAATCTCGGGTCTCCAAATCAAGGCGCTGTGACAAATCCGCAAGATTA 1140

QY 1140 TGGCGTGAACCAAAATCCGCGCGGCTCTACTGTAGAGCCCGGCTCCGCCGCAATTA 1199  
DB 1141 TGAAGCTGATCAAAAACGCCCCGACTACTGTGTGGGCAAGACGCGCTGAGAGCAATTT 1200  
QY 1200 AAACCAACCGCATTTTCCGCACTCTGAGCTGAACGCGTACGACCTTGCCTAACGCGCT 1259  
DB 1201 CCAGCAATCGGATTTTAAATTTTGGAACTAAACGGGTACGATCCCAATATGGGCTT 1260  
QY 1260 CCGTCTTCTCTCGGCTGGGCCCCAGAAAAGTTTCGAAAAACGCAACCATCTGCTGTTC 1319  
DB 1261 CCGTCTTCTCTGGATGGGCGACGAAAAATTCGCGCAAGAGAAACCAATCTGGCTGTTC 1320  
QY 1320 GGGCGGCAACCGAGGCAAGCAATCGCGGAAGCATGGCCAGCGCGCTGCGCTTCT 1379  
DB 1321 GGGCTGCACTACCGGGAAGCAATCGCGGAGGCGATAGCCCACTGTGCTTCT 1380  
QY 1380 ACGGCTGCTCACTGACCAATGAGAACTTTCCTTCAACGATTCGCTCGACAAAGATG 1439  
DB 1381 ACGGCTGCTCACTGACCAATGAGAACTTTCCTTCAACGATTCGCTCGACAAAGATG 1440  
QY 1440 TGAATCTGTGGAGAGAGGAGCAAGTGAACGCGCAAGTCTGTGATCTCGCCAAAGCATTC 1499  
DB 1441 TGAATCTGTGGAGAGAGGAGAAATGACCGCAAGTCTGTGATCTCGCCAAAGCATTC 1500  
QY 1500 TCGGCGGCAAGAGTGGCGGTGAGACCAAAAGTCAAGTCTGCGCCAGATCGATCCA 1559  
DB 1501 TCGGAGAGAGAGAGTGGCGGTGAGACCAAAAGTCAAGTCTGCGCCAGATCGATCCA 1560  
QY 1560 CCCCCTGATGTCACCTCCAAACCAACATGTGCGCGGTGATTTGAAGGAAACGACCA 1619  
DB 1561 CTCCTGATGTCACCTCCAAACCAACATGTGCGCGGTGATTTGAAGGAAACGACCA 1620  
QY 1620 CTTTGAACACAGACGCGCTTGAGAGACGGATGTTCAATTTGAATCAACCGCGCTC 1679  
DB 1621 CTTTGAACACAGACGCGCTTGAGAGACGGATGTTCAATTTGAATCAACCGCGCTC 1680  
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QY 4673 GGAGTGCCAA 4683
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RESULT 6
US-08-254-358-1
; Sequence 1, Application US/08254358
; Patent No. 5658785
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,358
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5658785and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-254-358-1

Query Match 69.8%; Score 3270.8; DB 2; Length 4680;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 812; Indels 21; Gaps 8;

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Qy 660 ACAAAGCTGGTGAACCACTTACCGCGGATGAGCCCACTCTGCCAATGCTTCCGG 719  
Dh 661 ACAAAGCTGGTGAACCACTTACCGCGGATGAGCCCACTCTGCCAATGCTTCCGG 720  
Qy 720 TGACCAAGACCGGTATGGCGCGGAGGGGGGAAACAAGTGTGAGAGTCAATCC 779  
Dh 721 TGACCAAGACCGGTATGGCGCGGAGGGGGGAAACAAGTGTGAGAGTCAATCC 780  
Qy 780 CCAACTTACCTCTGCGCAAGACTCAAGCCGAGCTGAGTGGCGTGAATTAAGAG 839  
Dh 781 CCAACTTACCTCTGCGCAAGACTCAAGCCGAGCTGAGTGGCGTGAATTAAGAG 840  
Qy 840 AGTATTAAGGCGCTGTTTAAACCTGCGCGAGCGCAACCGCTCGTGGCGCAACTGA 899  
Dh 841 AGTATTAAGGCGCTGTTTAAACCTGCGCGAGCGCAACCGCTCGTGGCGCAACTGA 900  
Qy 900 CCGACGTGAGCGAGCCAGAGAGCAAGAGAGATCTGAACCCCAATCTGAGCGCG 959  
Dh 901 CCGACGTGAGCGAGCGAGAGAGCAAGAGAGATCTGAACCCCAATCTGAGCGCG 960  
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Dh 961 CTGTATCCGCTCAAAAACTTCCGCAAGCTTCAATGAGCTGCTGGGTGCTGTGAGC 1020  
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Qy 1080 AGCGCGCTCCAACTCGCGGCTCCAGATCAAGAGCGCTCTGGAACAATGCGCAAGATCA 1139  
Dh 1081 AGCGCGCTCCAACTCGCGGCTCCAGATCAAGAGCGCTCTGGAACAATGCGCAAGATCA 1140  
Qy 1140 TGGCGCTGACCAATCGCGGCTCCGATCTGAGAGCGCTCGGCTCGGCGCGACATTA 1199  
Dh 1141 TGGCGCTGACCAATCGCGGCTCCGATCTGAGAGCGCTCGGCTCGGCGCGACATTA 1200  
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Dh 1201 AAACCAACCGCATTTACCGCATCTGAGCTGAGAGGCTAGACCTCTGACCGCGCT 1260  
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Dh 1321 GGGCGGACCAAGGAGCAACCACTGCGGAGAGCGATCGCCACGCTGCTTCT 1380  
Qy 1380 ACGGCTGGTGAACCTGAGCAACCACTTCTTCAAGATTTGCTGACCAAGATG 1439  
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Qy 1440 TGATCTGATGAGAGAGGAGCAAGATGACGGCCAAAGTCTGAGATCCGCCAAGCCATTC 1499  
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Qy 1500 TGGCGGACCAAGGTCGCTGAGCAACCAAGTGAAGTCTGCGCCAGATGATCCA 1559  
Dh 1501 TGGAGAGCAAGGTCGCTGAGCAACCAAGTGAAGTCTGCGCCAGATGATCCA 1560  
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Dh 2038 C---CGTGTGAGAACTCAACCGGTCTGTCTGCAAAAAGGAGTATCAAAACTGTGCT 2094  
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Dh 2392 CCGTCAACCGCGGAGTGAAGGCGCTTGAAGAGCAAGGCTTACGACAGCAGCTC 2451  
Qy 2457 AAAGCGGATGACATCGGTACTGCGGTATTAACAAGCGAGCGCGGCTTCAAGAGCGT 2516  
Dh 2452 AAAGCGGATGACATCGGTACTGCGGTATTAACAAGCGAGCGCGGCTTCAAGAGCGC 2511

OY	2517	CTGCAAGAAATACGTCCTTTTGGGGGGCAACTCTCGGGCGAGCATGTTCCAGGCCAAAGAG	25176
Db	2512	CTTAAAGAGAGTACGTCCTTTTGGGGGGCAACTCTCGGACGACAGTCCTTCCAGGCGAAAAG	251711
OY	25177	AGGGTCTTCGAACTTTTGGTCTGGTGTAGGAAAGGTGCTAAAGAGGGCTCTGGAAAAGAA	26366
Db	2512	AGGGTCTTTGAACCTCTGGGGCTGGTTAGGAACCTGTTAAAGACGGCTTCGGAAAAAAG	26311
OY	2637	CGTCCGGTAGAGCACTGCGCACACMAAGCCAGACTCTCTCGGGCATTTGGCAAGACAGGC	26396
Db	2632	AGGCCGGTAGAGCACTCTCTGTGGAGCGACAGCTCTCTCTGGGGAAACGGAAAAGCCGGGC	26911
OY	2637	CAGCAGCCCGCTTAAAAAGAGACTCAATTTTGGTCAACTGGCGACTCAAGTCAGTCCCT	27566
Db	2632	CAGCAGCCCTGGCAAGAAAAAGATTGAAATTTTGGTCAAGTGGAGACGCGACGTCAGTACTCT	27511
OY	2757	GACCCAGAACCTCTCTCGGGAACCTTCACCAACCCCGCTGCTGGGGGCACTAACTACATG	28166
Db	2752	GAACCCAGCCCTCTCGGACAGCAACACAGCCAGCCCTCTGTGCTGGGAACCTAACTACATG	28111
OY	2817	GCTTCAGCGGGTGGCGCACCAATGGCGACACAATAAGAAAGCCGCGACGAGTGGGTAT	28766
Db	2812	GCTACAGGCGATGGGGGACCAATGGCACAACAATAAGAGGGCGCGACGAGTGGGTAT	28711
OY	2877	GCTTCAGGAAATTTGGCATTTGGCATTTCCACATGGCTGGGCGACAAGTCATCAACACAGC	29366
Db	2872	TCCTCCGGAATTTGGCATTTGGCATTTCCACATGGATGGGCGACAAGTGCATCAACACAGC	29311
OY	2937	AACCGAATATGGGCTTTGGCCCACTATTAACAACCACTCTTACACAGCAATCTCCAGTCT	29966
Db	2932	AACCGAATCTGGGCTTTGGCCCACTATTAACAACCACTCTTACACAACTTCAAGCCAA	29911
OY	2997	TCAACGGGGGCGACGACAGCAACACACTACCTTCGGCTACAGCACCCCTGGGGGATTTT	30566
Db	2992	TCA---GGAAGCTCGAAGACGACATCATCTTTGGCTACAGCACCCCTGGGGGATTTT	30486
OY	3057	GATTTCAACAGATTCACACTGCCATTTCTACCAACGTGACGTGGACAGCATCATCAACAC	31166
Db	3049	GACTTCAACAGATTCACACTGCCACTTTTCAACAAGTACGTGGCAAAAGACTCATCAACAC	31086
OY	3117	AATTGGGGATTTCCGGCCCAAGAGACTCACTTCAAGCTTTCAACATTCMAAGTCAAGAG	31766
Db	3109	AACGGGGATTTCCGACCCMAAGACTCAACTTCAAGCTTTTAACTTCAAGTCAAAAGAG	31686
OY	3177	GTCACGAGAAATGATGGCGTCAACGACCAATCGCTAATAACTTACACAGACGGTCAAGTC	32366
Db	3169	GTCACGCAAAATGACGAGTACGACGACGATTCGCAATTAACCTTACACAGACGGTCAAGTC	32286
OY	3237	TTGTGCACTCGAGTACCAAGTCTCCGTAAGTCTCGGCTCTGGCGACACAGGCGTGCCTC	32966
Db	3229	TTTACTGACTCGAGTACCAAGTCTCCGTAAGTCTCGGCGTCTGGGCGACACAGATGCTCTC	32886
OY	3237	CCTCCGTTCCCGGCGGACGTGTTCAATTCGACGATACGGCTACTAACGCTCAACAT	33566
Db	3289	CCGCGCTTCCGACGACGATCTTCAATGATGGCGACAGTATGATATCTCAACCTCAACAC	33486
OY	3357	GGACGCGAGAGTGGGAGCGCTAATCCTTTACTGCGCGAAATTTTCCATGCGCAATG	34166
Db	3349	GGAGTCAAGGAGTGGAGCGCTCTTCAATTTACTGCGCGAGTACTTCTCTTCAAGT	34086
OY	3417	CTGAGAAACGGGCAATTAACCTTTACCTTACGCTACACCTTCAAGGACGTCCTTCAAGC	34766
Db	3409	CTGGGTACCGGAAACAATTTTACCTTCAAGCTTCAACCTTTTGAAGACGTTCTTTCAACGC	34686
OY	3477	AGCTACCGCGACAGCCAGACCTTGAACCGGCTGATGAATCCTCTCATGACACAGTACCTG	35366
Db	3469	AGCTACGCTCAAGCAGACAGTCTGGAACCGTCTCATGATCCTCTCATGACACAGTACCTG	35286
OY	3537	TATTACCTGGAACAGAACTCAACATCAAGTCGGGAAGTCCGAAAACAAGAACTTGTCTGTT	35966
Db	3539	TATTACTTGAAGACAAACACTTCAAGTGAACACACAGCAAGCTCAAGGCTTCAAGTT	35886
OY	3597	AGCGGTGGGTCTCAGCTGCGATGTCTGTTCAAGCCCAAAAATGGGCTACCTGACCTGCT	36566

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Db	3649	TACCGCCACAGCAGCGATATCAAAAGCATCTCGGATTAACACACAGTGAATCTCTGG	3708
Oy	3717	ACTGGTGTCTTAAATATATTAACCTTAATGGGCGTGAATCTATATCAACCTTGGCACTGCT	3776
Db	3709	ACTGGAGTCAACAAAGTACCACTCTCAATGGCAGAGACTCTGTGTGAATCCGGGCGCCGC	3768
Oy	3777	ATGGCTTCAACAAAGACGACAAAGACAAATTCTTTCCCATGAGCGGTGTATGATTTTTT	3836
Db	3769	ATGGCAAGCCACAGAGAGATGAAGAAAAGTTTTTCTTCAGAGGGGGTCTCATCTTT	3828
Oy	3837	GGAAAGGAGAGCGCGGAGCTTTCAAACACTGATATGACAAATGTATATACAGACGAA	3896
Db	3829	GGAGAGCAAGGCTCAGAGAAAACAATGTGAACATTGAAAAGTTCATATTAACAGACAA	3888
Oy	3897	GAGAAATCAAAAGCCACTAACCCCGTGGCCAACGAAAGATTTTGGACTGTGGACTCAAT	3956
Db	3889	GAGGAATTCGGAACAACCAATCCGTGGCTAOGGACGATATGGTTCGTATTCACCAAC	3948
Oy	3957	CTCCAGACAGACAGACAGACCCTTGGCAGCGGAGATGTGCATGTTATGGAGCTTACTT	4016
Db	3949	CTCCAGAGGCAACAGACAAGACGCTCCGACATGTCAACACACAGAGGCTTCTTCCA	4008
Oy	4017	GGAAATGTGTGGCAAGACAGAGATTAACCTGACAGGCTCTATTTGGGCCAAATTTCT	4076
Db	4009	GGCATGTCTGACAGACAGAGATGTACTTACGGGGCCCATCTGGGCAAGATTTCA	4068
Oy	4077	CACACGATGAGCACTTTCACCCGCTCTCTCAATGGCGGCTTTGCACTTAAGCACCCG	4136
Db	4069	CACACGAGGACATTTTTCACCCCTCTCCCTCATGGGTGGATTCGACTTAACACCCCT	4128
Oy	4137	CCTCTCAGATCTCATATAAAAAACAAGCTGTTCCTGTGGAATCCTCGGCAAGTTTTCG	4196
Db	4129	CCTCCACGATTCATCATGAAAGAACCCCGGTACTGTGGAATCCTTCACCACTTCAGT	4188
Oy	4197	GCTCAAAAGTTTGGCTCATTTATATCAACCCAGATTCACAGACA-AGTGAACGGTGAAT	4255
Db	4189	GCGGAAAGTTTGTCTTCTTATATCAACAAGTCTCCACGGGACACGGTACGGAGAT	4248
Oy	4256	TGAATGGAGCTGCAGAAAAGAAAACAGCAACGCTGGAATCCGCAAGTCACTATATC	4315
Db	4249	CGAGTGGAGCTGCAGAGAGAAAACAGCAACGCTGGAATCCGCAATTCAGTACATTC	4308
Oy	4316	TAACTATGCAAAATCTGCGCAAGTTGATTTCACTGTGACAAACATGACTTTTATCTGA	4375
Db	4309	CAACTACAAACAAGTCTGTTAATCGTGACTTAACGTGATACTAATGCGTGTATTCAGA	4368
Oy	4376	GCTTCGCCCATTTGGCACCCGTTACCTACACCCGCTCCCTGTAAATTTGTGTAAATCA	4435
Db	4369	GCTTCGCCCATTTGGCACCAATCTCGAATCTGTAAATTTGCTTGTAAATCAATA	4428
Oy	4436	AACGGTAAATTCGTCAGTTGAATTTGGTCTCATGTCCCTTAATCTTATCTGTCGA	4495
Db	4429	AACGTTTAATTCGTCAGTTGAATTTGGTCTCTGTGCTATTTCTTTATCTAGTTT	4488
Oy	4496	CCATAGCAACCGGTTACATTAACGTGTTAGTTGCGTTTCGCA- - -ATACCCCTAGT	4551
Db	4489	CCATGGCTAGTAGTAAATTAGCANTGGGCGGTTAATCATTTAACTAACAGAACCCCTAGT	4548
Oy	4552	GATGAGTTGCCCACTCCCTTATATGCGGCGCTCGCTCGGTGGGGCCGCAAGCAGA	4611
Db	4549	GATGAGTTGGCACTCCCTCTCTGCGCGCTCGCTCGCTCACTAAGCGCGGCGACAAA	4608
Oy	4612	GCTCGCGGTGTGGGACCTTTGGTTCGACAGGCCCAACCGAGCAGCGAGCGGCATAGA	4671
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Oy	4672	GGAGTGGCCAA 4683	

Db 4669 GCGAGTGCCCAA 4680

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RESULT 7
US-08-475-391-1
; Sequence 1, Application US/08475391
; Patent No. 5786211
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshalls, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,391
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,358
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 578621land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELERX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-475-391-1
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Query Match 69.8%; Score 3270.8; DB 2; Length 4680;  
Best Local Similarity 82.2%; Pred. No. 0;  
Matches 3859; Conservative 0; Mismatches 812; Indels 21; Gaps 8;

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QY 121 GCCAATCTCATCTAGGGGTTCTGAGAGGGGTGAGTCTGACGTGAATTACGTCATAG 180
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QY 301 GGTTTGAACGCGCAG-CGCCATGCGGGGTTTTCAGAGATTGTGATTAAAGTCCCAAGC 359
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Db 301 GGTTTGAACGCGCAGCCGCCATGCGGGTTTTTACGAGATTGTGATTAAAGTCCCAAGC 360
QY 360 ACCTTGAAGAGCATCTGCGCGGCACTTTCTGACAGCTTTGTGAACCTGGGTGGCGAAGG 419
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QY 480 CCGTGCCGAGAAAGCTTCAAGCGCACTTCTGTGCACTGCGCGCGGTGAGTAAGGCC 539
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Qy	1440	TGATCTGGTGGGAGGAGGCAAGATGACGGCCCAAGTCTGTGAGTCCGCCAAGGCATTC	1499
Db	1441	TGATCTGGTGGGAGGAGGAAAGATGACCGGCCCAAGTCTGTGAGTGTGGCAAGGCATTC	1500
Qy	1500	TCGGGGGCAAGCAAGTGTGGCGGTGGACCAAAAGTGCMAATCGTCCGCCAGATCCATCCCA	1558
Db	1501	TCGGAGGAAGCAAGGTGGCGGTGGACCAAAATGCAATCTCCGCCCAAGTACCCGA	1566
Qy	1566	CCCCCGTATCGTCACTCTCCAAACACCAACATGTGGCCGTGATTACGGAGAACAGACCA	1619
Db	1561	CTCCCGTATCGTCACTCTCCAAACCAACATGTGGCCGTGATTACGGAGAACCAACGA	1620
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Db	1621	CCCTTGACAACCAAGCAGCCGTTTGACAAGCCCGATGTTCAAAATTTGAATCAACCCGCGTTC	1680
Qy	1680	TGGAGCATGACTTTTGGCAAGGTGACAAAGCAGAAAGTCAAAAGATTTCTTCGCTGGGCGC	1739
Db	1681	TGGATCAATGACTTTTGGGAAGGTCAACCAAGCAGAAAGTCAAAAGATTTTTCGCGTGGGCGA	1740
Qy	1740	AGGATCACGTGACCGAGGTGGCGCATGAGTTCTATGTCAGAAAGGGGTGGAGCCAAACA	1799
Db	1741	AGGATCACGTGTTGATGAGTGGAGCATGAAATTTCTATGTCAGAAAGGGGTGGAGCCAAAGAA	1800
Qy	1800	GACCCGCCCCCGATGACCGCATTAATAACGAGCCCAACCGGGCGTCGCTCTAGTCCGCG	1859
Db	1801	GACCCGCCCCCGATGACCGCATTAATAATGAGCCCAACCGGGGTGGCGCATGATGTGGC	1860
Qy	1860	ATCCATGACGTCAAGCGCGGAAGAGCTCCGGTGAATTTGCGGACAGTACCAAAACA	1919
Db	1861	AGCCATGACGTCAAGACCGCGGA--AGCTTGATCAATTAACGACAGACAGTACCAAAACA	1917
Qy	1920	AATGTTCCGTCACCGGGGATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAA	1979
Db	1918	AATGTTCTCGTACGTTGGGCATGAATCTGAATGCTGTGTTCCCTGCAACAAATGCGAGAAA	1977
Qy	1980	TGAATTCAGAAATTTCAACATTTGCTTTCACGCAACGGGACACAGAGACTGTTCAGAATGTTCC	2039
Db	1978	TGAATTCAGAAATTTCAAAATTTCTGCTTCACTACGACAGAAAGACTGTTTAAGTGTCTTC	2037
Qy	2040	CCGGCGGTGCAGAAATCTCAACCGGT--CGTCAGAAAGAGACGTATCGAAATCTGTG	2096
Db	2038	C---CGTGTCAAGAAATCTCAACCCGTTTTCTGTCTCAAAAGCCGATCAGAAATCTGTGCT	2094
Qy	2097	CCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTTGCTGCTCGGCTCGCATCTGTCA	2156
Db	2095	ACATTCATCATATCATGAGGAAAGGTGCCAGA---CGCTTGACATGCTCGCATCTGTGCA	2151
Qy	2157	ACGTGGAATCTGATGACTGTGTTTCTGAGCAATTAATCACTTAACACGATAGGCTGCC	2216
Db	2152	ATGTGGAATTTGATGACTGATCTTTTGAACATTAATGATTTAAATCAGGTATGGCTGCC	2211
Qy	2217	GATGATTATCTTCAGATTGGCTCGAGGACCAACTCTCTGAAGGCATTTCGCACTGTGTG	2276
Db	2212	GATGATTATCTTCAGATTGGCTCGAGGACACTCTCTGTAAGGAATAAGCACTGTGTG	2271
Qy	2277	GACTTGAACCTGGAAGCCCGGAACCCAAAGCCAAACAGACAAAGCAGAGTCAGCGCG	2336
Db	2272	AAGCTCAAACTGTGGCCCAACCAACCAAGCCCGAGAGCGGCTAAGAGACGACGACAGG	2331
Qy	2337	GGTCTGGAGCTCTCGGTCTACAAGTACTCGGACCCCTTCAACGGACTCGACAAAGGGAG	2396
Db	2332	GGTCTGTGCTCTCTGGGTAAGTACTCGGACCCCTTCAACGGACTCTGACAAAGGAGAG	2391
Qy	2397	CCCGTCAACGGCGGGATGACAGCGGCTCTGAGACGACAAAGGCTTACGACCAAGCTC	2456
Db	2392	CCGGTCAACGAGGCGAGACGCGCGGCTCTGAGACGACCAAAAGCTTACGACCGGACGTC	2451
Qy	2457	AAAGCGGGTACAATCCGTACTGTGGGTATTAACCGCCGACGCCGAGTTTCAAGAGCT	2516
Db	2452	GACAGCGGAGCAACCCGTACTCTCAAGTACACACGCGCGAGTTTCAAGAGCTC	2511

QY	2517	CTGCAGAAAGAAATACGCTCTTTTGGGGGGCAACCTCGGGCGAGAGATCTTCACAGCCAAAG	2570
Db	2512	CTTAAAGAAAGATACGCTCTTTGGGGGGCAACCTCGAGCAGACAGTCTTCAGGCGAAAG	2571
QY	2577	AGGGTCTTCGAACCTTTTGTCTGGTTAGAGAGGTGTGAAGACGGCTCTTGAAAGAA	2638
Db	2572	AGGGTCTTTGAAACCTCTGGGCGCTGGTTAGGAACCTGTATTAGAAGGCTCCGGGAA	2631
QY	2637	CGTCCGGTATAGACATCGCCCAAMAGCCACATCTCTCTCGGGATTTGGCAAGCAGC	2696
Db	2632	AGGCGGTAGAGCACTCTCTGTGGAGCAACCTCTCTCGGGAACCGGAAAGGCGGGC	2691
QY	2697	CAGCAGCCCGCTAAAAAAGACTCAATTTTGGTCAGACTGCGCAGCTCAGATCAGTCCCC	2758
Db	2692	CAGCAGCCTCGAAGAAAGAAATGAATTTTGGTCAGACTGAGACGCAAGCTCAGTACT	2751
QY	2757	GAACCAACAACCTCTCGGAGAACTTCAGCAACCCCGCTGCTGTGGACCTTACAT	2816
Db	2752	GAACCCCAAGCCTCTCGGACACCAACAGCAACCCCTCTGGTCTGGGAATCAATACGAT	2811
QY	2817	GCTTACAGCGGTGGGGCAACCATGGCAGACAAATTAACGAAGGCGCGACGAGTGGGTAT	2876
Db	2812	GCTTACAGCGAGTGGGGCAACCATGGCAGACATTAACGAAGGCGCGACGAGTGGGTAT	2871
QY	2877	GCTTCAGGAAATTGGCAATTGCGATTCACATGCGTGGCGACAGAGTCATCACCAAGC	2936
Db	2872	TCTCTCGGAAATTGGCAATTGCGATTCACATGAGATGGCGACAGAGTCATCACCAAGC	2931
QY	2937	ACCGGAACATGGGCTTGGCCACCTATTAACAACCTCTTACAGCAAAATCTCCAGTCT	2996
Db	2932	ACCGGAACCTGGGCGCTGGCCACCTTACAAACCAACCTCTTACAAACAAATTTCCAGCCA	2991
QY	2997	TCAACGGGGGGCAGCAACGACCAACCACTACTCGGCTACAGACCCCTGGGGGATTTT	3056
Db	2992	TCA--GAGCCTCGAAGCAGACATACCTACTTTGGCTACAGACCCCTTGGGGGATTTT	3048
QY	3057	GATTTCAACAGATTTCACTGCGCATTTCTACACACGTGACTGGCAGCGACTCATCAAC	3116
Db	3049	GACTTCAACAGATTTCACTGCGCATTTTCAACAAGTACTGGCAAAAGCTCATCAAC	3108
QY	3117	AATTGGGGATTCGGCCCAAGAGACTCAATTCAAGCTCTTCAACATCCAGTCAAGAG	3176
Db	3109	AACGTGGGATTTCCAGCCCAAGAGACTCAATTCAAGCTTTTAACTTCAAGTCAAAAG	3168
QY	3177	GTCAAGCAGATGATGGCGTCACAGACCATCGCTATAACTTTACAGCAGCGGTTCAAGTC	3236
Db	3169	GTCAAGCAGAAATGACGGTAGACGACGATTCGCATAATACCTTACAGACGGGTTCAAGTG	3228
QY	3237	TTGTGGACTGGAGTACCAGTTCCCGTACGTCTCGGCTTGGGCACAGGGCTGCTC	3296
Db	3229	TTTACTGACTCGGAGTACCAAGCTCCCGTACGTCTCGGCTTGGGCATCAAGATGCTC	3288
QY	3297	CCTCGGTTCCCGGGAGAGTGTTCATATTCGAGAGTACGGCTACCTAACGCTCAACAT	3356
Db	3289	CCGCGTTCCAGAGAGAGTCTTATATGTGCAACGATATGATACCTCACCTGAACAAC	3348
QY	3357	GGCAGCCAGGAGTGGGACGCTCATCTTTTACTGCTGGAATATTTCCATGCGAGATG	3416
Db	3349	GGGAGTACGAGTAGGACGCTCTTCAATTTTACTGCTGAGGTACTTTCCATGCAATG	3408
QY	3417	CTGGAACAGGGCAATCTTAACTTACGCTACACCTTCAGAGACGTGCTTCCACAGC	3476
Db	3409	CTGGGATCCGGAACAATTTAACTTACGCTACACTTTTGAAGCGTTCTTTCCACAGC	3468
QY	3477	AGCTACGCGCACAGCCGAGGCTGAGACCGGCTGATGATCTCTCATCGACAGTACCTG	3536
Db	3469	AGCTACGCTCACAGCCGAGAGTCTGAGACCGTCTATGATCCTCTCATCGACAGTACCTG	3528
QY	3537	TATTAACCTGAACAGATCTCAGATCACTAGTCCGGAAGTCCCAAAACAAGACTTGCTGTT	3596
Db	3529	TATTAACCTGAACAGAACATCTCAAGTGAACCAACGACGAGTCAAGGCTTCAAGTTT	3588

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Qy 3597 AGCCGCGGTCTCCAGCTGCAGTGTCTGTCAGCCCAAAAACGTGCTACTGGAACCCCTGT 3656
Db 3589 TCTCAGGCGGAGGAGGTGATTCGGGACCAAGTCTAGAACTGGCTTCTGGAACCCCTGT 3648
Qy 3657 TACCGGACGACGCGCGTTTCTTAAACAAAACAGACAAACAACAGCACTTTACTGG 3716
Db 3649 TACCGCCGACGCGAGTATCAAAAGCATCTCGGATTAACAACAACAGTAATCTCGGG 3708
Qy 3717 ACTGGTCTTCAAAATATTAACCTTAAATGGGGTGAATCTTAATTAACCCCTGGCACTGCT 3776
Db 3709 ACTGAGATTACCAAGTACCACTTCAATGACAGAGACTCTCTGGTGAATCCGGGCGCCG 3768
Qy 3777 ATGGCTCTCACAAAAGACGACAAAGACAAGTCTTTCCCATGAGCGGTGTGATGATTTT 3836
Db 3769 ATGGCAAGCCCAACAAGGACGATGAAGAAAAGTTTTTCTCAGAGGGGTTCTCATCTTT 3828
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Db 3829 GGGAAAGCAAGGCTCAGAGAAAACAATGTGAACATTTGAAAAGTTCATATTAACAGACGA 3888
Qy 3897 GAGGAATCAAAAGCCTAACCCCGTGGCCACCGAAAAGTTTGGGACTGTGCGAGTCAAT 3956
Db 3889 GAGGAATCGAACAACCAATTCCTGGCTAGCGAGCACTATGTTCTGTAATCTAACAC 3948
Qy 3957 CTCCAGAGCAGACAGACAGACCTGCGACCGGAGATGTGCAATGTTATGGAGCCCTTACT 4016
Db 3949 CTCCAGAGAGGCAACAGACAGCTACCGAGATGTCAACAACAAGGGGTTCTTCA 4008
Qy 4017 GGAATGTGTGGCAAGACAGAGAGCTATACCTGCAAGGCTCTTATTTGGGCCAAAATTCCT 4076
Db 4009 GGCATGTGTGGCGAGACAGAGATGTGACCTTTCAGGGGGCCCATCTGGGCAAAAGTTCCA 4068
Qy 4077 CACAGAGATGACACTTTCACCCCGTCTCTCTCATGAGGCGGCTTTGACTTAAGACACCG 4136
Db 4069 CACAGAGAGACACTTTTCAACCCCTCTCTCTCATGAGGATTCGACTTAACACCCCT 4128
Qy 4137 CCTCTCAGATCTCATCAAAAACAACGCTGTCTCTGCGAATCTCTCCGAGAGTTTTCG 4196
Db 4129 CCTCCACAGATCTCATCAAGAACACCCCGGACTCTGGAAATCTTTCACCACTTCAGT 4188
Qy 4197 GCTACAAAGTTTGTCTTATTCATCAACCAAGTATTCACAGACA-AGTGAACGTGGAGAT 4255
Db 4189 GCGGCAAGTTTGTCTTCTTATCAACAAGTATTCACAGGACACGCTCACGTGGAGAT 4248
Qy 4256 TGAATGGAGGCTGCGAAGAAAACAAGCAACGCTGAATCCCGAAGTGCAGTATAC 4315
Db 4249 CGAGTGGAGGCTGCGAAGAAAACAAGCAACGCTGAATCCCGAATTCAGTACACTTC 4308
Qy 4316 TAACTATGCAAAATCTGCCAAGTTGATTTGACTGTGACAACAATGACTTTATATCTGA 4375
Db 4309 CAACCTAACAAAGTCTGTTAATCGTGAACCTTACGCTGATCTAATGCGTGTATTCAGA 4368
Qy 4376 GCTTCGCCCCCTTGGACACCCGTACTCAACCCGCTGTAATTTGTGTATTCATA 4435
Db 4369 GCTTCGCCCCCTTGGACACCAATACCTGATCTGTAATTTGTAATTCATA 4428
Qy 4436 AACCGTAAATTCGTGCTAGTTGAACCTTGGCTCATCTCTTATATCTTATCTGCTCA 4495
Db 4429 AACCGTAAATTCGTGCTAGTTGAACCTTGGCTCATCTCTGCTATTTCTTATCTAGTTT 4488
Qy 4496 CCATAGCAACCGGTTACACATTAACCTGTTAGTGGCTTCCGA- - -ATACCCCTTAGT 4551
Db 4489 CCATAGGCTAACGTAAATTAATAGCATGGCGGTTAATCAATTAATCAAGAAACCCCTAGT 4548
Qy 4552 GATGAGATTTGCCCATCTCTCTATGCGGCTGCTGCTGCTCGGTGGGGCGGCAAGACGA 4611
Db 4549 GATGAGATTTGCCCATCTCTCTGCGGCTGCTGCTGCTGCTGCTGAGCGCGGCGCAACAA 4608
Qy 4612 GCTTCGCGCTGCGGACCTTTGCTCCGACGCGCCCAACGAGCGAGCGGCGCATGGA 4671
Db 4609 GGTGCGCCGACGCGCGGCTTTGGCGGGCGGCTCAATGAGCGAGCGGCGCAGAGA 4668
Qy 4672 GGGAGTGGCCAA 4683

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Db 4669 GGGAGTGGCCAA 4680

RESULT 8
US-08-709-609-1
; Sequence 1, Application US/08709609
; Patent No. 5858775
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 585875and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-709-609-1

Query Match 69.8%; Score 3270.8; DB 2; Length 4680;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3859; Conservative 0; Mismatches 812; Indels 21; Gaps 8;

Qy 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGGCCGGGCGAACAAAGTGGCC 60
Db 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGGCCGGGCGAACAAAGTGGCC 60
Qy 61 CGAGCGCCGGGCTTGTGCCCGGGCGGCTCACTGAGCGAGCGAGCGCGCAAGAGGAGTG 120
Db 61 CGAGCGCCGGGCTTGTGCCCGGGCGGCTCACTGAGCGAGCGAGCGCGCAAGAGGAGTG 120
Qy 121 GCGCACTCCATCACTAGAGGTTCTCTGAGGGGTGAGTCCGTGACGTAAATTAAGTCTAG 180
Db 121 GCGCACTCCATCACTAGAGGTTCTCTGAGGGGTGAGTCCGTGACGTAAATTAAGTCTAG 180
Qy 181 GGTAGGAGAGTCTGTATTAGAGGTACGTAGTGTGTTTGGACATTTTGGCACACCAT 240
Db 181 GGTAGGAGAGTCTGTATTAGAGGTACGTAGTGTGTTTGGACATTTTGGCACACCAT 240
Qy 241 GTGGTCAAGCTGGTATTATTAAGCCGAGTACGACGAGGCTCTCATTTTGAAGCGGGA 300
Db 241 GTGGTCAAGCTGGTATTATTAAGCCGAGTACGACGAGGCTCTCATTTTGAAGCGGGA 300
Qy 301 GGTTTGAACGGCGAG-CCCATGCGGGGTTTAAAGATTTGATTAAGTATCCCGAGCG 359
Db 301 GGTTTGAACGGCGAGCGGCATGCGGGGTTTAAAGATTTGATTAAGTATCCCGAGCG 360

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QY	360	ACCTTGAGAGAGATCTGCCCGGCATTTCTGACAGACTTTTGAACTGGGTGGCCGAGAAAG	419
Db	361	ACCTTGACGGGATCTGGCCGGCATTTCGACAGCTTTGTGAACCTGGGTGGCCGAGAAAG	420
QY	420	AATGGAGATTGGCCGACAGATTCTGCATGTAGTCTGTGATCTGATTTGAGCAGGACCCCTGA	479
Db	421	AATGGAGATTGGCCGACAGATTCTGCATGTAGTCTGATTTGAGCAGGACCCCTGA	480
QY	480	CCGTGGCCGAGAGCTGCAGCGCGCACTTCGTGTCACCTGGCCGCGGTGAGTAAAGCCC	539
Db	481	CCGTGGCCGAGAGAGCTGCAGCGCGCACTTCGTGTCAGGAATGGCGCGGTGAGTAAAGCCC	540
QY	540	CGGAGAGCCCTCTCTTTGTTGAGTTGAGAAAGGGAGGCTCACTTCCACTCCCTCAATTTC	599
Db	541	CGGAGAGCCCTTTCTTTGTGCAATTTGAGAAAGGAGAGCTCACTTCCACTCAACGTGC	600
QY	600	TGTTGGAGACCAACGGGGGTCAATCATGTGCTGGGCGCTCTCTGTAGTCAATTAAGCG	659
Db	601	TCGTGAAACCAACGGGGGTGAATCATGTTTGGGAAGTTTCTGTAGTCAATTCGCG	660
QY	660	ACAGCTGTGTGACACCATCTACCGGGGATGAGCCGACCTTGCCCACTGTTTCGCG	719
Db	661	AAAACTAATTCAGGAATTTACCCGGGATGAGCCGCACTTTGGCAACTGTGTCGCG	720
QY	720	TGACCAAGACGGGTATGAGCGCGCGAGGGGGGAAAGGTGGTGGACGAGTCTACATCC	779
Db	721	TCACAAAGACCAAGAAATGCGCCCGAGGCGGGAACAGGTGTGATGATGATCTCAATCC	780
QY	780	CCAACTACTCTCTGCCCAAGTCAACGCCGAGCTCAGTGGCGGTGACTTAACATGAGAG	839
Db	781	CCAATTAATCTGTCTCCCAAAACCCAGCTGAGCTCAGTGGCGGTGACTTAATATGGAAC	840
QY	840	AGTATATTAAGGCGGTGTTTAAACCTGGCGAGCGGAACCGGTCTGTGCGCACCGACTGA	899
Db	841	AGTATTTAAGGCGCTGTGTTGAATCTCAAGAGCCGTAAACGTTGGTGGGCGACACTGA	900
QY	900	CCCACTGACGACGACCCAGAGAGCAAAACAGAGAAATCTGAACCCCAATTTGACGCGC	959
Db	901	CGACGTGTGCGAGACGACGAGGACGAACAAAGAAATCAGAAATCCCAATTTGATGGCG	960
QY	960	CTGTATCTCCGGTCAAAAACCTTCCGACGCTACATGAGCTGTGGTGGGTGGCTGTGAGAC	1019
Db	961	CGGTATCAGATCAAAAACCTTCAAGCAGATGATGAGAGCTGTGGTGGGTGGCTGTGAGAC	1020
QY	1020	GGGGCATCACTCCGAGAGAGAGTGTGATTCAGAGAGAACAGAGCCCTGTACATCTCCTCA	1079
Db	1021	AGGGGATTAATCTCGAGAGAGAGTGTGATTCAGAGAGAACAGAGCCCTCATACATCTCTTCA	1080
QY	1080	ACGCCGCTCAACTCGCGGTCCAGATCAAGGCCGCTCTGAGCAATGCCGCAAGATCA	1139
Db	1081	ATGCGGCTCTCAACTCGCGGTCCCAATCAAGGCTGCTTGGACAAATCGGGAAAGATTAA	1140
QY	1140	TGGGCTGACCAAAATCCGCGCCCGACCTACCTGTGAGGCCCGGCTCCGCCGCCGACATTA	1199
Db	1141	TGAGCTTACTTAAACCCGCCCCCGACTACCTGTGTGGGCGACGAGCCCTGTGAGGACATTT	1200
QY	1200	AAACCAACCGGATTTACCGCATCTCTGAGAGCTGAAGGGCTACGACCTCTCAACGCGGCT	1259
Db	1201	CCAGGAATCGGATTTATTAATTTTGGAACTTAAACGGGTACGATCCCAATATGGGCTT	1260
QY	1260	CCGTCTTTCTGGGCTGGGCGCAAGAAAAGTTGGAAAACGCAACCATCTGGCTGTTTG	1319
Db	1261	CCGTCTTTCTGGGAGGGGCGAAGAAAAGTTGGGMAAGGAAACCATCTGGCTGTTTG	1320
QY	1320	GGCGGGCACACGGGCAAGAACCAACATTCGCGAAGGCATCGCCACGCGGCGCTTCT	1379
Db	1321	GGCTGTGAACTACCGGAGAGACCAACATTCGCGAGGCCATGACCCACACTGTGCCCTTCT	1380
QY	1380	ACGGCTGGCTCACTGAGACCAATGAAACTTTCCTTCAAGATTGCTGTCAACAAGATGG	1439
Db	1381	ACGGGTGGTAACTGAGACCAATGAAACTTTCCTTCAAGACTGTGTGTCAACAAGATGG	1440

QY	1440	TGATCTGGTGGGAGGAGGAGCAAGATGAGCGCCAAAGTGTGGAGTCCGCAAGGCATTCC	1499
Db	1441	TGATCTGGTGGGAGGAGGAGGAAAGATGACCGCCAAAGTGTGGAGTCCGCAAGGCATTTC	1500
QY	1500	TCGCGCGAGCAAGAGGTGTGGCGGTGAGCAAAAAGTGCMAATCGCTCCCGCAGATCGATTCCA	1555
Db	1501	TCGGAGGAAGCAAGGTGTGGCGGTGAGCAAAAAGTGCMAATCGCTCCCGCAGATCGATTCCA	1566
QY	1560	CCCCGTGATCGTCACTTCCAAACACCAACATGTGCGCGGTGATTGACGGGAAACAGACCA	1611
Db	1561	CTCCCGTATCGTCACTTCCAAACACCAACATGTGCGCGGTGATTGACGGGAACTCAACGA	1620
QY	1620	CCTTGAGACACAGAGACCGCTTGCAGAGCCGGATGTCTAAATTGAACTCACCCGCGCTC	1677
Db	1621	CCCTTGAAACACAGAGACCGCTTGCAGAGCCGGATGTCTAAATTGAACTCACCCGCGCTC	1680
QY	1680	TGGAGCAGACTTTGGSCAAAGGTGACAAAGCAGGAAGTCMAAAGATTCTTCGCTGGAGCGC	1733
Db	1681	TGGATCATGACTTTGGGAAAGGTACCAAGCAGGAAGTCMAAAGATTCTTCGCGTGGGCAA	1744
QY	1740	AGGATCAGCTGACCGAGGTGTGGCGCATGAGTTCTACGTGAGAAAGGTTGAGAGCCAAACA	1799
Db	1741	AGGATCAGCTGTTGAGGTGTGAGCATGAAATCTACGTCAAAAAGGTTGAGAGCCAAAGAA	1800
QY	1800	GACCCGCCCCGAGTACCGCGGATTAAGCGAGCCCAAGCGGCGCTCCCTTCATGTCGGG	1855
Db	1801	GACCCGCCCCGAGTACCGCAATATTAAGTGAAGCCAAACGGGTTGCGCATGTTAGTCGCG	1866
QY	1860	ATCCATCGACGTACAGCGCGGAGAGAGTCCGGTGAATTGTCGCAAGATGACAAACA	1915
Db	1861	AGCCATCAGCTACAGCGCGGAGAGTCCGGTGAATTGTCGCAAGATGACAAACA	1917
QY	1920	AATGTTCTCGTCACGCGGGGATGCTTCAGATGCTGTTCCCTGCAAAACATGCGAGAA	1973
Db	1918	AATGTTCTCGTCACGTGGGATGAAATCTGATGCTGTTCCCTGCAAGAAATGCGAGAA	1977
QY	1980	TGAATCAGAAATTTCAACATTGTTCTTACGCAAGGAGCAGAGACTGTTACAGATGTTCC	2033
Db	1978	TGAATCAGAAATTTCAAAATCTGCTTCACTCACGCAAGAAAGACTGTTAGTGTCCTTTC	2037
QY	2040	CCGGCGGTGAGAAATTCACCGGT---CGACAGAAAGAGACGATGTGGAACTCTGTG	2099
Db	2038	C---CGTGTGAAATCTCMAACCCGTTTCTGTCTCAAAAAGCGATACAGAACTGTCT	2099
QY	2097	CCATTTCATCTGTGGGGGCGGGCTCCGAGATTGCTTGTGCGCGTGCATCTGTGCA	2155
Db	2095	ACATTTCATCATCATGTGGGAAAGGTGCCAGA---CGTTGCACTGTCTGTGCATCTGTGCA	2155
QY	2157	ACGTGAGCTTGAGATGACTGTGTTTTCTGAGCAATTAATGACTTTAAACAGATATGGTCC	2218
Db	2152	ATGTGGAATTTGAGATGACTGATCTTTTGAACAATTAATTAATATCAGGATGGCTCC	2219
QY	2217	GATGGTTATCTTCCAGATTGGCTGAGAGCAACTCTTGTGAGGCAATTCGGCATGTGG	2278
Db	2212	GATGGTTATCTTCCAGATTGGCTGAGAGCACTCTCTGTGAAGAAATTAAGACAGTGTGG	2279
QY	2277	GACTTGAACCTGAGGCCCGGAAACCAAGACCAACAGACGAAAGCAGGAGAGAGCGCGCG	2336
Db	2272	AAGCTCAAACTGTGCCCAACCAACCAAGGCCGAGAGCGGCAATAGGAGAGCAGACGAG	2337
QY	2337	GGTCTGTGCTCTCTGTGCTACAAATACCTCGAACCTTCAACGGAATTCGACAAAGGAGAG	2396
Db	2332	GGTCTGTGCTCTCTGTGCTACAAATACCTGTGGAACCTTCAACGGAATTCGACAAAGGAGAG	2399
QY	2397	CCGCTCAACGCGGCGAGTACAGCGGCGCTCGAGCAAGCAAGGCTTACGACACGACGCTC	2456
Db	2392	CCGCTCAACGAGGAGAGCGCGCGCGCTCGAGCAAGCAAGGCTTACGACCGGACGCTC	2451
QY	2457	AAAGCGGGGTGCAATTCGTTACCTGCGGATTAATACAGCCGAGCGCGAGTTTCAAGAGCGT	2516
Db	2452	GACAGCGGAGCAACCGTATCTAAGTACACACGCGAGCGGAGGTTTCAAGAGCGC	2511
QY	2517	CTGCAAGAGATACGTCTTTTGGGGGCACTCTCGGCGAGACGATCTTCAAGGCCAAGAG	2576

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 Db 2872 TCCTCCGGAATTGGCAATTGGCATTCACATGGATGGCGACAGAGTCATCAGCAGC 2931  
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 Db 2932 ACCCGAATATGGGCTTGGCCCACTTAACAACCACTCTACAGCAAAATCTCCAGTCT 2991  
 Qy 2997 TCAAGGGGGGCGAGCAAGCAACCACTACTTGGCTACAGCAACCCCTGGGGGATTTT 3056  
 Db 2992 TCA---GAGGCTCGAAGCAATATCTACTTGGCTACAGCAACCCCTGGGGGATTTT 3048  
 Qy 3057 GATTTCACAGATTCAGCTGCCATTTCTACCACTGACGTCGCGACGAGCTCATCAAC 3116  
 Db 3049 GACTTCACAGATTCAGCTGCCATTTCTACCACTGACGTCGCGAAGCATCATCAAC 3108  
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 Qy 3177 GTCAAGCAATGATGGCGTACGACGACCATGCTAATACTTACAGAGACGGTCAAGTC 3236  
 Db 3169 GTCAAGCAATGATGGCGTACGACGACCATGCTAATACTTACAGAGACGGTCAAGTC 3228  
 Qy 3237 TTGTGGACTCGAGTACAGTTCCTGTAAGTCTCTGGCTCTGGCGACAGGGCTGCTC 3296  
 Db 3229 TTACTGACTCGAGTACAGTTCCTGTAAGTCTCTGGCTCTGGCGCATCAAGATGCTC 3288  
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 Db 3349 GGGAGTCAGGAGTGAAGGCTCTTCACTTACTGCTGAGTACTTTCTTCTCAGATG 3408  
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 Db 3469 AGCTACGGTCAAGAGAGTGTGAGCGTCTCATGAATTCCTTCATGACCAAGTCTG 3528  
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 Db 3529 TATTACTTGAAGAGAACTCAATATGTCGGAATGGCAACCAAGCAAGTCAAGGCTTCA 3588  
 Qy 3597 AGCGTGGGTCTCCAGTGGCATGTCTGTTCAAGCCAAAACTGGCTACTGAGACCTGT 3656

Db 3589 TCTCAGCCGAGCGAGTGAATTCGGGACCAAGTCTAGGAATGGCTTCTTGACCTGT 3648  
 Qy 3657 TACCGGAGAGGCGGTTCTTAAGCAAGAAACAGACAAACAGCACTTACCTG 3716  
 Db 3649 TACCGGAGAGGAGTATTAAGACATCTGCGGATTAACAACAGTGAATACTGCTG 3708  
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 Qy 3897 GAGGAATCAAGGCACTAACCCCGTGGCAACGGAAGATTGGGACTGTGGAGTCAAT 3956  
 Db 3889 GAGGAATCCGAACCAATCCCGTGGCTACGAGCAGATGAGTGTCTGATCTACCAAC 3948  
 Qy 3957 CTCTAGACAGCAGACAGACCTTGGCAGCCGGAGATGTGATGATTAAGGACCTTACT 4016  
 Db 3949 CTCTAGAGAGGCAACAGACAGAGCTTACCGCAGATGTCAACACAAAGCGTTCTTCA 4008  
 Qy 4017 GGAATGGTGTGGCAAGACAGAGAGTATCTGCAAGGCTCTAATTTGGGCAAAATTCCT 4076  
 Db 4009 GGCATGATCTGGCAGGACAGAGATGTATCTTCAAGGCGCCATCTGGCAAAAGTCCA 4068  
 Qy 4077 CACACGAGTGAACATTTTCAACCCGCTCTCTCTCATGGGCGGCTTTGACTTAAGACCG 4136  
 Db 4069 CACACGAGGACATTTTCAACCCCTCTCCCTCATGGGTGATTCGACTTAACACCTT 4128  
 Qy 4137 CTTCTGAGATCTCTACAAACACCGCTTCTGCGAATCCTCCGAGAGTTTTCG 4196  
 Db 4129 CTTCTCAGATTTCTATCAAGAAACACCGGTACTGCGAATCTTTCGACACCTTCACT 4188  
 Qy 4197 GCTCAAAAGTTTGTCTATTCATCACCCAGTATTCACAGAGCA-AGTGAAGCTGAGAT 4255  
 Db 4189 GCGCAAAAGTTTGTCTTCTTCTATCACAGATCTCCACGCGGACGGTCAAGCTGAGAT 4248  
 Qy 4256 TGAATGGAGCTGAGAAAGAAACAGCAACCGTGAATCCGGAATGCAATATCATC 4315  
 Db 4249 CGAGTGGAGCTGAGAAAGAAACAGCAACCGTGAATCCGGAATGCAATATCATCTTC 4308  
 Qy 4316 TAACTATGCAAAATCTGCAACGTTGATTTCACTGTGAGCAACAATGCACTTAATCTGA 4375  
 Db 4309 CAACCTAACAAGCTGTGTAATGTTGACTTACCGTGAATCTAATGCGGTATCAGA 4368  
 Qy 4376 GCTCGCCCAATTGGACCCGTTACTCACCCGTCCTGTAAATTTGTGTAACTAATA 4435  
 Db 4369 GCTCGCCCAATTGGACCCGATACCTGACTCGTAATCTGTAAATTTGTTAATCAATA 4428  
 Qy 4436 AACCGTTAATCTGTGATGAACTTGGATCTCATGTCTTAAATCTTAATCTGCTCA 4495  
 Db 4429 AACCGTTAATCTGTGATGAACTTGGATCTCATGTCTTAAATCTTAATCTGCTT 4488  
 Qy 4496 CCAATGCAACCGGTTAACAATTAATCTGTAATGTCGCTTCGCA----ATACCCTAGT 4551  
 Db 4489 CCAATGCTACCTGATTAATTAAGCAGGCGGATTAATCAATTAACAAGAACCCCTAGT 4548  
 Qy 4552 GATGAGTGGCCCACTCCCTATAGCGCTGCTGCTGCTGGGCGCGCAGAGAGA 4611  
 Db 4549 GATGAGTGGCCCACTCCCTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4608  
 Qy 4612 GCTCTGCTGTGGGACCTTTGTGCTGCAAGGCCCAACGAGGAGCGAGCGCATAGA 4671  
 Db 4609 GGTGCGCCGAGCGCCGCGCTTGTCCCGGCGGCTCATGTAGCGAGGAGCGCCAGAGA 4668  
 Qy 4672 GGGAGTGGCCAA 4683  
 Db 4669 GGGAGTGGCCAA 4680

## RESULT 9

PCT-US95-07178-1  
Sequence 1, Application PC/TUS9507178  
GENERAL INFORMATION:  
APPLICANT: Johnson, Philip R.  
TITLE OF INVENTION: Adeno-Associated Virus Materials and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07178  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Grete E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31975  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4680 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US95-07178-1

Query Match 69.8%; Score 3270.8; DB 7; Length 4680;  
Best Local Similarity 82.2%; Pred. No. 0; Mismatches 812; Indels 21; Gaps 8;  
Matches 3859; Conservative 0;

QY 1 TTGGCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGCCGGGCGCAACAAAGTCCG 60  
DB 1 TTGGCACTCCCTCTGCGCGCTCGCTCGCTCACTGAGCCGGGCGCAACAAAGTCCG 60  
QY 61 CGAGCGCCCGGCTTTGCCCGGGCGGCTCACTGAGCGAGCGCGGAGAGAGAGTG 120  
DB 61 CGAGCGCCCGGCTTTGCCCGGGCGGCTCACTGAGCGAGCGCGGAGAGAGAGTG 120  
QY 121 GCCAATCTCATCTAGGGGTTCTGAGGGGGTGAAGTGAAGTGAATTAAGTCACTAG 180  
DB 121 GCCAATCTCATCTAGGGGTTCTGAGGGGGTGAAGTGAAGTGAATTAAGTCACTAG 180  
QY 181 GGTAGGAGAGTCTGTATTAAGAGTCACTGAGTGTGTCGACATTTTTCGACACCAT 240  
DB 181 GGTAGGAGAGTCTGTATTAAGAGTCACTGAGTGTGTCGACATTTTTCGACACCAT 240  
QY 241 GTGTGTCACGTGGGTATTTAAGCCCGAGTGAAGCGAGGCTTCCATTTTGAAGCGGGA 300  
DB 241 GTGTGTCACGTGGGTATTTAAGCCCGAGTGAAGCGAGGCTTCCATTTTGAAGCGGGA 300  
QY 301 GGTGTAACGCGAG-CGCCATGCCGGGGTTTGAAGATTGTATTAAGGTCCCGACGG 359  
DB 301 GGTGTAACGCGAGCGCGGCGCATGCCGGGGTTTGAAGATTGTATTAAGGTCCCGACGG 360  
QY 360 ACCTTGACGAGCATCTGCCCGGCAATTTCTGACAGCTTTGTGAATGGGTGGCGGAGAGG 419  
DB 360 ACCTTGACGAGCATCTGCCCGGCAATTTCTGACAGCTTTGTGAATGGGTGGCGGAGAGG 419

DB 361 ACCTTGACGAGCATCTGCCCGGCAATTTCTGACAGCTTTGTGAATGGGTGGCGGAGAGG 420  
QY 420 AATGGAGATTGCCCGCAGATTCTGACATGATCTGAATCTGATTAAGAGGACCCCTGGA 479  
DB 421 AATGGAGATTGCCCGCAGATTCTGACATGATCTGAATCTGATTAAGAGGACCCCTGGA 480  
QY 480 CCGTGGCCGAGAGGTGCGAGCGACTTCTGGTCCATGCGCGCGGTGATGAAGGCC 539  
DB 481 CCGTGGCCGAGAGGTGCGAGCGACTTCTGGTCCATGCGCGCGGTGATGAAGGCC 540  
QY 540 CGAGGCCCTCTTCTTGTTCAGTTCGAGAGGCGAGTCTCACTTCCACCTCCATATTC 599  
DB 541 CGAGGCCCTCTTCTTGTTCAGTTCGAGAGGCGAGTCTCACTTCCACCTCCATATTC 600  
QY 600 TGTGTGAGACCAAGGGGTCAATTCATGTGTGCGCGCTTCTGAGTCAATTAAGC 659  
DB 601 TGTGTGAGAACCAAGGGGTCAATTCATGTGTGCGCGCTTCTGAGTCAATTAAGC 660  
QY 660 ACAAGCTGTGACAGACCATCTACCGCGGGATCGAGCCGACCTGCTGATTCGCGG 719  
DB 661 AAAAATGATTCAGAGATTATTCGCGGGATCGAGCCGACTTTCGCAATCTGTTCGCGG 720  
QY 720 TGACCAAGACCGCTAATGCGCGCGAGGGGGAACAAAGTGTGAGACGAGTCAATCC 779  
DB 721 TCACAAAGACCAAGAAATGCGCGCGGAGCAAGAGTGTGAGTCAATCC 780  
QY 780 CCAACTATCTCTGCGCAAGACTAGCCGAGCTGCAAGTGGGCTGATCAATGAGG 839  
DB 781 CCAATTAATCTGCTCCCAAAACCCAGCTGCTGCAAGTGGGCTGATCAATGAGG 840  
QY 840 AGTATTAAGGCGGTGTTTAACTGCGCGGCAACCGCTGCTGAGCGACAGACCTGA 899  
DB 841 AGTATTAAGGCGGTGTTTAACTGCGCGGCAACCGCTGCTGAGCGACAGACCTGA 900  
QY 900 CCAAGCTGAGCAGACCCAGAGCAGAAAGAGAACTGTAACCCCAATTTCTGACGCGC 959  
DB 901 CCAAGCTGAGCAGACCCAGAGCAGAAAGAGAACTGTAACCCCAATTTCTGACGCGC 960  
QY 960 CTGTCAATCCGCTCAAAACCTCCGCAAGCTAATGAGCTGTGGTGGTGTGATGAC 1019  
DB 961 CTGTCAATCCGCTCAAAACCTCCGCAAGCTAATGAGCTGTGGTGGTGTGATGAC 1020  
QY 1020 GGGGCACTACCTCCGAGAGAGTGAATCCAGAGGACCGAGGCTCGTACATCTCTTCA 1079  
DB 1021 AGGGGATTAATCTCGAGAGAGTGAATCCAGAGGACCGAGGCTCGTACATCTCTTCA 1080  
QY 1080 ACGCGGCTCCCACTCGCGGTCCAGATCAAGCGCTGAGCAATGCGGCAAGATCA 1139  
DB 1081 ACGCGGCTCCCACTCGCGGTCCAGATCAAGCGCTGAGCAATGCGGCAAGATCA 1140  
QY 1140 TGGCGCTGACCAATTCGCGCGCGGACTAATCTGTGAGCTGCGCGCGGCAATTA 1199  
DB 1141 TGGCGCTGACCAATTCGCGCGCGGACTAATCTGTGAGCTGCGCGCGGCAATTA 1200  
QY 1200 AAACCAACCGCATTTAATCCGATCTGAGAGTGAACCGCTGAGCCCTGATGCGCGGCT 1259  
DB 1201 AAACCAACCGCATTTAATCCGATCTGAGAGTGAACCGCTGAGCCCTGATGCGCGGCT 1260  
QY 1260 CCGTCTTCTCGGCTGGGCCAGAAAAGTTTCGAAAACCAACCATCTGAGCTGTTTG 1319  
DB 1261 CCGTCTTCTCGGCTGGGCCAGAAAAGTTTCGAAAACCAACCATCTGAGCTGTTTG 1320  
QY 1320 GGGCGGCGACCAAGGCGCAAGCAATGCGGAGAGCTAGTCCGACGCGTGTCTTCT 1379  
DB 1321 GGGCGGCGACCAAGGCGCAAGCAATGCGGAGAGCTAGTCCGACGCGTGTCTTCT 1380  
QY 1380 ACGGCTGCTCACTGGAACCAATGAGAACTTTCCTTCAAGATTTGGTGTGACAAAGTGG 1439  
DB 1381 ACGGCTGCTCACTGGAACCAATGAGAACTTTCCTTCAAGATTTGGTGTGACAAAGTGG 1440  
QY 1440 TGAATCTGTGGAGAGAGGCAAGATGACGCGCAAGGTCGTGAGTCCGCGCAAGGCAATTC 1499  
DB 1441 TGAATCTGTGGAGAGAGGCAAGATGACGCGCAAGGTCGTGAGTCCGCGCAAGGCAATTC 1500

QY	1500	TCGCGCGCAGCAAGGTGGCGCTGGACCCAAACTGTCAATCGTCCGCCCAATTCGATCCCA	15539
Db	1501	TCGGAGGAGCAAGGTGGCGCGTGGACCAAGAAATGTCAATCGTCCGCCCAATTCGATCCCA	1560
QY	1560	CCCCCGTATCGTCACTCTCCAAACCAACAATGTGGCGGTGATTTGACGGGAACGACCA	1619
Db	1561	CTCCCGTATCGTCACTCTCCAAACCAACAATGTGGCGGTGATTTGACGGGAATCCACGA	1620
QY	1620	CTTTGAGCACCAAGCAGCCGTTTGACGACCCGATGTTCAAAATTGAACTCAACCCGCGTC	1679
Db	1621	CTTTGAAACACAGCAGCCGTTTGCAAGACCCGATGTTCAAAATTGAACTCAACCCGCGTC	1680
QY	1680	TGGAGCATGACTTTGGCAGAGGTGACAAAGCAGGAAGTCAAAGAGTCTTCCGCTGGGGGC	1739
Db	1681	TGGATCAATGACTTTGGGAAAGGTGACCAAGCAGGAAGTCAAAGACTTTTTCGGTGGGGCA	1740
QY	1740	AGGATCATGTGACCGAGGTGGCGCATGAGTTCTACGTCAAGAAAGGGTGGAGCCAAACAA	1799
Db	1741	AGGATCATGTGTTGAGGTGGAGCATGAAATTTCTACGTCAAAAGGGTGGAGCCAAAGAAA	1800
QY	1800	GACCCGCCCCCGATGACCGGATAAAGCGAGCCCAAGCGGGCTGCCTCACTCGCGG	1859
Db	1801	GACCCGCCCCCGATGACCGGATTAAGTAGAGCCCAAGCGGGTGGCGAGTCACTTGGCGC	1860
QY	1860	ATCTCATCGACTGACAGCGCGGAGAGCTCCGGTGGACTTTGGCGACAGTTACCAAAACA	1919
Db	1861	AGCCATGACCGTCAACCGCGG--AGCTTCGATCAACTTACGACACAGTTACCAAAACA	1917
QY	1920	AATGTTCTCGTACCGCGGCAATGCTTCAGATGCTGTTCCCTGCAAAACATGCGAGAAA	1979
Db	1918	AATGTTCTCGTACCGTGGGCATGAACTGATGCTGTTCCCTGCGAGAACATGCGAGAAA	1977
QY	1980	TGAATCAGAAATTTCAACTTTGCTTACGCGACGCGACAGAGACTGTTCAAGATGTTTTCC	2039
Db	1978	TGAATCAGAAATTTCAAAATATCTGCTTCACTACGCGACAGAAAGACTGTTTAAAGTGTTC	2037
QY	2040	CCGGGCTTCAGAAATCTCAACCGGT--CGTCAAGAAAGACGATGCGGAACTCTGTG	2086
Db	2038	C---CGTGCAGAAATCTCAACCCGTTTCTGTGTCAAAAAGCGGATCAGAAACTGTGCT	2094
QY	2097	CCATTCAATCATGCTGTGGGGCGGGCTCCGAGATTGCTGTGCTCGGCTGCATCTGTGCA	2156
Db	2095	ACATTCATCATATCATGTGGAAAGGTGCCAGA---CGCTTGACATGCTCTGCGATCTGTGCA	2151
QY	2157	ACGTGGATCTGGAGTACTGTGTGTTCTGAGCAATAAATGACTTTAAACAGATATGGCTGCC	2216
Db	2152	ATGTGGATTTGGATGACTGCACTCTTTGAAACAATAATATTAATTAATCAGATATGGCTGCC	2211
QY	2217	GATGTTTATCTTCCAGATTGGTGTGAGACAACTCTGTGAGGGATTCGGCAGTGTGTG	2276
Db	2212	GATGTTTATCTTCCAGATTGGTGTGAGACACTCTCTCTGAAGGAATTAAGCAAGTGTGTG	2271
QY	2277	GACTTGAAAACCTGAGACCCCGGAAACCCAAAGCCAAACAGACAAAGACAGAGACGACGG	2336
Db	2272	AAGTCTCAAACCTGCGCCCAACCAACCAAGCCCGAGAGCGGCATTAAGAGACAGCAGG	2331
QY	2337	GGTCTGTGTCTTCTTGCTTACAAGTACTCTGGAACCTTTCAACGCACTGACAGAGGGGAG	2396
Db	2332	GGTCTTGTGTCTTCTTGCTTACAAGTACTCTGGAACCTTTCAACGCACTGACAGAGGGGAG	2391
QY	2397	CCCGTCAACGCGGCGGAGTGCAGCGGCCCTCTGAGCAGCAACAGAGCTTAAGACCAAGCTC	2456
Db	2392	CCGGTCAACGAGGAGAGCGCGCGGCCCTCTGAGCAGCAACAAAGCTTAAGACCGGAGCTC	2451
QY	2457	AAAGGGGAGCAATCTCGTACTCTGGGTATTAACAAGCGCAGCGCGGATTTCAAGAGCGT	2516
Db	2452	GACAGCGAGACAACTCCGTACTCTCAAGTACAAACCAAGCGCGGAGGAGTTTCAAGAGCGC	2511
QY	2517	CTGCAAGAAATATCTTTTGGGGGCAACTCTGGGCGAGCAGTCTTCAAGCCCAAGAG	2576
Db	2512	CTTAAGAAAGATACCTCTTTTGGGGGCAACTCTGGAGCAGCAGTCTTCAAGCCCAAGAG	2571

QY	2577	AGGGTTCTCGAACCTTTTGGTCTGGTGGAGAAAGTCTTAAGAGCGTCTCTGGAAAAA	2636
Db	2572	AGGGTTCTTGAACCTCTGGGGCTGTGTGAGGAACCTTTAAGAGGGCTCTGGGAAAAAG	2631
QY	2637	CGTCCGGTAGAGCACTGCGCCACAAGAGCCAGACCTCTCTCGGGCACTTGGCAAGACAGGC	2696
Db	2632	AGGCCGGTAGAGCACTCTCTGTGGAGCCAGACTCTCTCTCGGGAACCGGAAGGCCGGC	2691
QY	2697	CAGAGCCCCGTAAAAAAGACTCAATTTTGGTCAGCTGGCGACTCAGAGTCAATCCCC	2756
Db	2692	CAGAGCGCTCGAAGAAAAAGATTGAATTTTGGTCAGACTGGAGCGCAGACTCAGTACCT	2751
QY	2757	GACCCACAACCTCTCTCGAAGAACTCTCAGCAACCCCCGCTGCTGGGACCTACTACAAATG	2816
Db	2752	GACCCCCAGCCTCTCGAGCAAGCCACACAGCCCCCTCTGTGTGGAACTTAATCGATG	2811
QY	2817	GCTTCAGCGGTGGCGCCAAATGGCAGACAAATTAACAAAGGCCGCGACGAGTGGTAAT	2876
Db	2812	GCTACAGGCAATGGCGCACCAATGGCAGACAAATTAACAGGGGCCGCGACGAGTGGTAAT	2871
QY	2877	GCCTCAGGAATTTGGCAATTGGATTCCACATGTGCTGGGCGACAGAGTCAATCACCAGCC	2936
Db	2872	TCCTCCGAAATTTGGCAATTGGATTCCACATGATGGGCGACAGAGTCAATCACCAGCC	2931
QY	2937	AACCGAACATGTGGCTTGTCCCACTAATTAACAACAACCTCTTAACAGCAAAATCTCGATGCT	2996
Db	2932	AACCGAACCTGTGGCTCTGCCCCCACTTAACAACAACCACTCTTAACAACAAATTTTCAGCCAA	2991
QY	2997	TCAACGGGGGGCAGCAACGACCAACACTGTCGGCTACAGACACCCCTGGGGGTAATTTT	3056
Db	2992	TCA--GGAGCTCGAAGCAATCACTTTGGCTACAGACCCCTTGGGGTAATTTT	3048
QY	3057	GATTTCACACAGATTTCACATGCACTTTTTCACACAGTACGTGACGCGACTCATCAACAC	3116
Db	3049	GACTTCACACAGATTTCACATGCACTTTTTCACACAGTACGTGCAAAAGACTCATCAACAC	3108
QY	3117	AATTGGGGAATTCGGCCCCAAGACACTCACTTCAAGCTTTCAACATCCAAATGCACAGAG	3176
Db	3109	AACGTGGGATTTCCAGCCCAAGAGACTCAACTTCAAGGCTCTTTAACTTCAAGTCAAGAG	3168
QY	3177	GTCACGAAGATGATGGGGTCAAGCAACCATGCTAATTAACCTTACACAGCGTTCAAGTC	3236
Db	3169	GTCACGAAGATGACGGTACGACACACATGATGTCCAATTAACCTTACACAGCGTTCAAGTC	3228
QY	3237	TTGTGCACTCGAGTACCAAGTTCCGTAAGTCTCTGCGCTCTGCGACACAGGGCTGCTC	3296
Db	3229	TTTATGACTCGAGGTACCAAGCTCCGTAAGTCTCTGCGCTCTGCGACACAGGATGCTC	3288
QY	3297	CCTCCGTTCCCGGGAGAGTGTATGATATTCGAGATAGCGCTACTTAAGCTCAACAAT	3356
Db	3289	CCGCGGTTCACAGAGAGTCTTATAGTGTCAACAGATATGATATCTCACCCCTGTAACAC	3348
QY	3357	GGCAGCCAGAGTGGGACGCTAATCCCTTATACGCTGGGAATTTTCCATCGCAGATG	3416
Db	3349	GGGAGTCAGGAGTGGAGCGCTCTTCAATTTTACTGCTGGAGTACTTTCTTCTCAAGATG	3408
QY	3417	CTGAGAAAGGCAATTACTTACCTTCAGCTACACTTCAGAGACGTCCTTTCCACAGC	3476
Db	3409	CTGGGTACCGGAACAACTTACTTCACTTCAAGTACACTTTTGAAGACGTTCCCTTCCACAGC	3468
QY	3477	AGCTACCGGCACAGCCAGACGCTTGAGCCGGCTGATGTAATCTCTCATGACCAAGTACTG	3536
Db	3469	AGCTACCGTCTCAGCCAGAGAGTCTGGAACGGTCTCATGTAATCCTCTCATGACCAAGTACTG	3528
QY	3537	TATTACCTGAACAACTCAATCAATCAATGCTCCGGAAGTCCCAAAACAAGACTTGTGCTTT	3596
Db	3529	TATTACTTGAACAAACAATCAATCAATGTCACAGTGAACCAACGCAAGTCAAGGCTTCACTTT	3588
QY	3597	AGCGGTGGGTCTCAGAGCTGCAATCTGTGTTACAGCCAAAAAATGGCTACCTGACCGCTGT	3656
Db	3589	TCTCAGGCCGAGCGAGTGAATCTTCGGGACCAAGTCTTAGAACTGGCTTCTCGACCCGCT	3648
QY	3657	TACCGGACGACCGGTTTTCTAAAAACAACAAACAGACACAAACAGCAACTTTACTGCTG	3716

Db 3649 TACGCCGACGACGATTCAAAGCATCTCGGATTAACAACAAGATATCTCGGG 3708  
Qy 3717 ACTGCTGCTTAAATATTAACCTTAATGAGCGTGAATCTTAATCAACCTCGGACTCT 3776  
Db 3709 ACTGAGCTTACCAAGTACCCTCAATGAGAGACTCTGTGTAATCCGGGGCCCCC 3768  
Qy 3777 ATGGCTCAACAAGACGACAAAGCAAGTCTTCCATGAGGGGTGTCAATGTTTTT 3836  
Db 3769 ATGGACCCCAAGAGACGATGAAGAAAGTTTTTCTCAGAGCGGGGTCTCATCTT 3828  
Qy 3837 GAAAAGAGAGCGCGGAGCTTCAACAACCTGCATTGAACAATGTGATGACAGACGA 3896  
Db 3829 GGGAAAGCAAGCTCAGAGAAAAAATGTAACATTTGAAAAGTATGATTAACAGACA 3888  
Qy 3897 GAGGAATCAAAAGCCTAACCCCGTGGCCACCGAAGATTGGACTGTGGCACTCAAT 3956  
Db 3889 GAGGAATCGGAACAACCAATCCGTGGCTAGGAGCAGTATGTTCTGTATCTCAAC 3948  
Qy 3957 CTCCAGACACAGACAGACCCCTGCGACCGAGATGTGCATGTATGGAGCCTTAACT 4016  
Db 3949 CTCAGAGAGGCAACAGACAGACACTACCGAGATGTCAACAACAAGGGGTCTTCCA 4008  
Qy 4017 GGAATGTGTGCAAGACAGACAGTATACCTGACAGGCTCTATTGGGCCAAATTTCT 4076  
Db 4009 GGCAATGCTGTGCAAGACAGAGATGTATCTTCAAGGGCCCATCTGGGCAAAAGTTCCA 4068  
Qy 4077 CACAGGATGACACTTTCACCCGTCTCTCATGAGGCGGCTTGAATTAAAGCACCG 4136  
Db 4069 CACAGGACGACATTTTCACCCCCTCTCCCTCATGGGTGATTCGGAATTAAACACCT 4128  
Qy 4137 CCTCTCATGATCTCTATCAAAAACGCGCTGTCTGGAATCTTCGGCAGAGTTTTCG 4196  
Db 4129 CCTCCAGATTTCTATCAAGAACCCCCGGTACCTGGAAATCTTTCACCACTTCAGT 4188  
Qy 4197 GCTCAAAAGTTTGTCTTCAATTCACCCAGTATTCACAGACA-AGTAGCGTGAAT 4255  
Db 4189 GCGGCAAGTTTGTCTTCTTCAATCAAGTATCTCAAGGACAGGCTCAGGTGGAAT 4248  
Qy 4256 TGAATGGAGCTGCAGAAAGAAACAGCAACGCTGGAATCCGAAATGACGATATATC 4315  
Db 4249 CGAGTGGAGCTGCAGAAAGAAACAGCAACGCTGGAATCCGAAATTCAGTACATTC 4308  
Qy 4316 TAACTATGCAAAATTCGCCAAGTGAATTCATCTGACACAACATGACCTTAATCTGA 4375  
Db 4309 CAACTAACAAGTCTGTTAATCGTGACTTAACGTTGATACTAATGCGGTATTCAGA 4368  
Qy 4376 GCTGCGCCCAATGAGCAACCCGTTAATCTGACCCGCTGTAATGTGTTAATCAATA 4435  
Db 4369 GCTGCGCCCAATGAGCAACGATACCTGATCTGTAATCTGTAATGTTTGAATCAATA 4428  
Qy 4436 AACCGTTAATTCGTGAGTTGAATCTTGTCTGATCTCTTAATCTTAATCTGCTCA 4495  
Db 4429 AACCGTTAATTCGTGAGTTGAATCTTGTCTGAGTATTTCTTCTTAATCAATTT 4488  
Qy 4496 CCATAGCAACCGGTTACATTAATCTGTAATGCGCTTGCGA----AATCCCTAGT 4551  
Db 4489 CCATAGCAACCGGTTAATTAAGCATGGGCGGTTAATCAATTAATCAAGAAACCCCTAGT 4548  
Qy 4552 GATGAGTTGACCACTCCCTCTATGCGGCTGCTGCGTGGTGGGCGCGGACAGACGA 4611  
Db 4549 GATGAGTTGACCACTCCCTCTGCGGCTGCTGCGTCACTAGGCGCGGACACAAA 4608  
Qy 4612 GCTCTGCGTGTGCGAATTTGTGCGAGGCGCCACGAGCGAGCGAGCAGTAA 4671  
Db 4609 GGTGCGCCGACGCGCGGCTTGGCCCGGCGGCTCAAGTGAAGCGAGCGCGCAGAGA 4668  
Qy 4672 GGGAGTGGCCAA 4683  
Db 4669 GGGAGTGGCCAA 4680

RESULT 10

US-09-807-802A-18  
; Sequence 18, Application US/09807802A  
; Patent No. 6759237  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, James M.  
; APPLICANT: Xiao, Weidong  
; TITLE OF INVENTION: Adeno-Associated Virus Serotype 1 Nucleic Acid Sequences,  
; FILE REFERENCE: GNPV.031USA  
; CURRENT FILING DATE: US/09/807, 802A  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/25694  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 4681  
; TYPE: DNA  
; ORGANISM: AAV-2  
US-09-807-802A-18  
Query Match 69.8%; Score 3267.8; DB 3; Length 4681;  
Best Local Similarity 82.3%; Pred. No. 0;  
Matches 3864; Conservative 0; Mismatches 807; Indels 22; Gaps 9;  
Qy 1 TTGGCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCGCGGACCAAGGTGCGC 60  
Db 1 TTGGCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCGCGGACCAAGGTGCGC 60  
Qy 61 CGAGCCCGGGCTTGGCCCGGCGGCTCACTGAGCGGAGCGGCGGAGAGGGAGTG 120  
Db 61 CGAGCCCGGGCTTGGCCCGGCGGCTCACTGAGCGGAGCGGCGGAGAGGGAGTG 120  
Qy 121 GCCAATCTCATCACTAGGGGTTCTGAGGAGGTGAGTCTGACGTGAATTAAGTCATAG 180  
Db 121 GCCAATCTCATCACTAGGGGTTCTGAGGAGGTGAGTCTGACGTGAATTAAGTCATAG 180  
Qy 181 GGTAGGAGGTCTGTATTAAGAGTCACTGAGTGTTCGACATTTTCGACACCAT 240  
Db 181 GGTAGGAGGTCTGTATTAAGAGTCACTGAGTGTTCGACATTTTCGACACCAT 240  
Qy 241 GTGTCAAGCTGGGTATTTAAGCCGAGTGAACGAGGCTCCATTTGAAGCGGGA 300  
Db 241 GTGTCAAGCTGGGTATTTAAGCCGAGTGAACGAGGCTCCATTTGAAGCGGGA 300  
Qy 301 GATTGAAACGCGCAG-CGCAATGCGGGGTTTACGAGATTGTATTAAGTCCCAAGC 359  
Db 301 GATTGAAACGCGCAGCCCGCAATGCGGGGTTTACGAGATTGTATTAAGTCCCAAGC 360  
Qy 360 ACTTTGACAGACATCTGCGCGCAATTTCTGACAGCTTTTGAATCGGTGCGGAAAG 419  
Db 361 ACTTTGACAGACATCTGCGCGCAATTTCTGACAGCTTTTGAATCGGTGCGGAAAG 420  
Qy 420 AATGGAGTTGCGCCGAGATTCTGACATGATCTGAATCTGAATGAGAGGCAACCCCTGA 479  
Db 421 AATGGAGTTGCGCCGAGATTCTGACATGATCTGAATCTGAATGAGAGGCAACCCCTGA 480  
Qy 480 CCGTGGCCGAGAACTGACGCGGCACTTCTGATCTCACTGCGCGCGGTGAGTAAGGCC 539  
Db 481 CCGTGGCCGAGAACTGACGCGGCACTTCTGATCTCACTGAGGAAATGCGCGGTGAGTAAGGCC 540  
Qy 540 CGAGGCGCTCTCTTGTGTCAGTTCAGAGAGGCGAGTCTTCACTTCACTCAATTC 599  
Db 541 CGAGGCGCTCTTGTGTCAGTTCAGAGAGGCGAGTCTTCACTTCACTCAATTC 600  
Qy 600 TGTGAGAGACACGAGGGGTCAATTCATGCTGGCGGCTCTGAGTGAATTAAGC 659  
Db 601 TGTGAGAGACACGAGGGGTCAATTCATGCTGGCGGCTCTGAGTGAATTAAGC 660  
Qy 660 ACAAGCTGTGACAGCACTACCGCGGAGTGAAGCGGACCTTCCCACTGTTGCGG 719

Dh 661 AAAAATGATTCAGAGATTTTACCGCGGATCGAGCCGACTTTGCCAAACTGTTCCGGG 720  
Qy 720 TGACCAAGAGCGGTAAATGGCGCCGGAGGGGGGAAACAAGTGTGGACGAGTCAATCC 779  
Dh 721 TCACAAAGACCAAGAAATGGCGCGAGGGGGAACAAGTGTGGATAGTCAATCC 780  
Qy 780 CCAACTACTCTCTGCCCAAGACTGAGCCGAGCTGCAATGGGCGTGAATAACATGAGG 839  
Dh 781 CCAATTACTGTCTCCCAAAACCCAGCGCTGAGCTCAGTGGGCGTGAATAATGAGAC 840  
Qy 840 AGTATATAGCGCGTGTAAACTGGCCGAGCCGAACCGCTGTGGCGACGACTGA 899  
Dh 841 AGTATTTAAGCGCGTGTAACTCAAGAGCGCTGAACCGTGTGGCGAGACTGA 900  
Qy 900 CCGCAGTCAGCCAGACCCAGAGAGCAACAAGAACTGAAACCCCAATCTGACGGC 959  
Dh 901 CGCAGCTGTGCGAAGCAGAGCAACAAGAACTCAAGATCCCAATTTGATGCGC 960  
Qy 960 CTGTATCCGGTCAAAAACCTCCGACGCTACATGAGCTGTGGGTGGCTGTGAGC 1019  
Dh 961 CGGTGATCAGATCAAAAACCTCAGCAGGTACATGAGCTGTGGGTGGCTGTGAGCA 1020  
Qy 1020 GGGGATCACTCCGAGAGCAATGTGATTCAGAGAGACCAAGCCTCTGATCTCTTCA 1079  
Dh 1021 AGGGATTTAATCTCGAGAGAGAGTGTATCAAGAGAGACAGGCTCATATCAATCTCTTCA 1080  
Qy 1080 ACGCGGCTCCCACTCGCGGTCCCGAGATCAAGGCGCTCTGGAACAATCGCGCAAGATCA 1139  
Dh 1081 ATGCGGCTCCCACTCGCGGTCCCGAGATCAAGGCTCTGGAACAATCGCGCAAGATTTA 1140  
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Qy 1200 AAACCAACCGCATTTTACCGCATCTCGAGCTGAAGGCTGACGACCTGCTTACCGCGCT 1259  
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Qy 1260 CCGCTTTCTCGGCTGGGCGCCAGAAAAGTTTCGAAAAACGCAACCATCTGCTGTTTG 1319  
Dh 1261 CCGTCTTTCTGGGATGGGCGACGAAAAGTTTCGAGAGAGAACCATCTGCGCTGTTTG 1320  
Qy 1320 GGGCGGCAACCGGCGCAAGACCAACATCGCGGAAGCCATCGCGCGCGTGCCTTCT 1379  
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Dh 1381 ACGGTTGTGTAACCTGAGCAATGAGAACTTCCCTTCAACGATGTGTGACAAAGATG 1440  
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Dh 1501 TCGGAGGAAGCAAGGTGCGGTGACCAAAATGCAATGCTCGGCCAGATTCATCCCA 1560  
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Qy 1860 ATTCATGACGTGACAGCGCGAAGAGCTCCGTGCACTTTGCCGACAGTACCAAAACA 1919  
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Dh 2038 C---CGTGTCAAGATCTCAACCGGTTCTGTCTCAAAAAGGCGTATCAAGAACTGTGCT 2094  
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Qy 2157 ACGTGAATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAACCAAGTATGCTGCC 2216  
Dh 2152 ATGTGATTTGATGATGATGATCTTTGACAAATTAATTAATCAGGTATGCTGCC 2211  
Qy 2217 GATGTTATCTTCCAGATTTGGCTGTGAGACAACTCTCTGAGGGCATTTGCGCAGTGTG 2276  
Dh 2212 GATGTTATCTTCCAGATTTGGCTGTGAGACAACTCTCTCAAGAAATTAACAGTGTG 2271  
Qy 2277 GACTTGAACCTGAGGCGCCGAAACCCAAAGCCAAACAGCAAAAGCAGACGAGCGG 2336  
Dh 2272 AAGCTCAACCTGAGCCACACACACAAACCCGAGAGGCGCATAGAGACAGCAGG 2331  
Qy 2337 GGTCTGTGCTTCTGTGCTACAGTACCTGAGACCTTTCACAGCACTGCAAGGCGGAG 2396  
Dh 2332 GGTCTGTGCTTCTGTGCTACAGTACCTGAGACCTTTCACAGCACTGCAAGGCGGAG 2391  
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Dh 2392 CCGGTCAACGAGGAGAGCGCGCGCTTGAAGCAAGCAAGGCTTTCAGACAGCTC 2451  
Qy 2457 AAAGCGGTGACAACTCGTACTCGGTATTAACAGCGCGAGCGGAGTTTCAGAGCGT 2516  
Dh 2452 GACAGCGAGACCAACCGTACTCAATGATCAACAGCGCGAGGAGTTTCAGAGCGC 2511  
Qy 2517 CTGCAAGAGATACGTCTTTTGGGGCAACCTCGGGGAGCAGTCTTTCAGGCGCAAGAG 2576  
Dh 2512 CTTAAAGAGATACGTCTTTTGGGGCAACCTCGGGGAGCAGTCTTTCAGGCGCAAGAG 2571  
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Dh 2572 AGGTTTCTGAACTTCTCGGCTGTGTGAGAGAGTCTTAAGACGCTCTCTGAGAAAG 2631  
Qy 2637 CGTCCGTGAGAGAGTGCACCAAGAGCAGACTCTCTCTCGGAGATTTGCAAGACAGG 2696  
Dh 2632 AGGCGGTGAGAGACTTCTCTGTGAGACAGACTCTCTCTCTCGGAGACCGAAAGCGGCG 2691  
Qy 2697 CAGCAGCGCTAAAGAGACTCAATTTTGTGATGAGCTTGGCGACTGAGAGTCAAGTCC 2756  
Dh 2692 CAGCAGCGCTGAAGAAAGATTTGAAATTTTGTGATGAGCTGAGAGCGGAGCTCAAGTCT 2751  
Qy 2757 GACCCACAACTCTCGAGAACTCCAGCAACCCCGCTGTGTGGGACTTAACAATG 2816  
Dh 2752 GACCCCGAGCTCTCGAGAGCAACCGAGAGCCCGCTGTGTGGGACTTAACAATG 2811  
Qy 2817 GCTTCAAGCGGTGCGACCAATGTGAGACAAATTAACGAAGCGCGGAGGTGGTAAAT 2876  
Dh 2812 GCTACAGGCAAGTGGCGACCAATGGCAGACAAATTAACGAAGGCGCGGAGGTGGTAAAT 2871







US-09-782-378A-1

69.3%; Score 3244.2; DB 3; Length 4675;

Query Match 82.2%; Pred. No. 0; Mismatches 808; Indels 28; Gaps 10;

Best Local Similarity 0; Conservative 0; Matches 3857;

1 TTGGCACTCCCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAACAAAGGTCCG 60  
1 TTGGCACTCCCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAACAAAGGTCCG 60  
1 TTGGCACTCCCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAACAAAGGTCCG 60  
61 CGAGCGCCGCGCTTTGCGCGCGCGCTCACTGAGCGCGCGCAAGAGGAGT 120  
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121 GCGCACTCATCACTAGGGGTTCTGAGAGGGTGAAGTGAAGTGAAGTGAAGTGAAG 180  
121 GCGCACTCATCACTAGGGGTTCTGAGAGGGTGAAGTGAAGTGAAGTGAAGTGAAG 180  
181 GGTAGGAGGTCCTGTATTAAGAGTCACTGAGTGTGTCGACATTTGCGACACCAT 240  
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241 GTGTCACGCTGGGTATTTAAAGCCGAGTGAAGCAGAGGCTCTCCATTTGAAGCGG 300  
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301 GGTTTGAAGCGGCGAG - GGCATAGCGGGGTTTAAAGATTTGATTTAAGTCCCGACG 359  
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360 ACCTTGAAGCAGCATCTGCGCGCATTTTCTGACAGCTTTGTGAACCTGGTGGCGGAG 419  
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540 CCGAGCGCGCTCTCTTTGTTGATTCGAGAGGCGAGTCTCTTCCACTCCATATTC 599  
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661 AAAAATCTATTCAGAGATTTACCGCGGGATCGAGCGGACCGCTGCGCAAGTGGTCCG 720  
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721 TCACAAAGACCAAGATGAGCGCGCGGAGGCGGAGAACAGAGTGTGAGCAGATGCTA 780  
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960 CTGTCATCCGCTCAAAAACCTTCGACGCTACATGAGCTGGTGGGCTGGTGGAGCC 1019  
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3896 AGAGAAATCAAAAGCACTTAACCCGCTGAGCAAGCAAGTGGAGTGGAGTCAAGTCA 3955  
3883 AGAGAAATCAAAAGCACTTAACCCGCTGAGCAAGCAAGTGGAGTGGAGTCAAGTCA 3942  
3956 TCTCAAGAGAGCAAGCAAGTCTGAGCGGAGAGTGGAGTGGAGTGGAGTGGAGTGGAG 4015  
3943 CTTCAAGAGAGCAAGCAAGTCTGAGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 4002  
4016 TGGAAAGAGAGCGGCGGAGCTTCAACATGCTGATTTGAGCAATGCTAATGATCAAGCA 4075  
4003 AGGATGTCTGAGAGAGAGAGTGTACTTTCAGAGGCGCAATGAGGCAAGATTTCC 4062  
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4136 GCTCTCAAGTCTTCAAAACAGCGCTGTCTCTGGAATCTTCTGAGAGTGGAGTGGAG 4195  
4123 TCTCTCAAGTCTTCAAAACAGCGGCTGTCTCTGGAATCTTCTGAGAGTGGAGTGGAG 4182  
4196 GCTTCAAGAGTGGCTTCAATCAACCGGATTTTCAAGAGCAAGTGGAGTGGAGTGGAG 4254  
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4255 TTTGAATGGAGCTTCAAG 4314

Dh 4243 TCGAGTGGAGCTCAGAGAGAAACAGCAGAACGCTGGAAATCCGAAATTCAGTACACTT 4302  
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Qy 4671 AGGAGTGGCCAA 4683  
Db 4663 AGGAGTGGCCAA 4675

## RESULT 12

US-09-782-378A-2

; Sequence 2, Application US/09782378A  
; Patent No. 691635  
; GENERAL INFORMATION:  
; APPLICANT: Hearing, Patrick  
; APPLICANT: Bahou, Madie  
; APPLICANT: Sandaou, Ziv  
; APPLICANT: Gantenko, Dmitri  
; TITLE OF INVENTION: Adenoviral Vectors  
; FILE REFERENCE: STONYB-04970  
; CURRENT APPLICATION NUMBER: US/09/782,378A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/237,747  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 4675  
; TYPE: DNA  
; ORGANISM: Human adeno-associated virus 2  
US-09-782-378A-2

Query Match 69.3%; Score 3244.2; DB 3; Length 4675;  
Best Local Similarity 82.2%; Pred. No. 0;  
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;

Qy 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCGCGGCGCAAAAGTGGCC 60  
Db 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCACTGAGGCGCGGCGCAAAAGTGGCC 60  
Qy 61 CGAGCGCCGGGCTTTGCCCGGGGCGGCTCAGTGAAGCGAGGCGCGAGAGGAGTG 120  
Db 61 CGAGCGCCGGGCTTTGCCCGGGGCGGCTCAGTGAAGCGAGGCGCGAGAGGAGTG 120  
Qy 121 GCCAACTCCATCACTAGGGGTTCTGAGAGGGGTGAGTCTGACGTGAATTCATAG 180  
Db 121 GCCAACTCCATCACTAGGGGTTCTGAGAGGGGTGAGTCTGACGTGAATTCATAG 180  
Qy 181 GGTTAGGAGGTCTGTATTAAGAGTCACTGAGTGTGTTTTCGACATTTTTCGACACCAT 240  
Db 181 GGTTAGGAGGTCTGTATTAAGAGTCACTGAGTGTGTTTTCGACATTTTTCGACACCAT 240

Qy 241 GTGTACGCTGGGTATTTTAAAGCCGAGTGAAGCAGCAGAGGCTCCATTTTGAAGCGGA 300  
Db 241 GTGTACGCTGGGTATTTTAAAGCCGAGTGAAGCAGCAGAGGCTCCATTTTGAAGCGGA 300  
Qy 301 GGTTTGAACGCGAG--CGCCATCGCGGGTTTTACGAGATTGTGATTGAAGTCCGAGCG 359  
Db 301 GGTTTGAACGCGAGCGCCATCGCGGGTTTTACGAGATTGTGATTGAAGTCCGAGCG 360  
Qy 360 ACCTTGAACGACATCTGCCCGGCAATTTTGAACGCTTTGTGAACCTGGGTGGCCGAGAGG 419  
Db 361 ACCTTGAACGACATCTGCCCGGCAATTTTGAACGCTTTGTGAACCTGGGTGGCCGAGAGG 420  
Qy 420 AATGGAGTTCGCGCGAGATTCTGAACATGATCTGAATCTGAATTGAGCAGGACCCCTGA 479  
Db 421 AATGGAGTTCGCGCGAGATTCTGAACATGATCTGAATCTGAATTGAGCAGGACCCCTGA 480  
Qy 480 CCGTGGCCGAGAACTGACAGCGGACTTCTGTGCACTGGCGCGCGGTGATTAAGGCC 539  
Db 481 CCGTGGCCGAGAACTGACAGCGGACTTCTGTGCAAGGATGGCCCGGTGATTAAGGCC 540  
Qy 540 CGGAGGCCCTCTTCTTTGTTCACTTGAAGAGGCGAGTCTTCCACTTCATATTC 599  
Db 541 CGGAGGCCCTTCTTTGTTCACTTGAAGAGGCGAGTCTTCCACTTCATATTC 600  
Qy 600 TGGTGAAGACCAAGGGGTCAATCCATGAGTGTGGGCGCTTCTGAGTCAATTAAGCG 659  
Db 601 TGGTGAAGACCAAGGGGTCAATCCATGAGTGTGGGCGCTTCTGAGTCAATTAAGCG 660  
Qy 660 ACAAGCTGTGACAGACCATCTACCGCGGATCGAGCCGACCTTGCCCAATGTTGGCG 719  
Db 661 ACAAGCTGTGACAGACCATCTACCGCGGATCGAGCCGACTTGGCCAACTGTTGGCG 720  
Qy 720 TGAACCAAGACGTAATGAGCGCGGAGAGGGGGAACAAGGTGTGAGCGATGATCATCC 779  
Db 721 TGAACCAAGACGTAATGAGCGCGGAGAGGGGGAACAAGGTGTGAGCGATGATCATCC 780  
Qy 780 CCAACTACCTCTGCCCAAGACTCAGCGCGAGTGAAGTGGGCGTGAATGAGAGG 839  
Db 781 CCAACTACCTCTGCCCAAGACTCAGCGCGAGTGAAGTGGGCGTGAATGAGAGG 840  
Qy 840 AGTATTAAGCGCGTGTTTAACTTGGCGAGCGCAACGCTGTGGCGCAGACTGA 899  
Db 841 AGTATTAAGCGCGTGTTTAACTTGGCGAGCGTGAACGCTGTGGCGCAGACTGA 900  
Qy 900 CCAAGTCAAGCCAGACCCAGAGCAAGAGAGATCTGAACCCCAATTCGAGCGCG 959  
Db 901 CCAAGTCAAGCCAGACCCAGAGCAAGAGAGATCTGAACCCCAATTCGAGCGCG 960  
Qy 960 CTGTCACTCCGTCAAAACTCCGCAAGCTACATGAGTGTGGGTGGCTGGTGAACC 1019  
Db 961 CTGTCACTCCGTCAAAACTCCGCAAGCTACATGAGTGTGGGTGGCTGGTGAACA 1020  
Qy 1020 GGGGCATCACTCCGAGAGCAGTGAATCCAGAGGACAGGCTGTGATCTCTTCA 1079  
Db 1021 GGGGCATCACTCCGAGAGCAGTGAATCCAGAGGACAGGCTGTGATCTCTTCA 1080  
Qy 1080 AGCGCGCTCACTCGCGGTCCAGATCAAGGCGCTCTGACATTAAGCGGAGATCA 1139  
Db 1081 AGCGCGCTCACTCGCGGTCCAGATCAAGGCGCTCTGACATTAAGCGGAGATCA 1140  
Qy 1140 TGGCGCTGAACAATCCGCGCGGACTACCTGTAGGCGCGCTCGCGCGCGAGATTA 1199  
Db 1141 TGGCGCTGAACAATCCGCGCGGACTACCTGTAGGCGCGCGCTCGCGCGAGATTA 1200  
Qy 1200 AAACCAACGCGATTTACCGCATCTGAGCTGAACGCTGAACCTGCTTACCGCGGCT 1259  
Db 1201 AAACCAACGCGATTTACCGCATCTGAGCTGAACGCTGAACCTGCTTACCGCGGCT 1260  
Qy 1260 CCGTCTTCTCGGCTGGGCGCGAGAAAGTTGCGAAAGCGCAACCATCTGGCTGTTTG 1319  
Db 1261 CCGTCTTCTCGGCTGGGCGCGAGAAAGTTGCGAAAGCGCAACCATCTGGCTGTTTG 1320

QY	1320	GGCCGGCCACCA	CGGGCAAGACCA	CAATGCGGAAGCCATCGCCACGCGTGGCTCT	1379		
Db	1321	GGCCCTGC	CAACTACCGGGAAGCA	CAATCGCGGAAGCCATGCCCCACCTGGGCTCT	1380		
QY	1380	ACGGCGCGGTCA	CACTGGGACCA	ATGAGACTTTCCTTCAACA	GATGGCGTCA	MAAGATG	1439
Db	1381	ACGGGTGGGTAA	CTGAGCAATGAGAACTTTCCTTCAACA	CTGTGTGCA	CAAGAATGG	1440	
QY	1440	TGATCTGGTGGG	AGAGGAGGCA	GATGACGGGCCAAGTGGTGA	GTCGCCCAAGGCAATTC	1499	
Db	1441	TGATCTGGGTGGG	AGAGGAGGAGAA	GATGACGCCCAAGTGGTGA	GTCGCCCAAGGCAATTC	1500	
QY	1500	TCGGCGGCA	GCAAGGTGGCGGTGAC	CAAAAGTCAGTGTCCGCCAATGCATCCCA	1558		
Db	1501	TCGGAGGAAGCA	MAAGGTGGCGGTGACCA	GAATGCAAGTCTCGGCCAATGACCCGA	1560		
QY	1560	CCCCCGTGA	TCGTCACTCTCA	CAACCAATGTGGCGGTGATTTGA	CGGGAACAGCAACA	1619	
Db	1561	CTCCCGTGA	TGCTCACTCTCA	CAACCAATGTGGCGGTGATTTGA	CGGGAACAGCAACA	1620	
QY	1620	CTTTCGAGCA	CCAGCAGCGCGTTG	CAAGACCGGATTTCAAAATTTGA	CTCACCCGCTC	1679	
Db	1621	CCTTGGAACA	CCAGCAGCGCGTTGCA	GAACCGGATTTCAAAATTTGA	CTCACCCGCTC	1680	
QY	1680	TGGAGCATGA	CTTTGGCAAGGTGAC	CAAAAGCAGAAGTCAAAGATTTTCCGCTGGGCGC	1739		
Db	1681	TGGATCATGA	CTTTGGGAAAGTCACA	CAAGCAGAAGTCAAAGATTTTTCGCTGGGCA	1740		
QY	1740	AGGATCAGCTGA	CCGAGGTGGCGCATGAGTTCT	AGTCAAGAAAGGTGGAGTCCACACA	1799		
Db	1741	AGGATCAGTGTG	ATGAGGTGAGCATGAAATCT	AGTCAAAAGGTGGAGTCCAGAA	1800		
QY	1800	GACCCGCCCCG	ATACACCGGATTA	AAAGCAGACCGGCGCTGCCCCATGTCGCGG	1859		
Db	1801	GACCCGCCCCG	ATACACCAATTA	AGTGAACCCAAACGGGTGGCAATGATTTGGCGC	1860		
QY	1860	ATCCATCGA	CGTCA	GC	CGGAAGAGCTCCGCTGGA	CTTTGCCAGACGTAACAAACA	1919
Db	1861	AGCCATCGA	CGTCA	GC	CGGAAGAGCTCCGCTGGA	CTTTGCCAGACGTAACAAACA	1917
QY	1920	AATGTTCTG	CTCAGCGCGG	CAATGCTTTTCCCTGCA	AAACATGCGAGAGA	1979	
Db	1918	AATGTTCTG	CTCAGCGG	CAATGATGCTTTTCCCTGCA	AAATGCGAGAGA	1977	
QY	1980	TGAATCAGA	ATTTCAACATTTGCT	CACGACCGGACCA	GAGACGTTCAGATGTTTTCC	2039	
Db	1978	TGAATCAGA	ATTTCAAAATCTG	CTCACCTCACGACAGAAAGACGTTTA	AGTGTCTTC	2037	
QY	2040	CCGGCGGTCA	GAATCTCA	CCGCT---CGTCAGAA	AGAGACGTATCGGAACTGTG	2096	
Db	2038	C---CGTGTCA	GAATCTCA	CCGCTTTCTGTCTG	CAAAAAGCGATCA	GAATCTGTCT	2094
QY	2097	CCATTCATCA	TCTGCTGGGCGGGCT	CCCCAGATGCTTTGCTCGGCTG	CGATCTGTCTCA	2156	
Db	2095	ACATTCATCA	TATCAATGGGAAAGGTG	CCAGA---CGCTTGA	CACTGCTCGCATCTGTGCA	2151	
QY	2157	ACGTGGATCTG	GAATGATCTGTGTTT	TGAGCAATTAATGACTTAA	ACAGATGATGGCTGC	2216	
Db	2152	ATGTGGAATTTG	ATGATCTGCACTTTTGA	CAATTAATATATTTAAATCA	AGATGATGGCTGC	2211	
QY	2217	GATGATTA	CTTTCAGATTGGCT	CGAGACAACCTCTG	AGGCAATTCGGCAGTGTGG	2276	
Db	2212	GATGATTA	CTTTCAGATTGGCTG	AGAGCACTCTTGA	AGGAATAAGCAATGTGGTG	2271	
QY	2277	GACTTGA	AACCTGGA	CCCCCGAAACCA	AGCACAACGCAAGACGACGCGCG	2336	
Db	2272	AAGCTCA	AAACCTGGCCCA	CAACCAAGCCCGCAGACGCAATTA	AGAGACGACGACGCG	2331	
QY	2337	GATCTGTG	ATCTTCCGGGCTCA	CAAGATCTCGGACCTTCA	ACGACTGGA	CAAGGGGAG	2396
Db	2332	GATCTGTG	ATCTTCCGGGCTCA	AGATCTCGGACCTTCA	ACGACTGGA	CAAGGGGAG	2391
QY	2397	CCCGTCA	ACGGCGAGATG	CA	CGGCGCTCTGAGACG---ACA	AGCTTACGACGACGCT	2455

Db	2392	CCGGTCAACGAGGCGAGGACCGCGGCGCTCGAGCACTGACAAAGCTTCAGACCGGACACT	24511
Oy	2456	CAAAACGGGATGCAATCCGTACTCGGGAATATACCAACGCCGACGCGAGTTTCAGAGACG	2515
Db	2453	CGACACGGAGACAAACCCGTACTTAAGTACAAACCGCCGACGCGAGTTTCAGAGACG	25111
Oy	2516	TCGCAAGAAAGTACGTCTTTTGGGGGCACTCGGGGAGACAGTCTTCAGGCCAAGAA	25757
Db	2512	CCTTAAAGAAAGTACGTCTTTTGGGGGCACTCGGGAGACAGTCTTCAGGCCAAGAA	25711
Oy	2576	GAGGATCTCGAATCTTTTGGTCTGGTGAAGAAAGTCTAAGACGGCTCTGGAAGAA	26355
Db	2572	GAGGATCTTGAACCTCTGGGGCTGGTGAAGAACTTGAAGACGGCTCGGGGAAAAA	26311
Oy	2636	ACGTCCGGTAAGACGTCCCAAAAGACCAAGACTCCCTCGGGCACTGGCAACAGAG	26959
Db	2632	GAGGCGGTAAGACCTCTCTGGGACCAAGACTCTCTCGGGCAACGGAAAGCGGG	26919
Oy	2696	CCAGACGCCCGGTAAAGAGACTCAATTTTGGTCAAGCTGAGCGCACTGAGTCACTCC	27555
Db	2692	CCAGACGCTGCAAGAAAAAGTTGAATTTTGGTCAAGCTGAGCGCACTGAGTCACT	27511
Oy	2756	CGACCCACAACTCTCGGAGAACTTCAGCAACCCCGCGCTGTGGGACCTTACAT	28155
Db	2752	TGACCCCGAGCTCTCGGACAGCCACGACGAGCCCTCTGTGGGAACTTAATACAT	28111
Oy	2816	GAGCTCAGGCGGTGGCGGACCAATGGGAGACAAATTAAGAAAGCGCGAGTGGGTA	28755
Db	2812	GAGTCAAGAGAGTGGCGCAACAAATGGAGACAAATTAAGAAAGCGCGAGTGGGTA	28711
Oy	2876	TGCTCAGAGAAATTGGCATTTGCGATTCCACATGGCTGGGCGACAGAGTCAATCAACCA	29355
Db	2872	TTCTCTCGGAAATTGGCATTTGCGATTCCACATGGGCGACAGAGTCAATCAACCA	29311
Oy	2936	CACCCGAACATGGGCTTTGCCCACTATTAACAACAACCTTTACAGCAAAATCTCCAGTGC	29955
Db	2932	CACCCGAACATGGGCTTTGCCCACTATTAACAACAACAACCTTTACAGCAAAATCTCCAGTGC	29911
Oy	2996	TTCAACGGGGGCGGACCAACGACCAACCACTATTCGGGTAACAGCAACCCCGGGGGTATTT	30555
Db	2992	ATCA---GGAACCTCGAAACGACAACTACCTTTGGCTACAGCAACCCCTTGGGGATTTT	3048
Oy	3056	TGATTTCAACAGATTCCATGCTCAATTTCTCAACAGTACGCGGACGACATCAACA	31155
Db	3049	TGACTTCAACAGATTCCATGCTCAATTTCTCAACAGTACGCGGACGACATCAACA	3108
Oy	3116	CAATTTGGGATTTCCGGCCCAAGAGACTCAACTTCAAGCTTCAACATCAAGTCAAGAA	31757
Db	3109	CAACTGGGATTTCCGACCCCAAGAGACTCAACTTCAAGCTTCAACATCAAGTCAAGAA	3168
Oy	3176	GATCAACGAAATGATGGCGTCAAGACATGCTATTAACCTTACAGACAGGTTCAAGT	32355
Db	3169	GATCAACGAAATGATGGCGTCAAGACATGCTATTAACCTTACAGACAGGTTCAAGT	3228
Oy	3236	CTTTCGGAATCGGAGTACGATTCGCCGTAAGTCTCGGCTCTGCGACCAAGGCTGCT	32959
Db	3229	GTTTACTACTTCGAGTACAGCTCCGTAAGTCTCGGCTCTGCGACCAAGGCTGCT	32888
Oy	3296	CCCTCCGTTCCCGCGGACGTGTTCAATGATTCGCAAGTACGGCTAACGCTCAACAA	33555
Db	3289	CCCGCGTTCCCGAGAGACGTCTTCAATGATTCGCAAGTACGGCTAACGCTCAACAA	3348
Oy	3356	TGGACGACGAGGAGTGGGACGCTATCTTTTACTGCTCGGAATATTTCCATGGCAGT	34155
Db	3349	CGGAGTACGAGGAGTGGGACGCTCTTCAATTTTACTGCTCGGAATATTTCTTCAGT	3408
Oy	3416	GCTGAGAACGGGACATTAATTTTACTGCTGAGTCACTTCAGAGACGCTTTCACAG	34755
Db	3409	GCTGAGTACGGGAAACATTTTACTGCTGAGTCACTTTTGAAGACGTTCTTTCACAG	3468
Oy	3476	CAGCTACGCGACACGACGAGCTGGAACGGCTGATGAATCTTCAATCAACAGTACT	35355

Db 3469 CAGCTACGCTCAGACGACGAGCTTGACCGCTCTCATGAATCCTCTCATGCACAGTACT 3528  
Qy 3536 GTATTACCTGAAACGAATCAATCAATCCGGAAGTCCCAAAACAAAGACTTGCTTT 3595  
Db 3529 GTATTACTTGACGAACAAACACTCCAAAGTGAACCAACGAGTCAAGGCTTCATTT 3588  
Qy 3596 TAGCCGTGGGCTCTCAGCTGGCATGTCTGTTCAGCCCAAAATGGCTACTGACCTTG 3655  
Db 3589 TTCTCAGGCCGAGAGGAGTGAATTTCCGAGACAGTCTGAGAACTGGCTTCTCTGACCTG 3648  
Qy 3656 TTACCGGACGACGCGCTTTCTTAAACAAACAGACAAACAAACAGCAACTTACTG 3715  
Db 3649 TTACCGGACGACGAGTATCAAGACATCTGCGGATTAACAACACAGTGAATCTCGTG 3708  
Qy 3716 GACTGGTCTTCAAAATTAATCTTAATGGCGTGAATCTTAATCAACCTCGACCTGC 3775  
Db 3709 GACTGGAGTACCAAGTACCACTCTAATGGACAGACACTCTGCGGAATC-----CGGC 3762  
Qy 3776 TATGGCTCACAACAAAGCAACAAAGAGTCTTTTCCATGACGCGTGTCTATGATTTT 3835  
Db 3763 CATGGCAAGCCACAAAGACAGATGAAGAAAGTTTTCCTCAGAGCGGGGTTCTCATCTT 3822  
Qy 3836 TGGAAAGAGAGCGCCGAGCTTCAACACGCACTGGCAATGTCTATGATCAAGACGA 3895  
Db 3823 TGGGAAGCAGGCTCAGAGAAAAACAATGTGAACATGAAAAAGTCAATGATTACAGACGA 3882  
Qy 3896 AGAGGAATCAAAAGCACTAACCCGTGCGACCGGAAGATTTGGAGCTGGGACGTAA 3955  
Db 3883 AGAGGAATCGGAACAAACAAATCCGTGCTACGAGAGATGATGTCTGATCTACCA 3942  
Qy 3956 TCTCCAGACGACGACAGACAGACCCCTGCGACGAGATGATGATTTATGGAGCTTACC 4015  
Db 3943 CTTCCAGAGAGGCAACAGACAGAGCTACCGGAGATGTCAACACAGAGCGCTTCTCC 4002  
Qy 4016 TGAATGTGTGGCAAGACAGACGATPACTGACGGTCTTATTTGGSCCAAATTC 4075  
Db 4003 AGGCATGTCTGGCGAGACAGAGATGTACTCTCAGGGGCGCCATCTGGGCAAGATTC 4062  
Qy 4076 TCACACGGATGGAACCTTCAACCCGCTCTCTCTCATAGGGCGCTTTGAGCTTAAGCAACC 4135  
Db 4063 AACACGGAGCGACATTTTCAACCCCTCTCTCTCATAGGGGATTTGGAGCTTAAGCAACC 4122  
Qy 4136 GCTCTCAGATCTCATCAAAAACACGCTGTCTTCTGCAATCTCCGGGACAGATTTTC 4195  
Db 4123 TCTCTCAAGATTTCTCATCAAGAACACCCCGGTACTGCGAATCCTTGACACACTTCAG 4182  
Qy 4196 GCGTCAAAAGTTTGTCTTATTCATCAACCAATTTCCACAGACA-AGTAGCGTGGAGA 4254  
Db 4183 TCGCGCAAAAGTTTGTCTTCTCATCAACAGTACTCCACGGGACACGGTCAAGCGTGGAGA 4242  
Qy 4255 TTGAATGGAGCTGCGAAGAAAGAAACAGCAACGCTGGAATCCCGAAGTGCAGTATCAT 4314  
Db 4243 TCGAGTGGAGCTGCGAAGAAAGAAACAGCAACGCTGGAATCCCGAATTCAGTACACTT 4302  
Qy 4315 CTAATATGCAAAATCTGCCAACGTTGATTTCACTGTGACAAACATAGACTTTATATCTG 4374  
Db 4303 CCAACTAACAAAGTCTGTATATGTGATTAACCTGAGATCTAATAGCGGTATTCAG 4362  
Qy 4375 AGCTCTGCGCCATTTGGACACCGCTTACTACCCGCTGTATTTGTGTATATCAAT 4434  
Db 4363 AGCTCTGCGCCATTTGGACACAGATATCTGACTCGTATCTGTATTTGCTGTATATCAAT 4422  
Qy 4435 AAACCGGTTAATGTGTCAAGTGAACCTTGGTCTCATGTCCCTTAATTTATCTATCTGTC 4494  
Db 4423 AAACCGGTTAATGTGTCAAGTGAACCTTGGTCTGTGCGTATTTCTTCTATCTATCTT 4482  
Qy 4495 ACCATAGCAACCGGTTACATTAACCTGTTAGTTCGCGA-----ATACCCCTAG 4550  
Db 4483 TCCATGGCTAGGTAGATTAAGATAGATGGCGGGTTAATCATTAACTAACAAGAACCCCTAG 4542  
Qy 4551 TGAATGAGTTGCCACTCTCTTATGCGCGCTCGCTCGCTGAGTGGGGCGGACAGAGAG 4610  
Db 4543 TGAATGAGTTGGCACTCTCTCTGCGCGCTCGCTCGCTCACTGAGGCGGGGCGACCAA 4602

Qy 4611 AGCTTGCGCGCTGCGGACCGCTTTGGTCCGAGGCCCCACGAGGAGAGCGAGCATAG 4670  
Db 4603 AGGTGCGCCACGACCGCCGGGCTTTGGCCGGCGGCTTGAAGTGAAGCAGCGCGCAGAG 4662  
Qy 4671 AGGAGTGGCCAA 4683  
Db 4663 AGGAGTGGCCAA 4675

RESULT 13  
us-10-111-708-1  
; Sequence 1, Application us/10111708  
; Patent NO. 6995010  
; GENERAL INFORMATION:  
; APPLICANT: UENO, Takashi  
; APPLICANT: MATSUMURA, Hajime  
; APPLICANT: TANAKA, Kei-ji  
; APPLICANT: IWASAKI, Tomoko  
; APPLICANT: UENO, Mitsuhiko  
; APPLICANT: FUJINAGA, Kei  
; APPLICANT: ASADA, Kiyozo  
; APPLICANT: KATO, Ikunoshin  
; TITLE OF INVENTION: GENE TRANSFER METHOD  
; FILE REFERENCE: UENO=9  
; CURRENT APPLICATION NUMBER: us/10/111,708  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: PCT JP00 07373  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: JP 11/308839  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4675  
; TYPE: DNA  
; ORGANISM: Adeno-associated Virus  
us-10-111-708-1

Query Match 69.3%; Score 3244.2; DB 4; Length 4675;  
Best Local Similarity 82.2%; Pred. No. 0;  
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;

Qy 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTAGAGCCGCGGACCAAGATCGCC 60  
Db 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTAGAGCCGCGGACCAAGATCGCC 60  
Qy 61 CGACGCGCGGCTTTGCGCGCGGCTTCACTAGAGCGAGCGGCGGACAGAGAGTG 120  
Db 61 CGACGCGCGGCTTTGCGCGCGGCTTCACTAGAGCGAGCGGCGGACAGAGAGTG 120  
Qy 121 GCCAATCCATCACTAGAGGCTCTGAGAGGGGTGAGAGGGGTGAGATCGTGAACGTATAG 180  
Db 121 GCCAATCCATCACTAGAGGCTCTGAGAGGGGTGAGAGGGGTGAGATCGTGAACGTATAG 180  
Qy 181 GGTAGGAGAGTCTGTATTAAGAGTCAAGTGAAGTGTGTCGACATTTTGGACACCAT 240  
Db 181 GGTAGGAGAGTCTGTATTAAGAGTCAAGTGAAGTGTGTCGACATTTTGGACACCAT 240  
Qy 241 GTGGTCAAGCTGGGATTTAAAGCCGAGTGAACAGAGGCTTCCATTTTGAAGCGGGA 300  
Db 241 GTGGTCAAGCTGGGATTTAAAGCCGAGTGAACAGAGGCTTCCATTTTGAAGCGGGA 300  
Qy 301 GGTTTGAACCGGAG-CCGCAATCGCGGGTTTAAAGATTTGAATTAAGTCCCGACG 359  
Db 301 GGTTTGAACCGGAGCGCGCAATCGCGGGTTTAAAGATTTGAATTAAGTCCCGACG 360  
Qy 360 ACCTTAGAGACATCTCCCGGCACTTCTGACAGCTTTGTGAACCTGGGTGGCCGAGAGG 419  
Db 361 ACCTTAGAGGCACTCCCGGCACTTCTGACAGCTTTGTGAACCTGGGTGGCCGAGAGG 420  
Qy 420 AATGGAGTTGCGCGCAATTTCTGACATGATCTGAATCTGAATTTGAGACAGGACCTCTGA 479

Dh 421 AATGGAGTTCGCCGACATTCGACATGATCTGAATCTGATGAGCAGGACCCCTGA 480  
Qy 480 CCGTGGCCGAGAAAGCTGAGCGCGA CTTCTTGSTCCA CTGGGCGCGCTGAGTAGGCC 539  
Db 481 CCGTGGCCGAGAAAGCTGAGCGCGA CTTCTTGCAAGAAATGGCGCGTGTGAATAGGCC 540  
Qy 540 CGAGAGCCCTCTTCTTTGTCAGTTGAGAAAGGCGAGTCTACTTCCACCTCCATATTC 599  
Db 541 CGAGAGCCCTTTCTTTGTGCAATTTGAAAGGAGAGAGACTACTTCCACATGCACTGCG 600  
Qy 600 TGTGTGAGACCA CGGGGGTCAATC CATGTGCTGCGCCGCTTCTGAGTCAGATTAGCG 659  
Db 601 TGTGTGAAACCA CGGGGGTGAATC CATGTGTTTGGAGCTTCTGAGTCAGATTAGCG 660  
Qy 660 ACAAGCTGTGACACATCTACCCGCGGAGTCGAGCCGACCTGTGCCAATGTGTTGCGGG 719  
Db 661 AAAAACTATTGAGAAATTTACCGCGGATCGAACCACTTTGCAAACTGTGTTGCGGG 720  
Qy 720 TGACCAAGACGCTAATGGCGCGGAGGGGGAA CAAGTGTGAGACGAGTCTCATCC 779  
Db 721 TCACAAAGACCAAGAAATGGCGCGGAGGGGAA CAAGTGTGAGAGTGAATGCTCATCC 780  
Qy 780 CCAACTACTCTCTGCGCAAGACTCAGCCGAGCTGCACTGAGCGCTGGA CTAA CATGAGG 839  
Db 781 CCAATTACTTGCTCCCAAAACCCAGCTCAGCTCAAGTGGCGTGA CTAA TATGAAAC 840  
Qy 840 AGTATATAAGCGCGTCTTAAACCTGCGCAGCGCAACCGCTCTGTGCGCAGCACTGA 899  
Db 841 AGTATTAAGCGCGCTGTTGAATCTCAGCGAGCGTAAACGTTGTGTGCGCAGCACTGA 900  
Qy 900 CCGACGAGCGCAGACCCAGAGAGCAAGCAAGATCTGAAACCCCAATCTGAGCGCG 959  
Db 901 CGCACGTGCGGAGACGAGAGCAAGCAAGAAATCAAGATCCCAATCTGATGCGC 960  
Qy 960 CTGTCACTCGGTCAAAAACTCCCGCAGCTACATGAGCTGTGCGGTGCTGTGAGCC 1019  
Db 961 CGGTGATCAGATCAAAAACTTCAGCCAGATGACATGAGCTGTGCGGTGCTGTGAGCA 1020  
Qy 1020 GGGGCACTACCTCCGAGAAAGCATGTGATCTCAGAGAGCAAGGCTCTGATCATCTCTTCA 1079  
Db 1021 AGGGATTAACCTCGAGAAAGATGTGATCTCAGAGAGCAAGGCTCTCAATCATCTCTTCA 1080  
Qy 1080 ACGCGGCTCCAACTCGCGGTCCCGATCAAGCGCGCTCTGGA CAATGCGGCAAGATCA 1139  
Db 1081 ATGGGCTCTCAACTCGCGGTCCCAATCAAGGCTGCTTGA CAATGCGGAAAGATTA 1140  
Qy 1140 TGGCGCTGACCAATCCGCGCCGACTA CTGTGAGCCCGCTCCGCGCACTTA 1199  
Db 1141 TGAAGCTGACTAAAAAGCGCCCGACTA CTGTGTGGGCGAGAGCCGTTGAGGACTTT 1200  
Qy 1200 AAACCAACCGATTTACCGCATCTCTGAGCTGAACGCTGAGCTTCTTACCGCGACT 1259  
Db 1201 CCACCAATCGATTTATTAATTTTGAATTAAGGATGAGTCTCCCAATATGCGGCTT 1260  
Qy 1260 CCGCTTTCTCGGCTGGGCCCGAGAAAGTTTCGAGAAACGCAACCATCTGGCTTTG 1319  
Db 1261 CCGCTTTCTCGGATGGGCTCAGAAAAAGTTTCGAGAAAGCAACCATCTGGCTTTG 1320  
Qy 1320 GGGCGGCAACGAGGAGCAACCATCTGCGAGAGCATCGCCACGCGCTGCTTCT 1379  
Db 1321 GGGCTGCACTAACGGAGAACCAACATCGCGAGGCAATAGCCACACTGTGCTTCT 1380  
Qy 1380 ACGGCTGTGCACTGAGCAATGAGAACTTTCCCTTCAAGATTGCTGCA CAAGATG 1439  
Db 1381 ACGGCTGTGTAACCTGAGCAATGAGAACTTTCCCTTCAAGACTGTGCA CAAGATG 1440  
Qy 1440 TGAATCTGTGAGAGGAGGCAAGATGACGCAAGGCTGTGAGTCCGCAAGGCAATTC 1499  
Db 1441 TGAATCTGTGAGAGGAGGAGGAGATGACGCAAGGCTGTGAGTCCGCAAGGCAATTC 1500  
Qy 1500 TCGGCGGCAAGAGTGCCTGTGACCAAAAGTCAAGTCTGTGCGCCAGATGCATCCA 1559  
Db 1501 TCGGAGGAAGAGGTGCGCTGTGACCAAAATGCAATGCTGTGCGCCAGATGACCGGA 1560

Qy 1560 CCCCCTGATGTCACCTCCAAACCAACATGTGCGCGGTGATTGACGGGAAACAGACCA 1619  
Db 1561 CTCCTGATGTCACCTCCAAACCAACATGTGCGCGGTGATTGACGGGAACTCAACGA 1620  
Qy 1620 CTTTGAAGCACACAGCGCTGTGAGAGACCGGATGTTCAATTTGAATCTCACCGCGCTC 1679  
Db 1621 CTTTGAAGCACACAGCGCTGTGAGAGACCGGATGTTCAATTTGAATCTCACCGCGCTC 1680  
Qy 1680 TGAAGCATGACTTTTGGCAAGGTGACAAAGCAGAAAGTCAAAAGATTCTTCCGTGGCGC 1739  
Db 1681 TGAATCATGACTTTTGGAGAGGTCA CAAAGCAGAAAGTCAAAAGACTTTTCCGTGGCGCA 1740  
Qy 1740 AGSATCACGTGACCGAGGTGGCATGAGTTCTAGTCAGAAAGGTTGAGCCAAACCA 1799  
Db 1741 AGSATCACGTGAGGTGGAGCATGAAATCTAGTCAGAAAGGTTGAGCCAAAGAAA 1800  
Qy 1800 GACCCGCCCGATGACGCGGATAAAGCGAACCGGCGCTGCTCACTGCTGCGG 1859  
Db 1801 GACCCGCCCGAGTACGCGCAATTAAGTGACCCCAACGGGTGCGGAGTCACTGTGCG 1860  
Qy 1860 ATCAATGACGTCAGACGCGGAGAGACTCCGTGACCTTTGCCAGAGTACCAAAACA 1919  
Db 1861 AGCCATGACGTCAGACGCGGAG--AGCTTGATCACTACGACAGACGATCACAAAACA 1917  
Qy 1920 AATGTTCTCGTACGCGGGCATGCTTCAAGTCTGTTCCCTGCAAAACATGCGAGAA 1979  
Db 1918 AATGTTCTCGTACGCGGGCATGAAATGATGCTGTTTCCCTGCAAAACATGCGAGAA 1977  
Qy 1980 TGAATCAGAAATTTCAACTTTGCTTCAACGACGAGGACAGAGACTGTTCAAGATGTTCC 2039  
Db 1978 TGAATCAGAAATTTCAAAATTCGTTCACTCACTCAGACAGAAAGACTGTTTAAAGTCTTC 2037  
Qy 2040 CCGCGTGTCAGAATCTCAACCGGT---CGTCAAGAAAGAGAGCTATCGGAACTGTG 2096  
Db 2038 C---CGTGTCAGAATCTCAACCGGTTCTGTGCTGCTCAAAAGAGGCTATCAGAACTGTGCT 2094  
Qy 2097 CCATTCATCATCTGCGGGGCGGCTCCGAGATTGCTGCTCGGCGCGCATCTGCGCA 2156  
Db 2095 ACATTCATCATATCATGAGGAAAGGTGCGAG--CGCTTGACATGCTGCGCATCTGCGCA 2151  
Qy 2157 ACGTGAATCTGATGATCTGTGTTCTGAGCAATTAATGACTTAACAGATATGAGTCC 2216  
Db 2152 ATGTGATTTGATGATCTGATCTTTGAACAATTAATTAATGATGATGCTGCC 2211  
Qy 2217 GATGTTATCTTCAAGATTGCTGAGACAACTCTCTGAGGCAATTCGCACTGTG 2276  
Db 2212 GATGTTATCTTCAAGATTGCTGAGGACACTCTCTCTGAAGAAATTAAGCACTGTG 2271  
Qy 2277 GACTTGAACCTGAGAGCCCGAAACCAAGGCCAACAGCAAAAGCAGAGAGAGCGCGG 2336  
Db 2272 AAGCTCAAACTGCGCCCAACCAACAAAGCCGAGGCGGCTPAAGAGAGACAGAG 2331  
Qy 2337 GGTCTGTGCTTCTGTGCTACAACTGCGGACTTTCACAGACTGCA CAAGGAGG 2396  
Db 2332 GGTCTGTGCTTCTGTGCTACAACTGCGGACTTTCACAGACTGCA CAAGGAGG 2391  
Qy 2397 CCGTCAACGCGGCGATGACGCGGCTTGAAGACG-ACAAAGCTTACGACAGACT 2455  
Db 2392 CCGTCAACGAGGAGACGCGCGGCTTGAAGACGATCAAAAGCTTACGACAGCGGAGCT 2451  
Qy 2456 CAAGCGGAGGAGCAATCTGCGGTATTAACAGCGGAGCGGAGTTTCAAGAGCG 2515  
Db 2452 CGACAGGAGAGCAACCGGATCTCAAGTATCAACAGCGGAGGAGTTTCAAGAGCG 2511  
Qy 2516 TCTGCAAGAGATAGTCTTTTGGGGCAACCTTGGGCGAGAGTCTTTCAGGCGCAAGAA 2575  
Db 2512 CTTTAAAGAGATAGTCTTTTGGGGCAACCTTGGGCGAGAGTCTTTCAGGCGCAAGAA 2571  
Qy 2576 GAGGTTCTGAACTTTTGTGCTGTGTTGAGAGAGTGTAAAGCGGCTCTTGAAGAA 2635  
Db 2572 GAGGTTCTGAACTTTTGTGCTGTGTTGAGAGAGTGTAAAGCGGCTCTTGAAGAA 2631



QY	2636	ACGTC	CCG	GTAA	GAC	AGT	GGCC	CA	AGAC	CC	GAC	CT	CT	CT	CG	GC	CA	ATT	GG	CA	A	G	A	C	A	G		2635	
Dp	2632	GAG	CC	CG	GT	A	G	A	C	T	CT	CT	GT	GG	AC	C	G	A	CT	CT	CT	CG	GA	A	C	CG	GA	A	2631
QY	2696	CC	AG	AG	CC	CG	CT	TA	AAAA	GA	GA	CT	CA	AT	TT	TT	GG	TC	AG	CT	CG	GC	AT	C	AG	AG	CT	CG	2755
Dp	2692	CC	AG	AG	CT	CT	CA	AAAA	AAAA	GA	TT	GA	AT	TT	TT	GG	TC	AG	CT	CG	GC	AT	C	AG	AG	CT	CG	2751	
QY	2756	CG	ACC	CA	CA	AC	CT	CT	CG	GA	AA	CT	CT	CG	CA	AA	CC	CC	CG	CT	GG	CA	CT	TA	CA	AT		2815	
Dp	2752	TG	AC	CC	CC	CA	GG	CT	CT	CG	GA	CC	CA	CG	CA	CC	CC	CC	CT	GT	GG	CA	CT	TA	CA	AT		2811	
QY	2816	GG	CT	TA	CG	GG	CG	GT	GG	CG	CA	TA	TA	GG	CA	CA	TA	TA	CG	AA	GG	CC	CG	CA	GG	AT	GG	2815	
Dp	2812	GG	CT	TA	CG	AG	CT	GG	CG	CA	TA	TA	GG	CA	CA	TA	TA	CG	AA	GG	CC	CG	CA	GG	AT	GG	2811		
QY	2876	TG	CC	TA	CA	GA	AA	AT	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	2935	
Dp	2872	TT	CT	CT	CG	GA	AA	AT	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	GG	CA	TT	2931	
QY	2936	CA	CC	CG	CA	CA	T	GG	CG	CT	TT	GG	CG	CA	CA	CT	CT	TA	CA	CA	CC	CT	CT	TA	CA	CA	AT	CT	2995
Dp	2932	CA	CC	CG	CA	CA	T	GG	CG	CT	TT	GG	CG	CA	CA	CT	CT	TA	CA	CA	CC	CT	CT	TA	CA	CA	AT	CT	2991
QY	2996	TT	CA	AC	GG	GG	GC	CA	GA	CA	CA	CA	CA	CT	TA	CT	GG	CT	TA	CG	CA	CC	CT	GG	GG	AT	TT	3055	
Dp	2992	AT	CA	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	3048		
QY	3056	TG	AT	TT	TA	CA	CA	GA	TT	TC	CA	CT	GG	CA	AT	TT	TC	CA	CA	GG	TC	GG	CA	GG	CA	CT	CA	3115	
Dp	3049	TG	AT	TT	TA	CA	CA	GA	TT	TC	CA	CT	GG	CA	AT	TT	TC	CA	CA	GG	TC	GG	CA	GG	CA	CT	CA	3108	
QY	3116	CA	AT	TT	GG	GG	AT	TT	CG	GC	CC	CA	GA	AG	CT	CA	CT	TA	CA	CA	CT	TA	CA	CA	CT	TA	CA	3175	
Dp	3109	CA	AT	TT	GG	GG	AT	TT	CG	GC	CC	CA	GA	AG	CT	CA	CT	TA	CA	CA	CT	TA	CA	CA	CT	TA	CA	3168	
QY	3176	GG	TC	CA	CG	CA	GA	TA	GT	GG	CG	TC	CA	CG	CA	CT	TA	TA	CT	TA	CG	CA	CG	TC	TA	CA	GT	3235	
Dp	3169	GG	TC	CA	CG	CA	GA	TA	GT	GG	CG	TC	CA	CG	CA	CT	TA	TA	CT	TA	CG	CA	CG	TC	TA	CA	GT	3228	
QY	3226	CT	TT	GG	CG	CA	CT	CG	GA	TA	CG	AT	CC	CG	TA	AG	CT	CG	GC	TC	CG	CA	CG	AG	GC	CT	3295		
Dp	3229	GT	TT	AA	CT	GA	CT	CG	GA	TA	CG	AT	CC	CG	TA	AG	CT	CG	GC	TC	CG	CA	CG	AG	GC	CT	3288		
QY	3296	CC	CT	CC	GG	TC	CC	GG	CG	AG	CT																		

Db	3709	GACTGGAGCTTACCAAGTACCACTCTCAATGGCAGAGACTCTCTGGTGAATC-----CGGC	3762
QY	3776	TATGGCCTCACAACAAGCACAAGAACAAGTCTTTTCCATGAGCGGTCTCATGATTTT	3835
Db	3763	CATGGCAAGCCACAAGAGCATGAGAAAGTTTCTTCTCAAGCGGGGTCTCATCTTT	3822
QY	3836	TGGAAAGAGAGCGCCCGGACCTTCAACACTGCATTGGACAAATGTCATGATCAGACGA	3895
Db	3823	TGGGAACCAAGGCTCCAGAGAAAACAATGTGAACATTGAAAAGGTCAAGATTACAGACGA	3882
QY	3896	AGAGGAATCAAAAGCCACTAAACCCCGTGGCCACCGAAGATTTGGGACTGTGGCAGTCAA	3955
Db	3883	AGAGGAATGGGAACAACCAATCCCGTGGCTCAGAGCAGTATGGTTCTGTATCTACCA	3942
QY	3956	TCTTCAAGCAGCAGCAGACAGACCTGTGGACCCGAGATGTGCATGTTATGGAGCCTTACC	4015
Db	3943	CCTCCAAAGAGGCAACAGACAAGAGGTACCCGAGAGTCAACAACAACAAGCGTTCTCC	4002
QY	4016	TGGAATGGTGTGGCAAGACAGAGCGTATCCTTGCAGAGGTCCTATTYGGCCAAAATTC	4075
Db	4003	AGGATATGTTCTGGCAGGACAGAGATGTGATCTTCAAGGGGCCATCTGGCAAAAGTTC	4062
QY	4076	TCACACGAGTGAACCTTTACCCGTCTCTCTCATGTGGCGGCTTTGGACTTAAAGCACC	4135
Db	4063	ACACACGAGCGAGCAATTTTCAACCCCTCTCCCTCATGGGTGAATTCGACCTTAAACACC	4122
QY	4136	GGCTTCCTCAGATCCTCATCAAAAACAAGCGCTGTTCCTGCGAATCTCCGCGCAGAGTTTC	4195
Db	4123	TCTTCCACAGATTTTTCATCAGAAACACCCGGTACTCTGCAATCTTTCGACACCTTCAG	4182
QY	4196	GGCTCAAAAGTTTGCTTCATTTCATCACCAAGTATTCACAGACA-AGTAGCGTGGAGA	4254
Db	4183	TGGCGAAAGTTTCTCTTCATCAACAGTACTCCACGGGACACGCTCAGCGTGGAGA	4242
QY	4255	TTGAATGGAGCTGCAGAAAAGAAACAGCAACGCTGGAAATCCCGAAGTCCAGATTCAT	4314
Db	4243	TCGATGGGAGCTGCAGAAAAGAAACAGCAACGCTGGAAATCCCGAATTCAGTACACTT	4302
QY	4315	CTAATCTATGCAAAATCTGCACAACGTTATTTCACTGTGGAACAACAATGACTTTATCTG	4374
Db	4303	CCAACTACAAACAATCTGTTAATGTGTGAACCTTACCGTGGATACTAATGGGCTGATTCAG	4362
QY	4375	AGCTTCGCCCCATTGGCAACCCGTTACTCACCCGTCCTCTGTAAATGTGTATTAAT	4434
Db	4363	AGCTTCGCCCCATTGGCAACAGAACTGACTGCTAATCTGTAAATCTTGTTAATTAAT	4422
QY	4435	AAACCGGTAAATTCGTGTCAAGTTGAACTTTGTGTCTCATGTCTTATATCTTATCTGTC	4494
Db	4423	AAACCGGTAAATTCGTGTCAAGTTGAACCTTGTGTCTGTGTATTTCTTTCTTATCTAGTT	4482
QY	4495	ACCATAGCAACCGGTTACACATTAACTGCTTAGTTGGCGTTGGGA---ATACCCCTAG	4550
Db	4483	TCCATGGCTAGTATGATTAAGTACGTGGCGGTTAATCATTTAACTACAGAAACCCCTAG	4542
QY	4551	TGAATGAGTTGCCACATCCCTCTATATGGCGCTGCTGCGTGGGGCGGAGACAG	4610
Db	4543	TGAATGAGTTGGCACTCCCTCTGTGGCGCTGCTGTCACTGAAGCGGGGACACAA	4602
QY	4611	AGCTTCGCGCTTCGGAACCTTGTGTCCGAGGCCCCACGAGCAGACGAGCGGCTAG	4670
Db	4603	AGGTTCGCCCAACGCGCGGGGTTTCCCGGGGGGCTCAGTGAAGACGAGCGCGCAGAG	4662
QY	4671	AGGAGATGTGCCAA	4683
Db	4663	AGGAGATGTGCCAA	4675

RESULT 14  
US-09-770-315-3  
; Sequence 3, Application US/09770315  
; Patent No. 6429001  
; GENERAL INFORMATION:



APPLICANT: Chiron Corporation  
; TITLE OF INVENTION: Recombinant AAV Packaging Systems  
; FILE REFERENCE: 20263-501  
; CURRENT APPLICATION NUMBER: US/09/770,315  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/178,536  
; PRIOR FILING DATE: 2000-01-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 3  
; LENGTH: 7557  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: recombinant DNA  
US-09-770-315-3

Query Match 66.5%; Score 3114.4; DB 3; Length 7557;  
Best Local Similarity 81.7%; Pred. No. 0;  
Matches 3705; Conservative 0; Mismatches 771; Indels 58; Gaps 7;

QY 18 GCGCGCTGCTGCTCCTCAGTGAAGCGGGGCGACCAAGTCCGCCAGCCCGGGCTTTCG 77  
DB 4 GCGCGCTGCTGCTCCTCAGTGAAGCGGGGCGACCAAGTCCGCCAGCCCGGGCTTTCG 63  
QY 78 CCGGCGGCTCTCAGTGAAGCGAGCGCGCAGAGAGGAGTGGCCAACTCCATCACTAG 137  
DB 64 TCGCGCGCTCTCAGTGAAGCGAGCGCGCAGAGAGGAGTGGCCAACTCCATCACTAG 123  
QY 138 GGG-----TTCTCGAGGGGTGG 155  
DB 124 TGGGACTTGCTAGTAACTTCTGTAATGATGCTATACGAAGTTATCCGAGGGGTGG 183  
QY 156 AGTCTGACGTGAATTAAGTCAATAGGTTAAGGAGTCTCTGATTAAGAGTCACTGAGT 215  
DB 184 AGTGTGACGTGAATTAAGTCAATAGGTTAAGGAGTCTCTGATTAAGAGTCACTGAGT 243  
QY 216 GTTTTGCACATTTTTCGACACCATGTGTCACGCTGGGTATTTAAGCCCGAGTGAAGAC 275  
DB 244 GTTTTGCACATTTTTCGACACCATGTGTCACGCTGGGTATTTAAGCCCGAGTGAAGAC 303  
QY 276 GCAGGCTCTCATTTTGAAGCGGAGGTTTGAACGCGAG--CGCCATGCCGGGGTTTAC 334  
DB 304 GCAGGCTCTCATTTTGAAGCGGAGGTTTGAACGCGAGCGCCATGCCGGGGTTTAC 363  
QY 335 GAGATTGATTAAGTCTCCAGCGACTTGAACGACATCTGCCCGGATTTTGAACGC 394  
DB 364 GAGATTGATTAAGTCTCCAGCGACTTGAACGACATCTGCCCGGATTTTGAACGC 423  
QY 395 TTTTGAACCTGGGTGGCGAGAGGAGTGGAGTTGCCGCCAGATTCTGACATGAGATCG 454  
DB 424 TTTTGAACCTGGGTGGCGAGAGGAGTGGAGTTGCCGCCAGATTCTGACATGAGATCG 483  
QY 455 AATCTGATTGACAGGACCCCTTGAACGCTGGCCGAGAGCTGCAGCGGACTTCTGTGC 514  
DB 484 AATCTGATTGACAGGACCCCTTGAACGCTGGCCGAGAGCTGCAGCGGACTTCTGTGC 543  
QY 515 CACTGCGCGCGCTGAGTGAAGGCCCCCGAGGCCCCCTTCTTTGTTCACTTGAAGAGGC 574  
DB 544 GAAATGGCGCGCTGAGTGAAGGCCCCCGAGGCCCCCTTCTTTGTTGCAATTTGAAGAGGA 603  
QY 575 GAGTCTACTTCCACCTCATATTCTGTTGAGAGCAGCGGGGTTCAATTCATGAGTGTG 634  
DB 604 GAGAGCTACTTCCACCTCATATTCTGTTGAGAGCAGCGGGGTTCAATTCATGAGTGTG 663  
QY 635 GCGCGCTTCTGAGTCAAGTTCAGCAAGCTGTGACAGCATCTACCGCGGATCGAG 694  
DB 664 GAGAGCTTCTGAGTCAAGTTCAGCAAGCTGTGACAGCATCTACCGCGGATCGAG 723  
QY 695 CCGAGCCCTGAGCACTGTTGCGGCTGACCAAGCGCTTAATGAGCGCGGAGGGGAGAC 754  
DB 724 CCGAGCTTGGCAAACTGTTGCGGCTGACCAAGCGCTTAATGAGCGCGGAGGGGAGAC 783

QY 755 AAGGTGAGCAGAGTGTACATCCCACTACCTCTCCCAAGACTCAGCCGAGCTG 814  
DB 784 AAGGTGAGTGAATGAGTGTACATCCCACTACCTCTCCCAAGACTCAGCCGAGCTG 843  
QY 815 CAGTGGCGGTGACTTAACATGAGAGATATTAAGCGCGTGTTTAACTCGCGAGCGC 874  
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QY 935 AATCTGAACCCCAATTCTGACGCGCTGTCAATCCGCTCAAAACCTCCGCACTGATCATG 994  
DB 964 AATCTGAATCCCAATTCTGATGCGCGGTGATCAAGTCAAAACCTTCAAGCGAGTACATG 1023  
QY 995 GAGCTGTGCGGTGCTGTGTGAGCCGGGCAATCACTTCCGAGAAAGCTGATCCAGAG 1054  
DB 1024 GAGCTGTGCGGTGCTGTGTGAGCAAGGGGATTAACCTTCGAGAAAGCTGATCCAGAG 1083  
QY 1055 GACCAAGCTGTGATCATCTCTTCAACGCGCGCTCAACTGCGGTCCAGATCAAGGCC 1114  
DB 1084 GACCAAGCTGTGATCATCTCTTCAATGCGCGCTTCAACTGCGGTCCAGATCAAGGCT 1143  
QY 1115 GCTCTGACAAATGCGCGCAAGATCATGCGCTGACCAAAATCCGCGCGCACTACCTGATA 1174  
DB 1144 GCTCTGACCAATGCGCGCAAAATTAATGAGCTTGAACCTGACCAAAACCTCCGATACCTGTG 1203  
QY 1175 GCGCCCGCTCGCGCGCGCAATTAACCAACCGCATTTACCGCATCTCGAGCTGAC 1234  
DB 1204 GCGCGAGCAGCCCGTGGAGGACATTTCCAGCAATCGGATTTTAATTTTGAATTAAC 1263  
QY 1235 GCGTACCAACCTGCTACGCGCGCTCTCTTCTTCCGCTGGCGCCAGAAAGTTCCGA 1294  
DB 1264 GCGTACCAATCCCAATATGCGCGCTCTCTTCTTGGAGTGGCGACGAAAGTTTCGCG 1323  
QY 1295 AAACGCAACACATCTGAGCTTTGGGCGGCGCACCAAGGCGCAAGACCAATCGCGGAA 1354  
DB 1324 AAAGGAAACACATCTGAGCTTTGGGCGGCGCTTGAACCTGACCAATGAGAACTTTCGC 1383  
QY 1355 GCGATCGCCCAAGCGCGTCCCTTCTACGCGCTGCTCAACTGAGCAATGAGAACTTTCGC 1414  
DB 1384 GCGATGAGTCCCAAGCGCGCTTCTTCAAGGCGCTTGAACCTGAGCAATGAGAACTTTCGC 1443  
QY 1415 TTCAACGATGCTGTCGACCAAGTGTGATCTGTGTGGAGGAGGCAAGATGACGCGCAAG 1474  
DB 1444 TTCAACGATGCTGTCGACCAAGTGTGATCTGTGTGGAGGAGGCAAGATGACGCGCAAG 1503  
QY 1475 GTCGTGAGTCCGCGCAAGGCGCATTTCTCGGCGCGCAAGAGTGCAGTGAACCAAAAGTGC 1534  
DB 1504 GTCGTGAGTCCGCGCAAGGCGCATTTCTCGGAGGAGCAAGAGTGCAGTGAACCAAAAGTGC 1563  
QY 1535 AAGTGTCCGCGCAAGTGCATCCCAACCCCGTGAATGTCATCTTCAACCAACCATGTGC 1594  
DB 1564 AAGTGTCCGCGCAAGTGCATCCCAACCCCGTGAATGTCATCTTCAACCAACCATGTGC 1623  
QY 1595 GCGGTGATGACGCGGAAACAGACCACTTGAAGACCAAGACCGGTGACAGACCGGATG 1654  
DB 1624 GCGGTGATGACGCGGAACTCAACGACCTTGAACCAAGACCGGTGACAGACCGGATG 1683  
QY 1655 TTCAAAATTTGAACACCCCGCTGTGAGCATGATTTGGCAAGTGAACCAAGCAGAA 1714  
DB 1684 TTCAAAATTTGAACACCCCGCTGTGAGCATGATTTGGCAAGTGAACCAAGCAGAA 1743  
QY 1715 GTCAAAGATTTCTTCCGCTGCGCGCAGAGTACGTCGACGAGGTGCGCATGAGTTCTAC 1774  
DB 1744 GTCAAAGATTTCTTCCGCTGCGCGCAGAGTACGTCGAGGTGAGGTGAGTGAATTTCTAC 1803  
QY 1775 GTCAGAAAGGTGAGGCAACACAGACCGCGCCCGCATGACCGCGGATTAAGAGGAGCC 1834  
DB 1804 GTCAGAAAGGTGAGGCAACAGAGACCGCGCCCGCATGACCGAGTGAATTAAGAGGCC 1863  
QY 1835 AAGCGGCTGCGCTCTCAGTCTGCGGATCATGACGTCAAGCGCGAAGAGCTCCGCTG 1894

Db 1864 AAACGGGTGCGGAGTCAGTTGGCCGAGCCATGACGTGACAGCGCGA---AGCTTCGATC 1920  
Qy 1895 GACTTGGCCGACAGGTACCAAAACAATGTTCTGTCACGGGGGATGCTTCAAGTGTG 1954  
Db 1921 AACTACGACAGAGTACCAAAACAATGTTCTGTCACGTGGGGATGAATCTGATGCTG 1980  
Qy 1955 TTTCCCTGCAAAACATGCGAGAGATGATGATCAAGATTTCAACATTTGGCTTCACGACGG 2014  
Db 1981 TTTCCCTGCAAGATGCGAGAGATGATGATCAAGATTTCAAAATATGCTTCACTACGGA 2040  
Qy 2015 ACCAGAGCTGTTCAAGATGTTTCCCGGCGGTGTCAGAAATCTCAACCGGT---CGTCAGA 2071  
Db 2041 CAGAAAGCTGTTAGAGTGTCTTCC---CGTGCAGATCTCAACCGTTCGTGTCGTC 2097  
Qy 2072 AAGAGAGATTCGGAACCTCTGTGCCATTCATCATCTGCTGGGGGGGCTCCGAGATT 2131  
Db 2098 AAAAAAGGATCAAAAACTGTGCTACATTCATTCATTCATGGAAGAGTCCAGA---C 2154  
Qy 2132 GCTTGTGCGGCTGCGATCTGGTCAACGTGATCTGATGACTGTGTTCTGAGCAATTA 2191  
Db 2155 GCTTGCATCTGCTGCGATCTGGTCAATGTGATTTGGATGACTGCATCTTTGAACAAATA 2214  
Qy 2192 ATGACTTAACCAAGTATGCTGCTGCGATGTTATCTTCAGATTGGCTCGAGACAACT 2251  
Db 2215 ATGATTTAATCAGGTATGCTGCTGCGATGTTATCTTCAGATTGGCTCGAGACACTCT 2274  
Qy 2252 CTTCGAGGGCAATTGCGGACGTGTGGGACTTGAACACTTGAGACCCGAAACCCAAAGCCAA 2311  
Db 2275 CTCTGAAGGAATTAAGACAGTGGTGAAGCTCAAACTGGCCCAACCAACCAAAAGCCCGC 2334  
Qy 2312 CCAGCAAAAGCAGAGACGACGGCCGGGGGTCTGGTGTCTCTGAGTCAAGTACTCTCGAGC 2371  
Db 2335 AGACGGGATTAAGAGACGACAGCAGAGGGGTCTTGTGTTCTTGGGTAACAGTACTCGAGC 2394  
Qy 2372 CTTCGAACGAGTCTCAACAAAGGGAGCCCGTCAACGCGCGGAGATGACGGCCCTCGAGCA 2431  
Db 2395 CTTCGAACGAGTCTCAACAAAGGGAGCCCGTCAACGAGGAGACGCGCCGCTCGAGCA 2454  
Qy 2432 CGAAGAGGCTTAACGACGAGACGCTCAAGCGGGTGAACATCCGTAACCTGCGGTATTAACA 2491  
Db 2455 CGACAAAGCTTAACGACGAGCTGACAGCGGAACAACCCGTAACCTCAAGTCAACACA 2514  
Qy 2492 CGCCGACGCGCAGTTCAGAGAGCGCTGTCAGAAAGATACGTCTTTTGGGGCAACCTCGG 2551  
Db 2515 CGCCGACGCGGAGTTCAGAGAGCGCTTAAGAGATACGTCTTTTGGGGCAACCTCGG 2574  
Qy 2552 GCGAGCACTCTTCAAGGCAAGAGAGGTTCTCGAACCTTTTGGTCTGTTGAGGAAG 2611  
Db 2575 ACGAGCACTCTTCAAGGCGAAGAGAGGTTCTTGAACTCTGGGGCTGTTGAGGAACC 2634  
Qy 2612 TGCATAAGCGGCTCTGGAAGAAACGTCGGTGAAGAGTCGCAACAAGAGCCAGATC 2671  
Db 2635 TGTATAAGCGGCTCTGGGAAAAAAGAGCGGTAGAGCACTCTCTGTGAGCCAGATC 2694  
Qy 2672 CTCCTCGGGCAATTGGCAAGACGAGCAGACCGCTAAAAAGAGACTCAATTTTGTCA 2731  
Db 2695 CTCCTCGGGAACCGGAAGGGCGGCGACAGCCTGCAAGAAAAAGATTTGATTTTGTGCA 2754  
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Db 2755 GACTGAGAACCGAGACTCAGTACCTGACCCCGAGCTCTCGGAACAGCCACAGAGCCCC 2814  
Qy 2792 CGCTGCTGTGGAGCTTACTAATGCTTCAGGCGGTGGCGCAACCAATGAGACAAATA 2851  
Db 2815 CTCTGTCTGTGGAACTAATAAGATGCTTAAGGACGATGGCGACCAAGTGAACAATA 2874  
Qy 2852 CGAAGCGCCGACGAGTGGGTAAATGCTCAAGAAATTTGGCATTTGCAATGGCT 2911  
Db 2875 CGAAGGCGCCGACGAGTGGGTAAATGCTCGGAAATTTGGCATTTGCAATGGAT 2934  
Qy 2912 GGGGCAAGAGTCAATCAACCAAGACCCGAACATGGGCTTGGCCCACTTAACAACA 2971

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Db 2995 CCTTACAAACAAATTTCCAGCCAAATCA---GGAGCTCGAAGCAATCACTACTTTGG 3051  
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Qy 3092 TGACTGCGAGGACTCATCAACAAATTTGGGATTTCCGCGCCAGAGACTCAACTTCA 3151  
Db 3112 TGACTGGCAAGACTCATCAACAACTGGGGATTCGAGCCAGAGACTCAACTTCA 3171  
Qy 3152 GCTCTCAACATCCAAATCAAGAGGTCAGAGCAAGATGAGGGGTCAAGCAATCGCTA 3211  
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Qy 3272 CGGCTTGCAGACCAAGGCTGCTCCTCGCTTCCGGCGAGAGTGTTCATGATTCGCA 3331  
Db 3292 CGGCTCGGCGCATCAAGAGTCCCTCCGCGGTTCCAGCAGAGCTCATGTGTGCACA 3351  
Qy 3332 GTACGGCTACTTAACGCTCAACAATGGCAGCAGAGGCGAGGAGCGCTCATCTTTACTG 3391  
Db 3352 GTATGATTAACCTACCTCTGAACAAGGAGTCAAGAGTCAAGAGTCTTCAATTTTACTG 3411  
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Qy 3452 CTTCGAGAGAGTGTCTTCCACAGAGCTTACCGGCAACGCCAAGACTTGAACGCGCTGAT 3511  
Db 3472 TTTTGAAGAGTGTCTTCCACAGAGCTTACCGCTCAAGCAGAGTGTGAGCGGTCTCAT 3531  
Qy 3512 GAATCTCTCATGAGACCAAGTACCTGTATTAACCTGAACAGAACTCAATGATCCGGAG 3571  
Db 3532 GAATCTCTCATGAGACCAAGTACCTGTATTAACCTGAACAGAACTCAATGATGAGAC 3591  
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RESULT 15
US-09-438-268-5
/ Sequence 5, Application US/09438268
/ Patent No. 6491907
/ GENERAL INFORMATION:
/ APPLICANT: Rabinowitz, Joseph E.
/ APPLICANT: Samulevki, Richard J
/ APPLICANT: Xiao, Weidong
/ TITLE OF INVENTION: VIRUS VECTORS AND METHOD OF MAKING AND ADMINISTERING
/ TITLE OF INVENTION: THE SAME
/ FILE REFERENCE: 5470-186
/ CURRENT APPLICATION NUMBER: US/09/438,268
/ CURRENT FILING DATE: 1999-11-10
/ EARLIER APPLICATION NUMBER: 60/107,840
/ EARLIER FILING DATE: 1998-11-10
/ EARLIER APPLICATION NUMBER: 60/123,651
/ EARLIER FILING DATE: 1999-03-10
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 8179
/ TYPE: DNA
/ ORGANISM: Virus
US-09-438-268-5

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Query Match	64.2%	Score 3008	DB 3	Length 8179
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Matches 3547; Conservative	0	Mismatches 750	Indels 19	Gaps 7

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Job time : 867 secs

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 13:05:23 ; Search time 149 Seconds  
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3989.148 Million cell updates/sec

Title: US-10-696-261-19

Perfect score: 4683

Sequence: 1 ttggccactccctctctgcg.....cgcatagaggagtgccaa 4683

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 506708

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3244.2	69.3	4675	US-11-327-357-1	Sequence 1, Appli
2	125	2.7	145	US-11-327-357-2	Sequence 2, Appli
3	118.2	2.5	4675	US-11-327-357-1	Sequence 1, Appli
4	117.8	2.5	145	US-11-327-357-2	Sequence 2, Appli
5	110	2.3	8322	US-11-269-117-6	Sequence 6, Appli
6	110	2.3	8322	US-11-269-117-6	Sequence 6, Appli
7	52	1.1	1309	US-10-953-349-16574	Sequence 16574, A
8	47.2	1.0	1191	US-10-953-349-33293	Sequence 33293, A
9	47	1.0	1302	US-10-953-349-33793	Sequence 33793, A
10	46.6	1.0	845	US-10-953-349-27324	Sequence 27324, A
11	45	1.0	45	US-10-513-348-6	Sequence 6, Appli
12	43.6	0.9	2152	US-10-953-349-38921	Sequence 38921, A
13	43.4	0.9	1439	US-10-953-349-32310	Sequence 32310, A
14	43.2	0.9	48	US-10-513-348-1	Sequence 1, Appli
15	43.2	0.9	681	US-10-984-694-2	Sequence 2, Appli
16	43.2	0.9	3508	US-11-071-896-6	Sequence 6, Appli
17	42.6	0.9	926	US-10-953-349-38418	Sequence 38418, A
18	41.8	0.9	1291	US-10-953-349-34039	Sequence 34039, A
19	41.6	0.9	681	US-10-984-694-6	Sequence 6, Appli
20	41.6	0.9	1235	US-10-953-349-27792	Sequence 27792, A
21	41.6	0.9	1478	US-10-953-349-32700	Sequence 32700, A
22	41.6	0.9	3546	US-11-071-896-9	Sequence 9, Appli
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26	41.6	0.9	6600	US-10-525-318-5	Sequence 5, Appli
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28	41	0.9	1147	US-10-953-349-16567	Sequence 16567, A
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33	40.8	0.9	3468	US-11-071-896-1	Sequence 1, Appli
34	40.8	0.9	3546	US-11-071-896-3	Sequence 3, Appli
35	40.8	0.9	3546	US-11-071-896-7	Sequence 7, Appli
36	40.6	0.9	3547	US-11-071-896-11	Sequence 11, Appli
37	40.6	0.9	1667	US-10-953-349-31278	Sequence 31278, A
38	40.4	0.9	696	US-10-953-349-16066	Sequence 16066, A
c	39	0.9	1570	US-10-953-349-27031	Sequence 27031, A
40	40.2	0.9	684	US-11-252-276-45	Sequence 45, Appli
41	40.2	0.9	717	US-11-252-276-47	Sequence 47, Appli
42	40.2	0.9	717	US-11-252-276-49	Sequence 49, Appli
43	40.2	0.9	1498	US-10-953-349-31731	Sequence 31731, A
44	40.2	0.9	1623	US-11-252-276-33	Sequence 33, Appli
45	40.2	0.9	1623	US-11-252-276-33	Sequence 33, Appli

ALIGNMENTS

RESULT 1									
US-11-327-357-1									
Sequence 1, Application US/11327357									
Publication No. US20060105983A1									
GENERAL INFORMATION:									
APPLICANT: BTG International Ltd									
APPLICANT: BEARD DR, PETER									
APPLICANT: RAU DR, KENNETH									
TITLE OF INVENTION: CYTOTOXIC AGENTS									
FILE REFERENCE: 142184A0									
CURRENT APPLICATION NUMBER: US/11/327,357									
PRIOR FILING DATE: 2006-01-09									
PRIOR APPLICATION NUMBER: 0009887.1									
NUMBER OF SEQ ID NOS: 6									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 1									
LENGTH: 4675									
TYPE: DNA									
ORGANISM: adeno-associated virus 2									
US-11-327-357-1									
Query Match									
Best Local Similarity 82.2%; Pred. No. 0;									
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;									
QY	1	TTGGCACTCCCTCTCTGCGGCTCGCTCGCTCACTAGAGCGCGGCAACAAAGTGGCC	60						
DB	1	TTGGCACTCCCTCTCTGCGGCTCGCTCGCTCACTAGAGCGCGGCAACAAAGTGGCC	60						
QY	61	CGAGCCCGGGCTTGGCCCGGCGCTCACTAGAGCGAGCGCCGAGAGGAGTG	120						
DB	61	CGAGCCCGGGCTTGGCCCGGCGCTCACTAGAGCGAGCGCCGAGAGGAGTG	120						
QY	121	GCCAACTCATCTAGAGGGTCTGAGAGGGTGAATCGTGAATTAACGTCTAG	180						
DB	121	GCCAACTCATCTAGAGGGTCTGAGAGGGTGAATCGTGAATTAACGTCTAG	180						
QY	181	GTTAGGAGGTCTGTATTAGAGTCACTAGTGTTTTGCACATTTTGCACACAT	240						
DB	181	GTTAGGAGGTCTGTATTAGAGTCACTAGTGTTTTGCACATTTTGCACACAT	240						
QY	241	GTTGTCACGCTGGTATTAAAGCCGAGTGAAGCAAGGAGTCCATTTTGAAGCGGA	300						
DB	241	GTTGTCACGCTGGTATTAAAGCCGAGTGAAGCAAGGAGTCCATTTTGAAGCGGA	300						
QY	301	GGTTGAAGCGGAG-CGCCATGCCGGGTTTACGAGATTGATTAAAGTCCCGAGC	359						
DB	301	GGTTGAAGCGGAG-CGCCATGCCGGGTTTACGAGATTGATTAAAGTCCCGAGC	359						



Dh 301 GGTITGAACGCGCAAGCCGCAATGCGGGTTTATGAGATTGTGATTAAGTCCCGACG 360  
Qy 360 ACCTTGACGAGCATCTGCGCGGCAATTTGTGACGTTTGTGAACCTGGGTGGCCGAGAAAG 419  
Dh 361 ACCTTGACGAGCATCTGCGCGGCAATTTGTGACGTTTGTGAACCTGGGTGGCCGAGAAAG 420  
Qy 420 AATGGAGTTCCCGCAGATTTCTGACATGATCTGAACTGATTTGAGAGGACACCCCTGA 479  
Dh 421 AATGGAGTTCCCGCAGATTTCTGACATGATCTGAACTGATTTGAGAGGACACCCCTGA 480  
Qy 480 CCGTGGCCGAGAAAGTGCAGCGCATCTTCTGTGCATGCGCGCCGCTGAGTAAGGCC 539  
Dh 481 CCGTGGCCGAGAAAGTGCAGCGCATCTTCTGACGGAATGCGCGCTGTGATGAAGGCC 540  
Qy 540 CGGAGGCCCTCTTCTGTGATTTGAGAAAGGGGAGTCCATCTTCCACTCCATATTC 599  
Dh 541 CGGAGGCCCTTCTTCTGTGAAATTTGAGAAAGGAGAGTCACTTCCACATGCACTGCG 600  
Qy 600 TGTGAGAACCAAGGGGTCAAAATCAGTGTGCTGGCGCTTCTGAGTCAAGATTAGCG 659  
Dh 601 TGTGAGAAACCAAGGGGTGAATTCATGTTTGGGAGCTTTCTGAGTCAAGATTGCGG 660  
Qy 660 ACAAGCTGTGTCAACATCTACCGCGGATGAGCCGACCTGCGCAACTGTGTTCCGG 719  
Dh 661 AAAAACTGATTCAGGAATTTAACCGCGGATCGAGCCGACTTTGCAAACTGTGTCGCG 720  
Qy 720 TGACCAAGACGGTAAATGCGCGGAGGGGAAACAAGTGTGAGACGATCAATCC 779  
Dh 721 TCACAAACACGAATGCGCGCGAGGCGGAGAACAGTGTGATGATGCTACATCC 780  
Qy 780 CCAACTACTCTCTGCGCAAGACTGACCGCGAGCTGCAATGAGCGTGAATAACATGAGG 839  
Dh 781 CCAATTAATCTGCTCCCAAAACCAAGCTGAGCTCAATGGGCGTGAATAATGAGAAC 840  
Qy 840 AGTATATAAGCGCGCTTTAAACTGTGCGGAGCGCAACCGCTGTGTGCGACGACTGA 899  
Dh 841 AGTATTTAAAGCGCTGTGTAATCTCAAGAGCGTTAAACGTTGTGTGCGAGACTGCA 900  
Qy 900 CCGACGTGAGCGAGCCGAGAGGAGAACAGGAATCTGAACCCCAATCTGACGCGC 959  
Dh 901 CGCACGTGTGCGACGAGAGGAGAACAGGAATCTGAATCTCAATCTGATGCGC 960  
Qy 960 CTGTGATCCGGTCAAAAACTTCGCGACGCTACATGAGACTGTGCGGTGCTGTGAGCC 1019  
Dh 961 CGGTGATCAGATCAAAAACTTCAGCAGGTACATGAGACTGTGCGGTGCTGTGAGCA 1020  
Qy 1020 GGGGATCACTCCGAGAGAGAGTGTATCCAGAGGACCAAGCTCTGTATCTTCTTCA 1079  
Dh 1021 AGGGGATTAATCTCGAGAGAGAGTGTATCCAGAGGACCAAGCTCTGTATCTTCTTCA 1080  
Qy 1080 ACGCGACTCTCCAACTCGCGGTCGCCAGATCAAGGCGGCTGTGAAACAATGCCGAAAGATCA 1139  
Dh 1081 ATGCGGCTCTCCAACTCGCGGTCGCCAAATCAAGGCTGCTTGTGAACAATGCCGAAAGATTA 1140  
Qy 1140 TGGCGCTGACCAAAATCGCGGCTCGACTACCTGTAGGCGCCGCTCGCCCGCGACATTA 1199  
Dh 1141 TGAAGCTGACATAAAACGCGCCCGACTACCTGTGTGCGCAGAGCGCTGTGAGGACATTT 1200  
Qy 1200 AAACCAACCGCATTTAACGCGATCTGTGAGCTGAAGGCTTACGACCTGTGCTACGCGGCT 1259  
Dh 1201 CCACCAATCGGATTTATATAATTTTGGAACTPAAACGGGTACGATCCCAAAATACGGGCTT 1260  
Qy 1260 CCGCTTTCTCGGCTGGGCGCCAGAAAAGTTTCGAAAAAGCAACCAATCTGGGCTTTG 1319  
Dh 1261 CCGTCTTTCTGGGATGGGCGACGAAAAGTTTCGCGAAGAGAACCAATCTGGGCTTTG 1320  
Qy 1320 GGGCGGCAACAGGCGCAAGACCAACATCGCGAAGCATCGCCACGCGCTGTGCTTCT 1379  
Dh 1321 GGGCTGCAACTACGGGAGAGCAACATCGCGAGGCGCATAGCCACACTGTGCTTCT 1380  
Qy 1380 ACGGCTGGTCAACTGAGCAATGAGAACTTTCTTCAAGATTGCGTGCACAAAGATG 1439  
Dh 1381 ACGGATGGTAAACTGAGCAATGAGAACTTTCCTTCAACGACTGTGTGCAAAAGATG 1440

Qy 1440 TGAATGTGGAGAGGAGGCAAGATGACGGCAAGGTCGTGAGTGTCCGCCAAGGCCATTC 1499  
Dh 1441 TGAATGTGGAGAGGAGGAGAGATGACCGCCAAAGGTCGTGAGTGTCCGCCAAGGCCATTC 1500  
Qy 1500 TCGCGGCAAGAGTGCAGGTGAGCCAAAGTGCAGAGTGTGCGCCAGATCGATCCA 1559  
Dh 1501 TCGGAGGAACCAAGTGCAGGTGAGCCAAAGTGCAGAGTGTGCGCCAGATCGATCCA 1560  
Qy 1560 CCCCCTGATTCGTACCTTCCAAACCAACATGTGCGCGGTGATTTGACGGGAACAGACCA 1619  
Dh 1561 CTCCCTGATTCGTACCTTCCAAACCAACATGTGCGCGGTGATTTGAGGGAACTCAACGA 1620  
Qy 1620 CTTTGAGACACAGCAGCCGTTGAGGACCGGATGTTCAATTTGAATCAACCGCGCTC 1679  
Dh 1621 CTTTGAGACACAGCAGCCGTTGAGGACCGGATGTTCAATTTGAATCAACCGCGCTC 1680  
Qy 1680 TGAAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAAGTCTTCGCTGGGCGC 1739  
Dh 1681 TGAATCATGACTTTGGGAAAGTCAACAAAGCAGGAAGTCAAAAGTCTTTCGCTGGGCAA 1740  
Qy 1740 AGGATCAAGTACCGAGTGGCGCATGAGTTTACGTCAGAAAGGTGAGCCACACAA 1799  
Dh 1741 AGGATCAAGTGTGAGTGGAGCATGAAATTTACGTCAAAAAGGTGAGCCAAAGAAA 1800  
Qy 1800 GACCGCGCCGATGACGCGGATPAAAGCAGCCAAAGCGGCGCTGCGCTCACTGCGCG 1859  
Dh 1801 GACCGCGCCGATGACGAGATPAAAGTACGTCAAAGCGGCGCTGCGCTCACTGCGCG 1860  
Qy 1860 ATTCATGACGTACAGCGCGAAAGAGCTCGGTGACTTTGCCGACAGTACCAAAACA 1919  
Dh 1861 AGCCATGAGGTACAGAGCGGAA--AGCTTCGATCAACTACGAGACAGGTACCAAAACA 1917  
Qy 1920 AATGTTCTGTCACGCGGAGATGCTCAGATGCTGTTCCCTGCAAAACAATGAGAGAA 1979  
Dh 1918 AATGTTCTGTCACGCGGAGATGATGATGCTGTTCCCTGCAAAACAATGAGAGAA 1977  
Qy 1980 TGAATCAAGATTTCAATTTGCTTCCGACGCGGACAGAGACTGTTCAAGATGTTTCC 2039  
Dh 1978 TGAATCAAGATTTCAAAATATGCTTCACTACGAGACAGAAAGCTGTTAAGATGCTTTC 2037  
Qy 2040 CCGCGGTGTCAAGATTTCAACCGGT---CGTCAAAAAGAGACGTATCGGAAACTGTG 2096  
Dh 2038 C---CGTGTCAAGATTTCAACCGGTCTGTCTGCTCAAAAAGGCTATCAAAACTGTGCT 2094  
Qy 2097 CAATTCATCATGCTGCGGCGGCTCCGAGATGCTGCTGCGCTGCGATCTGCTCA 2156  
Dh 2095 ACATTCATCATCATGCGGAGAAAGGTCCAGA---CGCTTCACTGCTGCGATCTGCTCA 2151  
Qy 2157 ACGTGAATCTGATGACTGTGTTCTGAGCAATAATGACTTAAACCAAGTATGCTGCC 2216  
Dh 2152 ATGTGATTTGATGATGATGATCTTTGAAACAATAATGATTTAAATCAGGTATGCGTCC 2211  
Qy 2217 GATGTATATCTTCCAGATTTGCTGAGGACCACTCTCTGAGGACATTCGCGAGTGTG 2276  
Dh 2212 GATGTATATCTTCCAGATTTGCTGAGGACCACTCTCTGAGGAAATAAACAAGTGTG 2271  
Qy 2277 GACTTGAACCTGGAAGCCCGGAAACCAAGCCAACAGGAAAGAGAGAGCGAGCGG 2336  
Dh 2272 AAGCTCAAACTGAGCCACCAACCAAAAGCCGACAGAGGAGCATTAAGAGAGAGAGG 2331  
Qy 2337 GGTCTGTGCTTCTGCTGCTCAAGTACTTGCAGCCCTTCAACGAGACTCGACAAAGGAG 2396  
Dh 2332 GGTCTGTGCTTCTGCTGCTCAAGTACTTGCAGCCCTTCAACGAGACTCGACAAAGGAG 2391  
Qy 2397 CCGTCAAGCGCGGAGTGAAGCGGCTTGAAGAG-ACAAGCTTACGACGACGCT 2455  
Dh 2392 CCGGTCAAGCGGAGAGCGCGCGGCTTGAAGAGAGTACAAAGCTTACGACGCGGCT 2451  
Qy 2456 CAAAGCGGTGACAAATCCGTATCTGCGGTATTAACACGCGGAGCGAGTTTCAAGAGCG 2515  
Dh 2452 CAGACGGGAGACAAACCGTATCTCAAGTACAAACACGCGGAGCGGAGTTTCAAGAGCG 2511

QY	2516	TCGTGAAGAATATGACTCTTTTGGGGGCACTCGGGGAGACGTCTTCCAGGCCAAGA	2575
Db	2512	CCTTAAAGAATAGTCTTTTGGGGGCACTCGGAGAGACGTCTTCCAGGCCAAGA	25711
QY	2576	GAGGGTTCTCGAACCCTTTTGGCTGGGTGAGGAAGGTCTAAGACGGCTCCGGAAAGA	2635
Db	2572	GAGGGTTCTTGAACCTCTGGGCTGGGTGAGGAACCTTTAAGACGGCTCCGGAAAGA	26311
QY	2636	AAGTCCGTAGAGCAGTCGCCACAAGACCGACCTCTCGGCACTTGGCAAGACAG	2695
Db	2632	GAGGCCGGTAAAGCACTCTCGTGGACCGACACTCTCTCGGAAACCGAAGAGCCGG	2691
QY	2686	CCAGCAGCCCCGTAAAAAGACTCAATTTTGGTCAGCTGGCGACTCAGACTGCTCC	2755
Db	2692	CCAGCAGCTCTCAGAAAAAGATTGAAATTTGGTCAGCTGGAGACGCACTCAGTACC	2751
QY	2756	CGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCGGCTGTGGGACCTACACAT	2815
Db	2752	TGACCCCAAGCTCTCGGACAGCCACCGACAGCCCCCTGTGGTCTGGGAACTAATACAT	2811
QY	2816	GAGTTTCAGCGGTGCGCAGCAATGGCAGACATTAACGAAGCGCGCAGCGAGTGGTTA	2875
Db	2812	GGCTACAGGCAGTGGCGCAACATGGCAGACATTAACGAGGGCGCGAGGAGTGGTTA	2871
QY	2876	TGCTCAGAGAAATTTGGCAATTGGGATTCACATGCTGGGCGACAGATCATCACCAAG	2935
Db	2872	TTCTCTCCGGAATTTGGCAATTGGGATTCACATGATGGGCGACAGAGTCATCACCAAG	2931
QY	2936	CACCCGAACATGGGCTTGGCCCACTTAACAACAACCTTAACAAGAAATCTCAGATGC	2995
Db	2932	CACCCGAACCTGGGCTTGGCCCACTTAACAACAACCTTAACAAGAAATTTCCAGCA	2991
QY	2996	TTCAACGGGGGCGCAGACCAAGCAACCACTACTTGGCTACAGACACCCCTGGGGATTT	3055
Db	2992	ATCA---GGAGCTCGAAGCAGACATCACTTGGCTACAGACACCCCTGGGGATTT	3048
QY	3056	TGATTTCAACAGATTCACATGCAATTTCTCACAGTACGGCAGCACTCATCAACA	3115
Db	3049	TGACTTCAACAGATTCACATGCACTTTTCAACAGTACGTGCAAGACATCATCAACA	3108
QY	3116	CAATTTGGGGAATTCGGGCCCAAGAGCTCACTTCAAGCTTTCAACATCCAAATCAAGA	3175
Db	3109	CAACTGGGGATTCGAGCCCAAGAGCTCAACTTCAAGCTTTTCAATTCAAATCAAGA	3168
QY	3176	GATCAAGACGAATGATGGCGTCAAGCAACATCGCTAAATACCTTACAGACGGTTCAAGT	3235
Db	3169	GGTCAAGCAAGATGACGGTAGAGCAAGCAATTTGCATTAACCTTACAGACGGTTCAAGT	3228
QY	3236	CTTGTCCGACTCGAGTACCAATTCCTCGTACGTCTCGGCTCTGGCGACCAAGGCTGCT	3295
Db	3229	GTTTACTGACTCGAGTACCAAGCTCCGTAAGTCTCGGCTCTGGCGACTCAAGGATGCT	3288
QY	3286	CCCTCCGTTCCCGGGGAGCGTGTATATATTCGAGATACGGCTACCTAACGCTCAACA	3355
Db	3289	CCCGCGTTCCCGAGAGCGTCTCATGTGTGCACAGATAGTAATCTCACCTCAACA	3348
QY	3356	TGGCAGCAGGAGATGGGAGCGCTATCTTTTACGCTCGGAATATTTCCCATCGCAGAT	3415
Db	3349	CGGAGTAGAGCATAGGACGCTCTTCAATTTTACGCTCGGAGTACTTTCTTTCAGAT	3408
QY	3416	GCTGAGAACGGGCAATTAATTTTACCTTCAGTCAACCTTCGAGGACGTGACTTTCACAG	3475
Db	3409	GCTGGGTACCGGAACAATTTTACCTTCAGTCAACCTTTTGAGGACGTTCTTTCACAG	3468
QY	3476	CAGCTACCGCGCAAGCCAGACCTTGGACCCGGTATGAATCTCTCATACACAGTACT	3535
Db	3469	CAGCTACCGCTACAGCCAGAGCTTGGACCGTCTCATGTATCTCTCATACAGTACT	3528
QY	3536	GTATTACTGTAACAGAACTCAATCACTCAGTCCGGAAGTCCCAAAAACAAGACTTGCCTTT	3595
Db	3529	GTATTACTTGGAGCAAAACATCTCAAGTGAACAACACGCAAGTAAAGCTTCACTT	3588
QY	3596	TAGCCGCGGTCTCCAGCTGGCAATCTGTTCAGCCCAAAAATGGTCACTGACCTG	3655

Db	3589	TTCTAGGCGGAGGAGTGTGACATTTCGGACCAAGTCAGAACTGGCTTCTCGAACCTTG	3648
Oy	3656	TTACCGGAGAGAGCGCGTTTCTTAAAAACAAAACAGACAACAACAACTTTACCTG	3715
Db	3649	TTACCGCCAGCAGGAGATGATCAAAGACATCTGCGGATACAAACAACATGTAATCTGCTG	3708
Oy	3716	GACTGGTCTTCAAAATATTAACCTTAATGGCGGTGAATCTATTAATCAACCTTGCACTGC	3775
Db	3709	GACTGGAAGCTACCAAGTACCACTCTCAATGGCAGAGACTCTCGGTGAATC-----CGGC	3762
Oy	3776	TATGGCTCTCACAAAGACGACAAAGACAAATTTCTTTCCATGAGCGGTGCATGATTTT	3835
Db	3763	CATGGCAAGCCACAAGAGCAGATGAAGAAAATTTTTTCTCAGAGCGGGGTTCTCATTT	3822
Oy	3836	TGGAAGAAGAGCGCGCGGAGCTTCAAAACATGCACTGGACATTTGGACATATCATACAGACA	3895
Db	3823	TGGAGAGCAGAGCTCAGAGAAAACAAATGTGAACTTGAAAAGGTCAATGATTAACAGACA	3882
Oy	3896	AGAGAAATCAAAGCCACTAAACCCCGTGGCCACCGAAGATTTGGGACTGTGGCAGTCAA	3955
Db	3883	AGAGAAATCGGAATCAACCAATCCCGTGGCTACGGAGCAGATGATGTTCTGATCTACCAA	3942
Oy	3956	TCTCCAGAGCAGCAGACACAGACCTTCGCAACCGGAGATGTGATGTATGGAAGCCTTACC	4015
Db	3943	CCTCCAGAGAGGCAACAGAGAGCAGCTACCGCAGATGTCAACACACAAAGGCGTTCTTCC	4002
Oy	4016	TGGAATGGTGTGGCAAGACAGAGAGCTATACCTGAGAGGCTCTATTGAGGCAAAATTCC	4075
Db	4003	AGGCAAGTCTGGCAGCAGACAGATGTGTACTTTCAGAGGCGCCATCTGGCAAAAGATTCC	4062
Oy	4076	TCACACGATGGACACTTTCACCCGCTCTCTCATGCGGCGCTTTGGACTTAAAGCACCC	4135
Db	4063	ACACACGAGCGGACATTTTACCCCTCTCCCTCATGGGTGATTCGGACTTTAAACACCC	4122
Oy	4136	GCTTCTCAGATCTCTCATCAAAAACAGCGCTGTTCCTGCGAATCTCTCGGACAGTTTTC	4195
Db	4123	TCCTTCACAGATTCATCAAGAAACACCCCGTACTCGCATCTTCGACACACTTCAG	4182
Oy	4196	GGCTACAAAGTTGGTTTCAATTCATCAACCCAGTATTTCCACAGAGACA-AGTAGCGTGGAGA	4254
Db	4183	TGCGCAAAAGTTGGTTTCTTCTTCAATCAACATCTCCAGCGGACACGGTCAAGCTTGAGA	4242
Oy	4255	TTGATGGGAGCTGCAGAAAGAAAACAGCAACGCTGGAAATCCGAAATGACGATATACAT	4314
Db	4243	TGAGATGGGAGCTGCAGAGAGAAAACAGCAACGCTGGAAATCCGAAATTCAGTACACTT	4302
Oy	4315	CTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACACAAATGACTTTATACTG	4374
Db	4303	CCAACTACAAAGCTGTGTTAATCGTGACTTACCGGTGATACAAATGCGCTGTATTCAG	4362
Oy	4375	AGCGTCGCGCCATTGGGACCGCGTTAACTCAACCGTCCTGTAAATGTGTATTAATCAAT	4434
Db	4363	AGCGTCGCGCCATTGGGACCGAGATCCGATCGTAATGTGTAATGTGTTTATTAATCAAT	4422
Oy	4435	AAACCGGTTAATGTGTCAAGTTGAACCTTGGTCTCAATGTCCTTAATTAATCTTATCTGCTC	4494
Db	4423	AAACCGTTAATGTGTTCATGTTGAATCTTGTGTCTGTCGTAATTTCTTCTTAATCTAGTT	4482
Oy	4495	ACCATAGCAACCGGTTACACTTAACTGTAGTTGGCGCTTTCGCGA---ATACCCCTAG	4556
Db	4483	TCCATAGCTACGTAGATTAAGTAGACATGGCGGTTAATCATTAATTAACAAAGAACCCCTAG	4542
Oy	4551	TGAATGGAATGCCACATCCCTCTAATGGCGCGCTGCTGCTGCGGTGGGGCGGCGAGAGAG	4610
Db	4543	TGAATGGAATTTGACCATCTCTCTCTGGCGGCTGCTGCTGCTACTAGAGGCGGGGACCA	4602
Oy	4611	AGCTTCGCGCTGTGCGGACCTTTGGTTCGACAGGCGCCACCGAGGAGCGAGCGCGATAG	4670
Db	4603	AGGTGCCCGGACGCCCGGGCTTTTCCCGGGGCGCTCAGTGAAGGAGCGGCGGACGAG	4662
Oy	4671	AGGAGTGGCCAA 4683	

Db 4663 AGGAGTGCGCAA 4675

## RESULT 2

US-11-327-357-2  
; Sequence 2, Application US/11327357  
; Publication No. US20060105983A1  
; GENERAL INFORMATION:  
; APPLICANT: BTG International Ltd  
; APPLICANT: BEARD DR, PETER  
; APPLICANT: RAJ DR, KENNETH  
; TITLE OF INVENTION: CYTOTOXIC AGENTS  
; FILE REFERENCE: 142184WO  
; CURRENT APPLICATION NUMBER: US/11/327,357  
; CURRENT FILING DATE: 2006-01-09  
; PRIOR APPLICATION NUMBER: 0009887.1  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 145  
; TYPE: DNA  
; ORGANISM: adeno-associated virus 2  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1)..(145)  
; OTHER INFORMATION: ITR  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (72)-  
; OTHER INFORMATION: Unpaired base  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (94)-  
; OTHER INFORMATION: Unpaired base  
; US-11-327-357-2

Query Match 2.7%; Score 125; DB 7; Length 145;

Best Local Similarity 100.0%; Pred. No. 2,7e-24; Mismatches 0; Indels 0; Gaps 0;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGCGCGGCGCAAGAGTGGCC 60  
Db 21 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGCGCGGCGCAAGAGTGGCC 80  
Qy 61 CGAGCGCCCGGCTTTGCGGCGGCTTCACTGAGCGGCGGCGGCGGAGAGGAGTG 120  
Db 81 CGAGCGCCCGGCTTTGCGGCGGCTTCACTGAGCGGCGGCGGCGGAGAGGAGTG 140  
Qy 121 GCCAA 125  
Db 141 GCCAA 145

## RESULT 3

US-11-327-357-1/c  
; Sequence 1, Application US/11327357  
; Publication No. US20060105983A1  
; GENERAL INFORMATION:  
; APPLICANT: BTG International Ltd  
; APPLICANT: BEARD DR, PETER  
; APPLICANT: RAJ DR, KENNETH  
; TITLE OF INVENTION: CYTOTOXIC AGENTS  
; FILE REFERENCE: 142184WO  
; CURRENT APPLICATION NUMBER: US/11/327,357  
; CURRENT FILING DATE: 2006-01-09  
; PRIOR APPLICATION NUMBER: 0009887.1  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4675  
; TYPE: DNA

; ORGANISM: adeno-associated virus 2  
US-11-327-357-1

Query Match 2.5%; Score 118.2; DB 7; Length 4675;

Best Local Similarity 87.8%; Pred. No. 1e-21; Mismatches 18; Indels 0; Gaps 0;  
Matches 129; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGCGCGGCGCAAGAGTGGCC 60  
Db 4675 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGCGCGGCGCAAGAGTGGCC 4616  
Qy 61 CGAGCGCCCGGCTTTGCGGCGGCTTCACTGAGCGGCGGCGGCGGAGAGGAGTG 120  
Db 4615 CGTCGGGCGACCTTTGGTCCCGGCTTCAGTGAGCGGAGCGGCGGAGAGGAGTG 4556  
Qy 121 GCCAATCCATCACTAGGGTTCTCG 147  
Db 4555 GCCAATCCATCACTAGGGTTCTCG 4529

## RESULT 4

US-11-327-357-2/c  
; Sequence 2, Application US/11327357  
; Publication No. US20060105983A1  
; GENERAL INFORMATION:  
; APPLICANT: BTG International Ltd  
; APPLICANT: BEARD DR, PETER  
; APPLICANT: RAJ DR, KENNETH  
; TITLE OF INVENTION: CYTOTOXIC AGENTS  
; FILE REFERENCE: 142184WO  
; CURRENT APPLICATION NUMBER: US/11/327,357  
; CURRENT FILING DATE: 2006-01-09  
; PRIOR APPLICATION NUMBER: 0009887.1  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 145  
; TYPE: DNA  
; ORGANISM: adeno-associated virus 2  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1)..(145)  
; OTHER INFORMATION: ITR  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (72)-  
; OTHER INFORMATION: Unpaired base  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (94)-  
; OTHER INFORMATION: Unpaired base  
; US-11-327-357-2

Query Match 2.5%; Score 117.8; DB 7; Length 145;

Best Local Similarity 88.3%; Pred. No. 2,2e-22; Mismatches 17; Indels 0; Gaps 0;  
Matches 126; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGCGGCGGCGCAAGAGTGGCC 60  
Db 145 TTGGCCACTCCCTCTCTGCGGCTCGCTCGCTCACTGAGCGGCGGCGCAAGAGTGGCC 86  
Qy 61 CGAGCGCCCGGCTTTGCGGCGGCTTCACTGAGCGGCGGCGGCGGAGAGGAGTG 120  
Db 85 CGTCGGGCGACCTTTGGTCCCGGCTTCAGTGAGCGGAGCGGCGGAGAGGAGTG 26  
Qy 121 GCCAATCCATCACTAGGGTTCT 145  
Db 25 GCCAATCCATCACTAGGGTTCT 1

## RESULT 5

US-11-269-117-6

```
; Sequence 6, Application US/11269117
; Publication No. US20060110364A1
; GENERAL INFORMATION:
; APPLICANT: LIN, et al.
; TITLE OF INVENTION: VECTOR-MEDIATED DELIVERY OF POLYNUCLEOTIDES ENCODING SOLUBLE VEGF
; FILE REFERENCE: 28967/40835B
; CURRENT APPLICATION NUMBER: US/11/269,117
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: US 11/208,696
; PRIOR FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/602,926
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 6
; LENGTH: 8322
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AAV vector
US-11-269-117-6
```

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Query Match          2.3%; Score 110; DB 7; Length 8322;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGCGGACCAAGGTGCGC 60
DB 4625 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGCGGACCAAGGTGCGC 4684
QY 61 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGAG 110
DB 4685 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGAG 4734
```

```
RESULT 6
US-11-269-117-6/c
; Sequence 6, Application US/11269117
; Publication No. US20060110364A1
; GENERAL INFORMATION:
; APPLICANT: LIN, et al.
; TITLE OF INVENTION: VECTOR-MEDIATED DELIVERY OF POLYNUCLEOTIDES ENCODING SOLUBLE VEGF
; FILE REFERENCE: 28967/40835B
; CURRENT APPLICATION NUMBER: US/11/269,117
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: US 11/208,696
; PRIOR FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/602,926
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 6
; LENGTH: 8322
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: AAV vector
US-11-269-117-6
```

```
Query Match          2.3%; Score 110; DB 7; Length 8322;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGCGGACCAAGGTGCGC 60
DB 116 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTAGAGCGCGGACCAAGGTGCGC 57
QY 61 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGAG 110
DB 56 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGGAG 7
```

```
RESULT 7
US-10-953-349-16574
; Sequence 16574, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 16574
; LENGTH: 1309
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-16574
```

```
Query Match          1.1%; Score 52; DB 6; Length 1309;
Best Local Similarity 46.1%; Pred. No. 0.00022;
Matches 175; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
```

```
QY 1011 TGTGGAACCGGGGATCACTCCGAGAAGAGTGAATCCAGAGACGAGGCTGTGACA 1070
DB 638 TGTGGAAGCTGTGATCTCTGTCGCGCGGCACTCCATGCGGTGCGGCACTCTCTCT 697
QY 1071 TCTCTTCAACGCGGCTTCCAACTGCGGTCGCGTCCAGATCAAGCGGCTGTGACAATGCCG 1130
DB 698 TCACCGGCGGCTCAACGCGCGCGCGGAGAGATCAACCGGCTCAACGCAACTTCTCA 757
QY 1131 GCAAGATATAGCGCTGACCAATTCGCGCGGCACTACTGATGAGCCCGCTCGCCCG 1190
DB 758 ACCAAGATGTCACCAAGGCGCCCAACCGGCTGTGTCAACAGCTTCGCAATGAGACT 817
QY 1191 CCGACATTAAACCAACCGCATTTACCGCATCTGAGACTGAACGCTACGACCTGCGCT 1250
DB 818 ACGAGACGCTGTCCAAATGTCATGCCGCGTTACACGCGGCTGCGCAAGATCAGCGACT 877
QY 1251 ACGCGGCTCGGCTTTCTGCGGTGGGCGCCAGAAAAGTTGGAAAACGCAACCACTCT 1310
DB 878 TCTCTGACAAACCTTCTACCAACAACTGCGCAGATGTCAGCTTCAACTCCGACT 937
QY 1311 GGTCTTTGGGCGCGGCAACGCGGCAAGACCAATCGCGGAGCACTCCGACGCGG 1370
DB 938 GGCAGCTCATGACCCACACGAGGCGCAGGCGTCAAGTCAAGTACCGCAACGCGCA 997
QY 1371 TGCCCTTCTACGCGTGCCTC 1390
DB 998 CGCTCTGGGACGCGGACTTC 1017
```

```
RESULT 8
US-10-953-349-33293
; Sequence 33293, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 33293
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
```

```
US-10-953-349-33293
Query Match          1.0%; Score 47.2; DB 6; Length 1191;
```

Best Local Similarity 44.3%; Pred. No. 0.0039;  
Matches 193; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

Qy	1009	GCTGTGGACCGGGGCACTACCTCCGGAGACGAGTGAATCCAGAGAGACAGAGCTTGTA	1066
Db	473	GCTGGCGGGGAACAACCTGACGTACAGAGTCCCGCGGGGGCGGCGACGGGGCGGGTTC	532
Qy	1069	CATCTCTCTTCAACGGCGGCTCCAACTCGCGGTCCAGATCAAGGCGGCTTGGAACAATGC	1128
Db	533	CAGGGAGACGGAGCGCAACAGAGAACCTCCCTCGCGGTCTGCACCGCGGCGAGCTGT	592
Qy	1129	CGGCAAGATCATGGGGCTGACCAATCCGGCGCCGACTAAGCTGTGAGCCCGCTCGCC	1188
Db	593	CGGCAACTTCAACGGCGAAGAACTTCACCGCGAGGACATGGTGGTGCCTCCGGGCGCGCA	652
Qy	1189	CGCCGACATTTAAACCAACCGGATTTACGGCATCTGAGCGMAACGGATTCAGACCTCGC	1248
Db	653	CACGGTCGGCGCTCCACTGTCTCTTTCACCAACCGGCTCTAGCGGCTTACGACAGC	712
Qy	1249	CTACGCCGGCTCCGTCTTCTCGGCTGGGCGCCAGAAAGATTGCGAAAACGCACCAACCAT	1308
Db	713	CAGGAGAGTGCACCCCACTCATGAGTCCGCTAGCCCTCCTGTCGGGGCATCTGCCC	772
Qy	1309	CTGGCTGTTTGGGCGCGGCACCACGGGGCAAGACCAACATCGCGAAGGCATTCGCCACGC	1368
Db	773	GTCCAAACCAAGCCAGTCTTCTCCCAACACCAACCAACATGACCTTCATACACGCCCGC	832
Qy	1369	CGTGCCCTTTACGGCTGCTGCACTGGACCAATAGAACTTTCCTTCAACGATTTGGGT	1428
Db	833	GCTGTGCACAAACAGTACTAGTCGTGGCTCGCCAAACAACCTCGGCTCTTTCAGCTCCGA	892
Qy	1429	CGACACAGTGTGATC	1444
Db	893	CCAGGCTCTGCTCACCC	908

```

RESULT 9
US-10-953-349-33793
? Sequence 33793, Application US/10953349
? Publication No. US20060107345A1
? GENERAL INFORMATION:
? APPLICANT: ALEXANDROV, Nickolai et al.
? TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
? FILE REFERENCE: 2750-1579PUS2
? CURRENT APPLICATION NUMBER: US/10/953,349
? CURRENT FILING DATE: 2004-09-30
? NUMBER OF SEQ ID NOS: 40252
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 33793
? LENGTH: 1302
? TYPE: DNA
? ORGANISM: Zea mays subsp. mays
US-10-953-349-33793

```

Query Match	1.0%;	Score 47;	DB 6;	Length 1302;
Best Local Similarity	45.6%;	Pred. No. 0.0046;		
Matches 204; Conservative	0;	Mismatches 240;	Indels 3;	Gaps 1;

QY	1072	CTCCTTCAACGCGCCTTCCAATCTCGGCTCCAGATCAAGGCGCTTGACAAATGCGCG	1131
Db	489	CGCGCGCGACGTCACAACTCCGCGCGCGGCCACAGGGGAAGACCGCGCTGCACCTGGCGCG	548
QY	1132	CAAGATCATGCGCGTGACCAATCGCGGCCGACTACTGTGAGGCCCGCTCGCGCGC	1191
Db	549	CGAGTGTGTTCTCC---CCGATATGTGTCCGTGTGTTGACACACAGCGCACCCAG	605
QY	1192	CGACATTAAACCAACGCGCATTTTACCGCATCTTGAGGTGAACGCGTACGACCTTGCTTA	1251
Db	606	CGCAGGACGCTCGACGCGCGTACCCGCTGACGCTGTCGAGGCGCTCACATCAGAATT	665
QY	1252	CGCGGCTCGGCTTTTCTCGGCTGGGCCAAGAAAGGTTGGAAACGCAACACCATCTG	1311

Db	666	CCTGTTCAAGGGGCCCCCGTCCGGGGGCTCACGACATGAGGCCAAAGACTCAGGCTGTG	725
Qy	1312	GCTGTTGGGCGCGCACATCGGCGAAGCAACATGCGGAGGCATCGCCACGCCCT	1371
Db	726	CCTTGAGCTCTGTGAGTCCGCGGTGATGTTGATACCAACGCGCAGCTCGACCGCGCGGGA	785
Qy	1372	GCCCTTTCAGGGCTGCCGTCACCTGACACCATGAGAACTTTCCTTCAACGATGGGTGGA	1431
Db	786	CGACGCCCGGGGAAAGCCAGCAGCGCGCGCGGCGGCGAACTTCCCCAGAGACGACGCCAGGA	845
Qy	1432	CAAGATGTTGATCTGTGTGGAGAGAGGGCAAGATGACGGCCAAAGTCTGTGATCCGCCAA	1491
Db	846	CAGCTTGATGAGCTGTACGATGAATCCACCTCATGTATCCAGGGCCAGGAGATGCGCGGC	905
Qy	1492	GGCCATTCTCGCGCGGACGACAGATGCGC	1518
Db	906	TGCGCGGTGGCGCGCGGTGAGGCGAG	932

```

RESULT 10
US-10-953-349-27324
; Sequence 27324, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27324
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-27324

```

Query Match	Similarity	1.0*	Score	46.6	DB 6	Length	845
Best Local	Similarity	46.0*	Pred.	No. 0.0047			
Matches	203	Conservative	0	Mismatches	229	Indels	9
							Gaps
							1
1061	GCTCTGTCATCTCTCTTCAACGCGCCTCCAACTCGCGGATCCGAGTCAAGCCGCTCTG	1120					
249	GACTTCGAGCTCGCCTCTCAAGCGCGGAGCGGACCGGCTCGCCTCTCGCGCGCGCG	308					
1121	GACCAATGCGGCAAGATCATGCGCTGACCAATTCGCGCCGACTACCTGTGAGCCCC	1180					
309	GAGCTCTTCCCGGACCTGATCCCGCTCGGCTCGCCTCTCTCTCTCTGCTCTTCAAC	368					
1181	GCTCGCGCGCGGACATTAAACCAACCGCATTTACGCGATCTCGAGCTGAACGGCTAC	1240					
369	CACGAAAAAGCGGACCTGCGCGCGCGCGCGCGCTCTCTCTCGCGGACCTACCGACTCC	428					
1241	GACCTTGCTACGCGCGGCTCCGCTTTCTTGCGCTGGGCGCCAGAAAAGTTTGGAAAAAGC	1300					
429	GACACACCTCTGGACCTCGCGGGGATCAGGCGCTTCGCGGACGCGCTCTGTGAGCGCAAC	488					
1301	AACACCATCTGGCT-----GTTTGGGCGGCGACCAACGGGCAAGAACCATGCGG	1351					
489	GGCGTCCAGCTGCTCTGTGACACACTCTCGCGGCTCTCTCGAGTGTGACATCCGAGAGGGC	548					
1352	GAAGCCATTCGCCACGCGCGTCCCTTCAAGGCTGCGTCACTGGACCAATGAGACTTT	1411					
549	GAGCGGGTGACCAATTCCTGGCGGCTCGGAGAACCTCATTCGACTTCGCGCCACATTC	608					
1412	CCCTTCAACGATTCGCTGACCAACATGATGTATCTGTGTGGAGGAGGCAATGACGGCG	1471					
609	GCCCACTCTGTCTGTGACCGGACCAAGATGCTCCGGTGGCTGTGGCCCGGTGTCAAGGCC	668					
1472	AAGGTGTGAGTTCGCGCAAG	1492					
669	CGGACCTTCGAGGCGCAACGAG	689					

RESULT 11  
US-10-513-348-6  
; Sequence 6, Application US/10513348  
; Publication No. US20060093589A1  
; GENERAL INFORMATION:  
; APPLICANT: Warington, Kenneth H.  
; APPLICANT: Opie, Shaun R.  
; APPLICANT: Muzyczka, Nicholas  
; TITLE OF INVENTION: VP2-MODIFIED RAAV VECTOR COMPOSITIONS AND USES THEREFOR  
; FILE REFERENCE: 4300.016100  
; CURRENT APPLICATION NUMBER: US/10/513,348  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: PCT/US04/05205  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: PCT/US03/13583  
; PRIOR FILING DATE: 2003-05-01  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-513-348-6

Query Match 1.0%; Score 45; DB 6; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2889 TGGCATTGCGATTCCACATGCTGGGCGCAAGATCATACCAACC 2933  
DB 1 TGGCATTGCGATTCCACATGCTGGGCGCAAGATCATACCAACC 45

RESULT 12  
US-10-953-349-38921  
; Sequence 38921, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 38921  
; LENGTH: 2152  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-38921

Query Match 0.9%; Score 43.6; DB 6; Length 2152;  
Best Local Similarity 42.6%; Pred. No. 0.048;  
Matches 284; Conservative 0; Mismatches 379; Indels 3; Gaps 1;

QY 999 TGGTGGGTGGGTGGATGACCGGGCATCACTCCGAGAGAGATGCCAGAGACC 1058  
DB 412 TGAATCCCGGGTCCCGCGCAAGCCCATGATGGGGTGCATTCAGGGGCGAGGAAAC 471  
QY 1059 AGGCTGTATCATCTCTTCAAGCGCGCTCCACTCGCGGTCCAGATCAAGCGCTC 1118  
DB 472 AGTTCTCGCGCGAGAGATCAAGCTTCATGATCTGAACAAGATGAAGAGAGCGCGAGG 531  
QY 1119 TGGAAATGCGCGCAAGATCAAGGCGGTGACCAATCCGGCGCGCATTAACCTGTAGGCC 1178  
DB 532 CTTAACCTGCGCAAGCAACCAATCAAGAAAGCTGTGTGTCATCCGGCTTAACCTCAAGCACT 591  
QY 1179 CCGCTCCGCGCGAGCATTAACAACCAAGCATTTACCGCATCTGTGAGTGAAGCGCT 1238

DB 592 CCCAGCGCGAGGCCAACAGAGACGCCGGCGTATCTCCGGCTCAACGTATGCCATCA 651  
QY 1239 AGACCTGCTCTTACCGCGGCTCCGTCTTTCTTGGCTGGGCCCAAGAAAGTTCCGAAAC 1298  
DB 652 TCAAGAGACCCACCGCGCGCATGCAATAGGGCTCGAACAAAGTGTGACACGACG 711  
QY 1289 GCAACACCATCTGGCTGTTTGGGCGCGGCACACAGGGGCAAGCAACAATCGCGAAGCA 1358  
DB 712 GCGAAGAAAGTCTTCACTTCTTCACTTCGGCGGGGTAACCTTGAACGTTCTGCTCTCA 771  
QY 1359 TCGCCACGCGGTGCTCTTCTTCAAGCTGCTCACTGACCAATGAACTTTCCCTTCA 1418  
DB 772 CCATGAGAGAGGAGCATCTTTAGAGTCAAGGACACGCGCGGACACCCACCTCGGAGGCG 831  
QY 1419 ACGATTGCTGACAAAGATGATGATGTGTGGG--AGAGAGCAAGATGACGCGCAAG 1475  
DB 832 AGGACTTGAACAACGCGCTGTGAAACAATTGTCAGAGAGTTCAAAGAGAAACAAG 891  
QY 1476 TCGTGAAGTCCGCGCAAGGCAATTCCTGCGCGGACAGAGTGGCGGTGACCAAAAGTCA 1535  
DB 892 AGACATCACTGGCAACCCCAAGGCGCTCCGCGACTAGAACCGCTGCGAGAGGCTA 951  
QY 1536 AGTCGTCCGCCAGATGATCCACCCCGTATGCTCACTTCAACCAACATGTGCG 1595  
DB 952 AGAGAGCGCTCTCCCTCCACCGCGCAACACACATGATGATCGCTTATAGAGGCA 1011  
QY 1596 CCGTATGACGGGAAACGACACACCTTTCAGACACACAGCGCTTGAAGAGCGGATGT 1655  
DB 1012 TCGACTTCAACGACATCAACCGGTGCGGTTCGAGAGCTCAACATGACCTTCC 1071  
QY 1656 TCAAT 1661  
DB 1072 GCAAGT 1077

RESULT 13  
US-10-953-349-32310  
; Sequence 32310, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 32310  
; LENGTH: 1439  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-10-953-349-32310

Query Match 0.9%; Score 43.4; DB 6; Length 1439;  
Best Local Similarity 50.2%; Pred. No. 0.044;  
Matches 107; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 1312 GCTGTTTGGCGCGGCAACAGGCAAGCAATCGCGGAAGCATCGCCAGCCGT 1371  
DB 232 GCTGTGCGCGGTGTCGCGGGAAGCGGCGACAGACAGAGCGGTGTCGCGGATGCT 291  
QY 1372 GCCCTTACGCGCTGCTCAACTGGAACCAATGAGAACTTTCCCTTCAAGATGTGCTGA 1431  
DB 292 GTTCTGCAACAGTGAAGAGAGCGGCGCGCTTCTTCACTTAACCGCTTACCGGCGC 351  
QY 1432 CAAGTGTGATCTGTTGGAGAGAGGCAAGATGACGCGCAAGGCTGAGTGGCGCA 1491  
DB 352 GCGGTGCGATTCAGTGGCGGCGGAGCAACCCGATCAAGGTGCGGAGTGAACAC 411  
QY 1492 GGCATTTCTCGCGGCAAGAGTGTGCGGTGA 1524

Db 412 CAACTGTTGCGGCTTCTCCGTGCGCATGGA 444

## RESULT 14

Sequence 1, Application US/10513348  
Publication No. US20060093589A1  
GENERAL INFORMATION:  
APPLICANT: Warrington, Kenneth H.  
APPLICANT: Opie, Shaun R.  
APPLICANT: Muzyczka, Nicholas  
TITLE OF INVENTION: VP2-MODIFIED RAAV VECTOR COMPOSITIONS AND USES THEREFOR  
FILE REFERENCE: 4300.016100  
CURRENT APPLICATION NUMBER: US/10/513,348  
PRIORITY FILING DATE: 2004-10-29  
PRIORITY APPLICATION NUMBER: PCT/US04/05205  
PRIORITY FILING DATE: 2004-02-19  
PRIOR APPLICATION NUMBER: PCT/US03/13583  
PRIOR FILING DATE: 2003-05-01  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-513-348-1

## Query Match

Best Local Similarity 0.9%; Score 43.2; DB 6; Length 48;  
Best Local Similarity 93.8%; Pred. No. 0.0091;  
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2194 GACTTAAACCGATGCTGCTGCCATGCTTATCTTCCAGATTGGCTCG 2241  
Db 1 GATTTAATCAGTCTGCTGCCATGCTTATCTTCCAGATTGGCTCG 48

## RESULT 15

US-10-984-694-2  
Sequence 2, Application US/10984694  
Publication No. US20060093679A1  
GENERAL INFORMATION:  
APPLICANT: TSIEH, Roger Y.  
APPLICANT: WANG, Lei  
TITLE OF INVENTION: METHODS FOR ENGINEERING POLYPEPTIDE  
TITLE OF INVENTION: VARIANTS VIA SOMATIC HYPERMUTATION AND POLYPEPTIDES MADE  
FILE REFERENCE: 39754-0976A US  
CURRENT APPLICATION NUMBER: US/10/984,694  
CURRENT FILING DATE: 2004-11-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 681  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Nucleic acid encoding the fluorescent protein  
OTHER INFORMATION: mRFP1.2  
US-10-984-694-2

## Query Match

Best Local Similarity 0.9%; Score 43.2; DB 6; Length 681;  
Best Local Similarity 44.5%; Pred. No. 0.034;  
Matches 171; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 1018 CCGGGGATCACTCCGAGAAAGATGATCCAGAGAGCCAGGCTTGTACATCTCTT 1077  
Db 162 CCGGCTTGGCTGCGATCTGTCTCCCTCAGTTATGATGAGGCTCCAGGCTTACGT 221  
QY 1078 CAAGCCGCTTCAACTGCGGCTCCAGATCAAGCCGCTTGAACAATGCCGAGAGAT 1137  
Db 222 GAAGCAACCCCGCAGATCCCGACTACTGAAGCTGTCTTCCCGAGGGCTTCAAGTG 281

QY 1138 CATTGGCTGACCAATCCCGGCCGACTACTGTAGGCCCGCTCCGCCGCCGACAT 1197  
Db 282 GGAAGCGCTGATGAACTTTCAGAGACGGCGGCTGTGTACCGTACCCAGATCTCTCCT 341  
QY 1198 TAAACCAACCGCATTTTACCGCATCTGAGCTGAAACGGCTTACGACCTTGTACGCCGG 1257  
Db 342 GCAAGACGGCGAGTTTATCTTACAAGGTGAAGCTGCGGCAACCACTTCCCTCCGACGG 401  
QY 1258 CTCGCTTTTCTCGGCTGGGCCCAAGAAAAGTTTCGAAAACGCAACCACTGTGCTGT 1317  
Db 402 CCCGTAATGCAAGAAAGACCATGCGTGGAGGCTCTCTCCGAGCGATGATCCCGA 461  
QY 1318 TGAGCCGCGCCACCAAGGCAAGACCAATGCGGAGAGCCATGCGCCAGCCGCTGCTCT 1377  
Db 462 GGAAGCGGCTCTGAAAGGCGAGATCAAGATGAGGCTTAAGTAAAGACCGGCCACTTA 521  
QY 1378 CTACGGCTGCGTCAACTGACCAA 1401  
Db 522 CGACGCCGAGGTCAAGACCACTTA 545

Search completed: June 13, 2006, 13:22:07  
Job time : 152 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 12:06:09 ; Search time 2682 Seconds  
(without alignments)  
12174.139 Million cell updates/sec

Title: US-10-696-261-19

Perfect score: 4683

Sequence: 1 ttggccactccctctctgcg.....cgcatagaggagtgccaa 4683

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq 8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4683.8	99.6	4683	AAf23749	AAf23749 AAV6 DNA
2	4683.8	99.6	4683	ADL13983	ADL13983 Adeno-ss
3	4683.8	99.6	4683	ADG39763	ADG39763 AAV-6 gen
4	4253.2	90.8	4718	AAAD00772	AAAD00772 Adeno-ss
5	4253.2	90.8	4718	ADG76507	ADG76507 Adeno-ss
6	4253.2	90.8	4718	ADL13984	ADL13984 Adeno-ss
7	4253.2	90.8	4718	ADG39758	ADG39758 AAV-1 gen
8	3831.4	81.8	4239	ADN39402	ADN39402 Adeno-ss
9	3831.4	81.8	4239	ADZ46598	ADZ46598 HSV-AAV s
10	3802	81.2	4347	ADW39398	ADW39398 Adeno-ss
11	3802	81.2	4347	ADZ46594	ADZ46594 HSV-AAV s
12	3802	81.2	4347	AEF81093	AEF81093 Adeno-ss
13	3678.4	78.5	4721	ADG76502	ADG76502 Adeno-ss
14	3678.4	78.5	4721	ADG39764	ADG39764 AAV-7 gen
15	3678.4	78.5	4721	ADV67509	ADV67509 Nucleotid
16	3678.4	78.5	4721	ADZ27030	ADZ27030 Adeno-ss
17	3443.2	73.5	4382	ABO80410	ABO80410 AAV9 rep
18	3404.6	72.7	4385	ADG76506	ADG76506 Adeno-ss

19	3370.4	72.0	4393	9	ACF05811	ACF05811 Adeno-ss
20	3370.4	72.0	4393	10	ADG76505	ADG76505 Adeno-ss
21	3370.4	72.0	4393	12	ADG39765	ADG39765 AAV-8 gen
22	3370.4	72.0	4393	14	ADV67510	ADV67510 Nucleotid
23	3370.4	72.0	4393	14	ADZ27032	ADZ27032 Adeno-ss
24	3296.2	70.4	4679	4	AAI66974	AAI66974 Adeno-ss
25	3296.2	70.4	4679	6	ABK89694	ABK89694 Adeno-ss
26	3296.2	70.4	4679	10	ABV76133	ABV76133 Adeno-ss
27	3296.2	70.4	4679	14	AEA48850	AEA48850 Bovine ad
28	3296.2	70.4	8698	4	AAH26325	AAH26325 wild-type
29	3294.6	70.4	4679	4	AAf23750	AAf23750 AAV2 DNA
30	3285	70.1	4679	12	ADG39757	ADG39757 AAV-2 gen
31	3270.8	69.8	4680	2	AAT09008	AAT09008 wild-type
32	3270.8	69.8	4680	9	ABX14497	ABX14497 wild-type
33	3270.8	69.8	4680	9	ADA50070	ADA50070 Adeno-ss
34	3270.8	69.8	4680	10	ADG81075	ADG81075 Adeno-ss
35	3270.8	69.8	4680	12	ADG92079	ADG92079 wild-type
36	3270.8	69.8	4680	14	AEA848083	AEA848083 Adeno-ss
37	3244.2	69.3	4675	4	AAH41481	AAH41481 Adeno-ss
38	3244.2	69.3	4675	4	AAf89931	AAf89931 Nucleotid
39	3244.2	69.3	4675	6	ABA02989	ABA02989 Adeno-ss
40	3244.2	69.3	4675	6	ABG69879	ABG69879 Human ade
41	3244.2	69.3	4675	6	ABG69880	ABG69880 Human ade
42	3244.2	69.3	4675	10	ADG76508	ADG76508 Adeno-ss
43	3244.2	69.3	4675	15	AEF10041	AEF10041 Adeno-ss
44	3244.2	69.3	4675	15	AEF10040	AEF10040 Adeno-ss
45	3182.8	68.0	4722	4	AAf23748	AAf23748 AAV3B DNA

## ALIGNMENTS

RESULT 1  
AAf23749  
ID AAF23749 standard; DNA; 4683 BP.  
XX  
XX AAF23749;  
XX  
XX 28-MAR-2001 (first entry)  
XX  
XX  
XX AAV6 DNA sequence.  
XX  
XX AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS;  
XX  
XX atherosclerosis; sickle cell anemia; thalassemia;  
XX  
XX blood clotting disorder; diabetes; ss.  
XX  
XX Adeno associated virus.  
XX  
XX US6156303-A.  
XX  
XX 05-DEC-2000.  
XX  
XX 11-JUN-1997; 97US-00873168.  
XX  
XX 11-JUN-1997; 97US-00873168.  
XX  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Russell DW, Rutledge EA;  
XX  
XX WPI; 2001-060164/07.  
XX  
XX Adeno-associated virus serotype 6 and viral vector derived from it for  
XX  
XX gene therapy of cystic fibrosis, cancer, acquired immunodeficiency  
XX  
XX syndrome, sickle cell anemia, thalassemia and diabetes.  
XX  
XX Claim 1; Fig 1; 50pp; English.  
XX  
XX The present invention relates to adeno-associated virus serotypes. The  
XX  
XX present sequence is the DNA sequence of one such serotype (AAV6). AAV6  
XX  
XX can be used to construct AAV viral vectors for use in gene therapy for a  
XX  
XX range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis,  
XX  
XX sickle cell anaemia, thalassemia, blood clotting disorders and diabetes.

CC The AAV viral vectors have increased transduction efficiency of a  
CC particular host cell as the AAV virion containing the AAV vector genome  
CC can be modified to express a capsid protein of an AAV serotype that  
CC transduces the selected host cell

XX Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;

Query Match 99.6%; Score 4663.8; DB 4; Length 4683;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
QY 1 TTGGCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCCGGCGCAACAAAGTCCG 60
Db 1 TTGGCACTCCCTCTCTGCGGCTGCTGCTCACTGAGCCGGCGCAACAAAGTCCG 60
QY 61 CGAGCCCGGGGCTTTGCCCCGGGCGCTCAGTGAACGACGACGCCGACAGAGAGATG 120
Db 61 CGAGCCCGGGGCTTTGCCCCGGGCGCTCAGTGAACGACGACGCCGACAGAGAGATG 120
QY 121 GCCAACTCATCACTAGGGGTTCTCGAGGGGTGAGTCTGAAGTGAATTACGTCATAG 180
Db 121 GCCAACTCATCACTAGGGGTTCTCGAGGGGTGAGTCTGAAGTGAATTACGTCATAG 180
QY 181 GGTAGGAGGTCTCTGATATTAAGGTCAAGTGTGTTTGCACATTTTGCACACCAT 240
Db 181 GGTAGGAGGTCTCTGATATTAAGGTCAAGTGTGTTTGCACATTTTGCACACCAT 240
QY 241 GTGTGACGCTGGGTATTTAAGCCGAGTGAACGACGAGGCTTCCATTGGAACGGGA 300
Db 241 GTGTGACGCTGGGTATTTAAGCCGAGTGAACGACGAGGCTTCCATTGGAACGGGA 300
QY 301 GGTGTAACGCGACGCGCATGCGGGGTTTTCAGATTTGATTAAGTCCCGACGGA 360
Db 301 GGTGTAACGCGACGCGCATGCGGGGTTTTCAGATTTGATTAAGTCCCGACGGA 360
QY 361 CTTTGACGAGCATCTGCCGSCATTTCTGACAGCTTTGTGAATGAGTGGCCGAGAA 420
Db 361 CTTTGACGAGCATCTGCCGSCATTTCTGACAGCTTTGTGAATGAGTGGCCGAGAA 420
QY 421 ATGGAGGTGCGCGCAGATTCTGACATGAGATCTGAATCTGATTAAGAGGAAACCC 480
Db 421 ATGGAGGTGCGCGCAGATTCTGACATGAGATCTGAATCTGATTAAGAGGAAACCC 480
QY 481 CGTGGCGAGAAAGTGTGACGCGCACTTCTGTGTCACTGCGCGCGCTGAATTAAG 540
Db 481 CGTGGCGAGAAAGTGTGACGCGCACTTCTGTGTCACTGCGCGCGCTGAATTAAG 540
QY 541 GGAAGCCCTCTTTCTTTGTTCAAGTTGAGAGGCGAGTCTTAATTCTTCAATTTCT 600
Db 541 GGAAGCCCTCTTTCTTTGTTCAAGTTGAGAGGCGAGTCTTAATTCTTCAATTTCT 600
QY 601 GGTGAGACCAACGCGGGGTCAATCAATGATGTCGCGCGCTTCCGAGTCAAGTTAAG 660
Db 601 GGTGAGACCAACGCGGGGTCAATCAATGATGTCGCGCGCTTCCGAGTCAAGTTAAG 660
QY 661 CAAGCTGTGACGACATCTACCGCGGAGTGAAGCCGCTTCCCAATGTTTCCGCGT 720
Db 661 CAAGCTGTGACGACATCTACCGCGGAGTGAAGCCGCTTCCCAATGTTTCCGCGT 720
QY 721 GACCAAGACGCGTATGAGCGCGGAGGGGGGAAACAAGTGTGACGAGTCTAATCTCC 780
Db 721 GACCAAGACGCGTATGAGCGCGGAGGGGGGAAACAAGTGTGACGAGTCTAATCTCC 780
QY 781 CAACTAACCTCTGCGCAAGACTCAAGCCGAGCTGAGTGGCGGTGATTAATGAGAGA 840
Db 781 CAACTAACCTCTGCGCAAGACTCAAGCCGAGCTGAGTGGCGGTGATTAATGAGAGA 840
QY 841 GTATATAAGCGCGTATTAAACCTGCGGACGCAACGCGTCTGCGGACGACCTGAC 900
Db 841 GTATATAAGCGCGTATTAAACCTGCGGACGCAACGCGTCTGCGGACGACCTGAC 900
QY 901 CCAGCTCAGCCAGACCCAGAGCAAGACAGAGAGATTTGAACCCCAATTCTGACGCGCC 960
Db 901 CCAGCTCAGCCAGACCCAGAGCAAGACAGAGAGATTTGAACCCCAATTCTGACGCGCC 960
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Db 901 CCAGCTCAGCCAGACCCAGAGCAAGACAGAGAGATTTGAACCCCAATTCTGACGCGCC 960
QY 961 TGTATCCGGTCAAAAACCTCCGACGCTACATGAGACTGTGGGGGTGGGAGCG 1020
Db 961 TGTATCCGGTCAAAAACCTCCGACGCTACATGAGACTGTGGGGGTGGGAGCG 1020
QY 1021 GGGCATCACTCCGAGAGAGATGATCCAGAGAGACAGGCTCTGATACCTCTTCAA 1080
Db 1021 GGGCATCACTCCGAGAGAGATGATCCAGAGAGACAGGCTCTGATACCTCTTCAA 1080
QY 1081 CGCCGCTTCAACTCTGCGGTGCCAGATCAAGCCGCTCTGAGCAATGCCGCAAGATCAT 1140
Db 1081 CGCCGCTTCAACTCTGCGGTGCCAGATCAAGCCGCTCTGAGCAATGCCGCAAGATCAT 1140
QY 1141 GGGGCTGACAAATCCGCGCCGACCTACGTTAGGCGCCGCTCCGCGCGCATTTAA 1200
Db 1141 GGGGCTGACAAATCCGCGCCGACCTACGTTAGGCGCCGCTCCGCGCGCATTTAA 1200
QY 1201 AACCAACCGCATTTACCGCATCTCTGAGCTGAACGAGCTACGACCTTACCGCGGCTC 1260
Db 1201 AACCAACCGCATTTACCGCATCTCTGAGCTGAACGAGCTTACGACCTTACCGCGGCTC 1260
QY 1261 GGTCTTTCTGCGCTGGGCCCAAGAAAGTTGCGAAAACGACACCATCTGCTTTGG 1320
Db 1261 GGTCTTTCTGCGCTGGGCCCAAGAAAGTTGCGAAAACGACACCATCTGCTTTGG 1320
QY 1321 GCGGCGCACCAAGGGGCAAGACCAATCGGGAAGCCATGCGCCAGCGGCTTCTA 1380
Db 1321 GCGGCGCACCAAGGGGCAAGACCAATCGGGAAGCCATGCGCCAGCGGCTTCTA 1380
QY 1381 CGGCTGCGTCAACTGACCAATGAGAACTTTCCCTTCAACGATTTGCTGACAAAGATG 1440
Db 1381 CGGCTGCGTCAACTGACCAATGAGAACTTTCCCTTCAACGATTTGCTGACAAAGATG 1440
QY 1441 GATTTGTTGGAAGAGGCGCAAGATGACGCGCAAGTGTGTGAGTCCGCCAAGGCAATCT 1500
Db 1441 GATTTGTTGGAAGAGGCGCAAGATGACGCGCAAGTGTGTGAGTCCGCCAAGGCAATCT 1500
QY 1501 CGGCGGACGAAAGGTGCGCGTGGACCAAAAGTGCAGTCTGCGCCAGATGATCCAC 1560
Db 1501 CGGCGGACGAAAGGTGCGCGTGGACCAAAAGTGCAGTCTGCGCCAGATGATCCAC 1560
QY 1561 CCCCGTATGTCATCCTTCAACACCAACATGTGCGCGGTATTTGACGGGAAACGACAC 1620
Db 1561 CCCCGTATGTCATCCTTCAACACCAACATGTGCGCGGTATTTGACGGGAAACGACAC 1620
QY 1621 CTTGAGACCAACGACCGCTTTGACGAGCCGGAATGTTCAATTGGAATCAACCCGCGTCT 1680
Db 1621 CTTGAGACCAACGACCGCTTTGACGAGCCGGAATGTTCAATTGGAATCAACCCGCGTCT 1680
QY 1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGAGTCTTCCGCTGGGCGCA 1740
Db 1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGAGTCTTCCGCTGGGCGCA 1740
QY 1741 GGATCAAGTGAACGAGGTGCGCATGAGTTCATGTCAGAAAGGTTGAGACCAACAG 1800
Db 1741 GGATCAAGTGAACGAGGTGCGCATGAGTTCATGTCAGAAAGGTTGAGACCAACAG 1800
QY 1801 ACCCGCCCCGATGACCGCGGATTAAGAGCGAGCCCAAGCGGGCTTCCCTCAATCGGGA 1860
Db 1801 ACCCGCCCCGATGACCGCGGATTAAGAGCGAGCCCAAGCGGGCTTCCCTCAATCGGGA 1860
QY 1861 TCCATGACGTCAGACGCGGAGAGTCCGATGAGACTTTGCGGACAGTATCCAAACAA 1920
Db 1861 TCCATGACGTCAGACGCGGAGAGTCCGATGAGACTTTGCGGACAGTATCCAAACAA 1920
QY 1921 ATGTTCTGTCACGCGGCGCATGCTTCAAGTGTCTTCCCTGCAAAACATGCGAGAGAT 1980
Db 1921 ATGTTCTGTCACGCGGCGCATGCTTCAAGTGTCTTCCCTGCAAAACATGCGAGAGAT 1980
QY 1981 GAATCAAAATTTCAACATTTGCTTCAAGCACGGGACCAAGAGACTGTTCAAAATGTTTCCC 2040
Db 1981 GAATCAAAATTTCAACATTTGCTTCAAGCACGGGACCAAGAGACTGTTCAAAATGTTTCCC 2040
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QY 2041 CGGCGTGCAGATCTCAACCGGTGTCGAAAGAGGACGTATGGGAAACTCTGTCAT 2100  
DB 2041 CGGCGTGCAGATCTCAACCGGTGTCGAAAGAGGAGTATCGGAAACTCTGTCAT 2100  
QY 2101 TCATCATCTGCTGGGGCGGGCTCCGAGATGCTTGTCTGGCTCGATCTGCTCAACGT 2160  
DB 2101 TCATCATCTGCTGGGGCGGGCTCCGAGATGCTTGTCTGGCTCGATCTGCTCAACGT 2160  
QY 2161 GGATCTGGATGATCTGTGTTTCTGAGCAATAATGACTTAACCAAGTATGCTGCGATG 2220  
DB 2161 GGATCTGGATGATCTGTGTTTCTGAGCAATAATGACTTAACCAAGTATGCTGCGATG 2220  
QY 2221 GTTATCTTCCAGATTGGCTCGAGGACAACTCTCGAGGAGGCAATTGGGAGGTGGGACT 2280  
DB 2221 GTTATCTTCCAGATTGGCTCGAGGACAACTCTCGAGGAGGCAATTGGGAGGTGGGACT 2280  
QY 2281 TGAACCTGAGAGCCCGGAAACCCAAAGCCAAACAGCAAAAGCAGAGCAGCGCCGGGGTC 2340  
DB 2281 TGAACCTGAGAGCCCGGAAACCCAAAGCCAAACAGCAAAAGCAGAGCAGCGCCGGGGTC 2340  
QY 2341 TGGTCTTCTTGGCTACAAATGCTCTGGAACCTTCAACGAGCTCGACAAAGGGGAGCCCG 2400  
DB 2341 TGGTCTTCTTGGCTACAAATGCTCTGGAACCTTCAACGAGCTCGACAAAGGGGAGCCCG 2400  
QY 2401 TCAACGCGGCGGATGCAAGCGGCTCGAGCAGCAAAAGGCTTACGACAGAGCTCAAG 2460  
DB 2401 TCAACGCGGCGGATGCAAGCGGCTCGAGCAGCAAAAGGCTTACGACAGAGCTCAAG 2460  
QY 2461 CGGGTGAACAATCCGTAACCTGCGGTATTAACAAGCGGAGCGGAGTTTCAAGAGCGTCTGC 2520  
DB 2461 CGGGTGAACAATCCGTAACCTGCGGTATTAACAAGCGGAGCGGAGTTTCAAGAGCGTCTGC 2520  
QY 2521 AAGAAATACGTCTTTTGGGGGCAACCTCGGCGAGCAGTCTTCCAGGCCAAAGAGAGGG 2580  
DB 2521 AAGAAATACGTCTTTTGGGGGCAACCTCGGCGAGCAGTCTTCCAGGCCAAAGAGAGGG 2580  
QY 2581 TTCTCGAACCTTTTGGTGTGTTGAGGAGGAGGCTTAACAGCGGCTCTGAGAAAGAAAGCTC 2640  
DB 2581 TTCTCGAACCTTTTGGTGTGTTGAGGAGGAGGCTTAACAGCGGCTCTGAGAAAGAAAGCTC 2640  
QY 2641 CGGTAGAGCAGTCCGCAACAGAGCGAGACTCCTCTCGGGCAATTGGCAAGACAGGCCAGC 2700  
DB 2641 CGGTAGAGCAGTCCGCAACAGAGCGAGACTCCTCTCGGGCAATTGGCAAGACAGGCCAGC 2700  
QY 2701 AGCCGCTTAAAAAGAGACTCAATTTTGTGTCAGACTGCGGACTCAGAGTCAGTCCCGAGC 2760  
DB 2701 AGCCGCTTAAAAAGAGACTCAATTTTGTGTCAGACTGCGGACTCAGAGTCAGTCCCGAGC 2760  
QY 2761 CACAACTCTGGGAGAACCTTCCAGAACCCCGGCTGTGTGGAGACTTACAAATGGCTT 2820  
DB 2761 CACAACTCTGGGAGAACCTTCCAGAACCCCGGCTGTGTGGAGACTTACAAATGGCTT 2820  
QY 2821 CAGCGGTGGGCGCACCAATGGCAGCAATTAAGAGGCGCGCAGAGTGGGTATGCTT 2880  
DB 2821 CAGCGGTGGGCGCACCAATGGCAGCAATTAAGAGGCGCGCAGAGTGGGTATGCTT 2880  
QY 2881 CAGAAATTTGCGATTGCGATTTCACATGGCTGGGCGAGCAGAGTCATCAACAGCACCC 2940  
DB 2881 CAGAAATTTGCGATTGCGATTTCACATGGCTGGGCGAGCAGAGTCATCAACAGCACCC 2940  
QY 2941 GAAACATGGGCGCTTGGCCCACTTATACCAACCTTACAGCAAAATTCACATGCTTAA 3000  
DB 2941 GAAACATGGGCGCTTGGCCCACTTATACCAACCTTACAGCAAAATTCACATGCTTAA 3000  
QY 3001 CGGGGGCGAGCAAGCAACCACTACTTGGGCTACAGCACCCCTGGGGGATTTTGAAT 3060  
DB 3001 CGGGGGCGAGCAAGCAACCACTACTTGGGCTACAGCACCCCTGGGGGATTTTGAAT 3060  
QY 3061 TCAACAGATTCCACTGCGATTCTTCAACAGCTGACGAGCTGCAACCAAT 3120  
DB 3061 TCAACAGATTCCACTGCGATTCTTCAACAGCTGACGAGCTGCAACCAAT 3120

QY 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAAGTCAAGAGGTCA 3180  
DB 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAAGTCAAGAGGTCA 3180  
QY 3181 CGACGAATGATGGGCTCCAGACATCGCTAATTAACCTTACAGAGCGGTTCAAGTCTTGT 3240  
DB 3181 CGACGAATGATGGGCTCCAGACATCGCTAATTAACCTTACAGAGCGGTTCAAGTCTTGT 3240  
QY 3241 CGGACTCGGAATACCAATGCTCCCGTACGTCTCGGCTCTGGCCACCAAGGCTGCTCCCTC 3300  
DB 3241 CGGACTCGGAATACCAATGCTCCCGTACGTCTCGGCTCTGGCCACCAAGGCTGCTCCCTC 3300  
QY 3301 CGTTCCCGGCGGAGCGTGTTCATGATTCGCGAGTACGAGTACCTTAACGCTCAACATGSCA 3360  
DB 3301 CGTTCCCGGCGGAGCGTGTTCATGATTCGCGAGTACGAGTACCTTAACGCTCAACATGSCA 3360  
QY 3361 GCCAGGAGTGGGAGCGCTCATCTTTTATCTGCTGGAATATTTCCATCGCAGATGCTGA 3420  
DB 3361 GCCAGGAGTGGGAGCGGCTCATCTTTTATCTGCTGGAATATTTCCATCGCAGATGCTGA 3420  
QY 3421 GAACGGGCAATTAACCTTACCTTACAGTACACTTTCAGAGAGCTGCTTCCACAGCAGCT 3480  
DB 3421 GAACGGGCAATTAACCTTACCTTACAGTACACTTTCAGAGAGCTGCTTCCACAGCAGCT 3480  
QY 3481 ACGGCAACAGCCAGAGCGCTGAGCCGGCTGATGAATCCCTCATGCAACAGTACCTGAT 3540  
DB 3481 ACGGCAACAGCCAGAGCGCTGAGCCGGCTGATGAATCCCTCATGCAACAGTACCTGAT 3540  
QY 3541 ACTGGAACAGAACTCACAAATCAGTCCGGAAGTGGCCAAACAAAGACTTGTGTTAGCC 3600  
DB 3541 ACTGGAACAGAACTCACAAATCAGTCCGGAAGTGGCCAAACAAAGACTTGTGTTAGCC 3600  
QY 3601 GTGGGTCTCCAGCTGGCATGTCTGTTACGCCAAATAATGCGTACCTGGAACCTGTTACC 3660  
DB 3601 GTGGGTCTCCAGCTGGCATGTCTGTTACGCCAAATAATGCGTACCTGGAACCTGTTACC 3660  
QY 3661 GGGGGTCTCCAGCTGGCATGTCTGTTACGCCAAATAATGCGTACCTGGAACCTGTTACC 3720  
DB 3661 GGGGGTCTCCAGCTGGCATGTCTGTTACGCCAAATAATGCGTACCTGGAACCTGTTACC 3720  
QY 3721 GTGCTTCAAAATATTAACCTTAAATGGGCGTGAATCTATATCAACCTGGCACTGTATGG 3780  
DB 3721 GTGCTTCAAAATATTAACCTTAAATGGGCGTGAATCTATATCAACCTGGCACTGTATGG 3780  
QY 3781 CCTCACACAAAGAGCAAGAAACAAGTCTTCCCATGAGGGGTGTCATGATTTTGGAA 3840  
DB 3781 CCTCACACAAAGAGCAAGAAACAAGTCTTCCCATGAGGGGTGTCATGATTTTGGAA 3840  
QY 3841 AGGAGAGCGCGGAGCTTCAAAACACTGATTTGGAACAATGTCATGATCAACAGCAAGAG 3900  
DB 3841 AGGAGAGCGCGGAGCTTCAAAACACTGATTTGGAACAATGTCATGATCAACAGCAAGAG 3900  
QY 3901 AAATCAAGCCACTTAACCCCGTGCCACCGAAAGATTTGGGACTGTGGCACTCATCTCC 3960  
DB 3901 AAATCAAGCCACTTAACCCCGTGCCACCGAAAGATTTGGGACTGTGGCACTCATCTCC 3960  
QY 3961 AGAGCAGAGCAGACAGCCCTGCGACCGGAGATGTGCAATGTTATGGAGCTTACCTGAA 4020  
DB 3961 AGAGCAGAGCAGACAGCCCTGCGACCGGAGATGTGCAATGTTATGGAGCTTACCTGAA 4020  
QY 4021 TGGTGGCAAGACAGAGAGCTAATACCTGCGAGGCTCCATTTGGGCAAAATTCCTCA 4080  
DB 4021 TGGTGGCAAGACAGAGAGCTAATACCTGCGAGGCTCCATTTGGGCAAAATTCCTCA 4080  
QY 4081 CGGATGGAACATTTTCAACCGGTCTCTCATGAGGCGGCTTGAATTAAGCACCCGCTC 4140  
DB 4081 CGGATGGAACATTTTCAACCGGTCTCTCATGAGGCGGCTTGAATTAAGCACCCGCTC 4140  
QY 4141 CTCAATCTCATCAAAACACGCTGCTCTGCGAATCTCTCGGCAAGATTTTGGCTA 4200  
DB 4141 CTCAATCTCATCAAAACACGCTGCTCTGCGAATCTCTCGGCAAGATTTTGGCTA 4200  
QY 4201 CAAAGTTTGTTCATTCATCAACCAAGTATTCACAGGCAAGTACGAGTGAAT 4260

Db 4201 CAAAGTTGCTTCATTCATCACCCGATATTCACAGCAAGTAGCGGTGAGATTGAT 4260  
Qy 4261 GGGAGCTGCAGAAAAGAAAAGCAACCGCTGGAAATCCCGAAGTGCAGATATCATCTAACT 4320  
Db 4261 GGGAGCTGCAGAAAAGAAAAGCAACCGCTGGAAATCCCGAAGTGCAGATATCATCTAACT 4320  
Qy 4221 ATGAAAATATGCGCAACGTTGATTTCACTGTGAGCAACATGAGACTTATATGAGCCTC 4380  
Db 4221 ATGCAAAATCTGCCAAGCTTATTTCACTGTGAGCAACATGAGACTTATATGAGCCTC 4380  
Qy 4381 GCGCCATTGGCAGCCCGTTACTCACCGCTCCCTGTAAATGTGTGTATATCAATPAACCG 4440  
Db 4381 GCGCCATTGGCAGCCCGTTACTCACCGCTCCCTGTAAATGTGTGTATATCAATPAACCG 4440  
Qy 4441 GTTAATTCGTGCTGAGTGAATTTGGTGTCAATGTCCTATATATCTATATCTGACCACTA 4500  
Db 4441 GTTAATTCGTGCTGAGTGAATTTGGTGTCAATGTCCTATATATCTATATCTGACCACTA 4500  
Qy 4501 GCAACCGGTTACATTAATGCTAGTGTGCGCTTCGGAATACCCCTAGTGAAGT 4560  
Db 4501 GCAACCGGTTACATTAATGCTAGTGTGCGCTTCGGAATACCCCTAGTGAAGT 4560  
Qy 4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620  
Db 4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620  
Qy 4621 TCTGGGAGCTTTTGTGTGCTCGAGGCGCCACCGAGCGAGCGAGCGAGCGAGCGAGTGC 4680  
Db 4621 TCTGGGAGCTTTTGTGTGCTCGAGGCGCCACCGAGCGAGCGAGCGAGCGAGCGAGTGC 4680  
Qy 4681 CAA 4683  
Db 4681 CAA 4683  
RESULT 2  
ADL13983 ID ADL13983 standard; DNA; 4683 BP.  
XX  
AC ADL13983;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Adeno-associated virus serotype 6 complete DNA.  
XX  
KW ss: cytoskeletal; neuroprotective; antiinflammatory; gene therapy;  
KW expression construct; adeno-associated virus;  
KW integration efficiency element; inverted terminal repeat; integration;  
KW chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma;  
KW retinoblastoma; inflammatory disease; arthritis;  
KW neurodegenerative disease.  
XX  
OS Adeno-associated virus 6.  
XX  
PN MO200308734-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 09-APR-2003; 2003WO-US011191.  
XX  
PR 09-APR-2002; 2002US-0371044P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Falck-Pedersen BS, Philpott N;  
XX  
DR WPI; 2003-833723/77.  
XX  
PT New expression construct comprising a nucleic acid sequence encoding an  
PT adeno-associated virus integration efficiency element, useful for  
PT treating cancer e.g. lung cancer or colon cancer or inflammatory disease  
PT e.g. arthritis.

XX  
PS Disclosure; SEQ ID NO 2; 62pp; English.  
XX  
CC The invention relates to an expression construct comprising a nucleic  
CC acid sequence encoding an adeno-associated virus integration efficiency  
CC element (AAV IES), which is devoid of AAV inverted terminal repeats (AAV  
CC ITRs) and site-specifically integrates into a host cell chromosome when  
CC provided to the host cell in conjunction with an AAV Rep protein. The  
CC expression construct can be used as a therapeutic factor for treating a  
CC mammal for a pathologic state which is cancer, including lung cancer,  
CC colon cancer, renal cancer, anal cancer, bile duct cancer, bladder  
CC cancer, bone cancer, brain cancer, spinal chord cancer, breast cancer,  
CC cervical cancer, lymphoma, endometrial cancer, esophageal cancer,  
CC gallbladder cancer, gastrointestinal cancer, laryngeal cancer, leukemia,  
CC liver cancer, multiple myeloma, neuroblastoma, ovarian cancer, pancreatic  
CC cancer, prostatic cancer, retinoblastoma, skin cancer, stomach cancer,  
CC testicular cancer, thymus cancer or thyroid cancer. Other pathologic  
CC state includes inflammatory disease (arthritis), neurodegenerative  
CC disease, a disease of an organ attributed to the presence of increased or  
CC decreased level of a particular gene product(s). This sequence  
CC corresponds to the AAV serotype 6 complete DNA including the IEE  
CC sequence.  
XX  
SQ Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;

Query Match 99.6%; Score 4663.8; DB 10; Length 4683;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTCTGCGCGCTCGCTCACTGAGCCCGGCGACCAAGTTCGCC 60  
Db 1 TTGGCCACTCCCTCTCTCTGCGCGCTCGCTCACTGAGCCCGGCGACCAAGTTCGCC 60  
Qy 61 CGAGCCCGGGGCTTTGGCCGGGCGGCTCTCAGTGAAGGAGCGAGCGAGGAGGAGT 120  
Db 61 CGAGCCCGGGGCTTTGGCCGGGCGGCTCTCAGTGAAGGAGCGAGCGAGGAGGAGT 120  
Qy 121 GCCAACTCCTCACTAGAGGGTCTCTGAGGAGGTGAGTCTGACGTGAATTAAGTCATAG 180  
Db 121 GCCAACTCCTCACTAGAGGGTCTCTGAGGAGGTGAGTCTGACGTGAATTAAGTCATAG 180  
Qy 181 GGTAGGAGAGTCTCTGATTAAGAGTCACTGAGTGTGTTGGCAATTTGGCACACAT 240  
Db 181 GGTAGGAGAGTCTCTGATTAAGAGTCACTGAGTGTGTTGGCAATTTGGCACACAT 240  
Qy 241 GTGGTACGCTGGGTATTAAGCCCGAGTAGACCGAGGCTCCATTGTAAGCGGGA 300  
Db 241 GTGGTACGCTGGGTATTAAGCCCGAGTAGACCGAGGCTCCATTGTAAGCGGGA 300  
Qy 301 GGTGTAACCGGAGCGCCATGCGGGGTTTACGAGATTTGATTAAGTCCCAAGCGA 360  
Db 301 GGTGTAACCGGAGCGCCATGCGGGGTTTACGAGATTTGATTAAGTCCCAAGCGA 360  
Qy 361 CTTGAGAGAGATCTGCGCCGATTTCTGACACTTTGTGAATCTGGGTGGCGAAGGA 420  
Db 361 CTTGAGAGAGATCTGCGCCGATTTCTGACACTTTGTGAATCTGGGTGGCGAAGGA 420  
Qy 421 ATGGAGATTGCGCGCAGATTTCTGACATGATCTGAATCTGATTGAGCAGCACTCCAG 480  
Db 421 ATGGAGATTGCGCGCAGATTTCTGACATGATCTGAATCTGATTGAGCAGCACTCCAG 480  
Qy 481 CGTGGCGAAGAGTGCAGCGCACTTCTGTGTCACATGCGCGCGGTGTAAGGCC 540  
Db 481 CGTGGCGAAGAGTGCAGCGCACTTCTGTGTCACATGCGCGCGGTGTAAGGCC 540  
Qy 541 GGAAGCCCTCTCTTTGTTGATTTGAGAGAGGCGAGTCTTACTTCCACTCCATATCT 600  
Db 541 GGAAGCCCTCTCTTTGTTGATTTGAGAGAGGCGAGTCTTACTTCCACTCCATATCT 600  
Qy 601 GGTGAGACCAAGGAGGTTCAATTCATGAGTGGGCGCTCTCTGAGTCAATTAGCGA 660  
Db 601 GGTGAGACCAAGGAGGTTCAATTCATGAGTGGGCGCTCTCTGAGTCAATTAGCGA 660

Qy 661 CAAAGTGTGACAGACCAATCTACCGGGATCGAGCCGACCTGTCCCAATGTGTTGCGGT 720  
| | | | |  
Db 661 CAAAGTGTGACAGACCAATCTACCGGGATCGAGCCGACCTGTCCCAATGTGTTGCGGT 720  
Qy 721 GACCAAGACGGGTAAATGCGCGCGGAGGGGGGAAACAAGTGTGACGAGTGTACATCC 780  
| | | | |  
Db 721 GACCAAGACGGGTAAATGCGCGCGGAGGGGGGAAACAAGTGTGACGAGTGTACATCC 780  
Qy 781 CAACATCCTCTGCGCCCAAGACTCAGCCCGAGCTGAGTGGGGTGTGACTTAACATGAGAGA 840  
| | | | |  
Db 781 CAACATCCTCTGCGCCCAAGACTCAGCCCGAGCTGAGTGGGGTGTGACTTAACATGAGAGA 840  
Qy 841 GTATATAAGCGCGTGTAAACCTGAGCGGCAAAACGGCTGTGGCGACAGACTGAC 900  
| | | | |  
Db 841 GTATATAAGCGCGTGTAAACCTGAGCGGCAAAACGGCTGTGGCGACAGACTGAC 900  
Qy 901 CCACGTGACCGCAGACCCAGAGACAGAACAGAGAAATCTGAAACCCCAATTCTGACGCGC 960  
| | | | |  
Db 901 CCACGTGACCGCAGACCCAGAGACAGAACAGAGAAATCTGAAACCCCAATTCTGACGCGC 960  
Qy 961 TGTCAATCCGCTCAAAAACCTCCGCAACGCTACATGAGCTGGTGGGTGGCTGTGAGACG 1020  
| | | | |  
Db 961 TGTCAATCCGCTCAAAAACCTCCGCAACGCTACATGAGCTGGTGGGTGGCTGTGAGACG 1020  
Qy 1021 GGGCATCACTCCAGAGACAGTGGATCAGAGAGACAGGCGCTGTGATCATCTCTTCAA 1080  
| | | | |  
Db 1021 GGGCATCACTCCAGAGACAGTGGATCAGAGAGACAGGCGCTGTGATCATCTCTTCAA 1080  
Qy 1081 CGCGGCTTCCAACTCGCGGTCCAGATCAAGGCGCGCTGTGACAAATGCGCGCAAGATCAT 1140  
| | | | |  
Db 1081 CGCGGCTTCCAACTCGCGGTCCAGATCAAGGCGCGCTGTGACAAATGCGCGCAAGATCAT 1140  
Qy 1141 GGGCTGACCAAAATCCGGCGCGGACTACTGTGTAGGCGCGCTCGCGCGCGGCAATTAA 1200  
| | | | |  
Db 1141 GGGCTGACCAAAATCCGGCGCGGACTACTGTGTAGGCGCGCGCTCGCGCGCGGCAATTAA 1200  
Qy 1201 AACCAACGGCATTTTACCGCATCTCTGAGCTGAAACGGCTACGACCTGTGCTAGCGGCTC 1260  
| | | | |  
Db 1201 AACCAACGGCATTTTACCGCATCTCTGAGCTGAAACGGCTACGACCTGTGCTAGCGGCTC 1260  
Qy 1261 CGTCTTTCTGCGCTGGGCGCCAGAAAAGGTTGGAACACGCAACATCTGGCTGTGG 1320  
| | | | |  
Db 1261 CGTCTTTCTGCGCTGGGCGCCAGAAAAGGTTGGAACACGCAACATCTGGCTGTGG 1320  
Qy 1321 GCCCGCCACACGGGCAAGACCAATATGCGGAAACCTTCGCCACGCGGCTCTTCTA 1380  
| | | | |  
Db 1321 GCCCGCCACACGGGCAAGACCAATATGCGGAAACCTTCGCCACGCGGCTCTTCTA 1380  
Qy 1381 CGGCTGCGTCAACTGGAACCAATGAGACCTTCCCTTCAACGATGGGTCGACAGAGTGGT 1440  
| | | | |  
Db 1381 CGGCTGCGTCAACTGGAACCAATGAGACCTTCCCTTCAACGATGGGTCGACAGAGTGGT 1440  
Qy 1441 GATCTGTTGGAGAGAGGCAAGATGACGCGCAAGGTCGTGAGTCCGCGCAAGGCCATCT 1500  
| | | | |  
Db 1441 GATCTGTTGGAGAGAGGCAAGATGACGCGCAAGGTCGTGAGTCCGCGCAAGGCCATCT 1500  
Qy 1501 CGGCGGCAAGAGTGTGCGCTGTGACCAAAAGTGTGTCGCGCCGACATGATCCAC 1560  
| | | | |  
Db 1501 CGGCGGCAAGAGTGTGCGCTGTGACCAAAAGTGTGTCGCGCCGACATGATCCAC 1560  
Qy 1561 CCCCGTGTGCTGACCTCTCAACACCAACATGATGCGCGGTGATTGAAGGGAACAGCACAC 1620  
| | | | |  
Db 1561 CCCCGTGTGCTGACCTCTCAACACCAACATGATGCGCGGTGATTGAAGGGAACAGCACAC 1620  
Qy 1621 CTTGAGACACAGACGCGGTTGACAGACCGGATGTTCAAAATTTGAATCTCACCGCGCTCT 1680  
| | | | |  
Db 1621 CTTGAGACACAGACGCGGTTGACAGACCGGATGTTCAAAATTTGAATCTCACCGCGCTCT 1680  
Qy 1681 GGAGATGACCTTTGGCAAGTGTGACAAAGCAAGAAATCAAGATCTTCCGCTGGGCGCA 1740  
| | | | |  
Db 1681 GGAGATGACCTTTGGCAAGTGTGACAAAGCAAGAAATCAAGATCTTCCGCTGGGCGCA 1740  
Qy 1741 GGATCACTGTGACCGAGTGTGGCGCATGAGTCTTACGTCAAGAAAAGGTTGAGGCCAACAAAG 1800  
| | | | |

Db 1741 GGATCACTGTGACCGAGTGTGGCGCATGAGTCTTACGTCAAGAAAAGGTTGAGGCCAACAAAG 1800  
| | | | |  
Qy 1801 ACCCGCCCCCGATGACCGGATTAAGAGAGCCCAAGCGGCGCTGCCCCCTTACGTGGCGA 1860  
| | | | |  
Db 1801 ACCCGCCCCCGATGACCGGATTAAGAGAGCCCAAGCGGCGCTGCCCCCTTACGTGGCGA 1860  
Qy 1861 TCCATCGACGTCAGACCGGGAAGAGACGTCGGGTGACTTGGCCGACAGGTACCAAAACAA 1920  
| | | | |  
Db 1861 TCCATCGACGTCAGACCGGGAAGAGACGTCGGGTGACTTGGCCGACAGGTACCAAAACAA 1920  
Qy 1921 ATGTTCTGTCACCGCGGACATGCTTACAGATCTGTTCCTCTGCAAAACATGCGAGAGAT 1980  
| | | | |  
Db 1921 ATGTTCTGTCACCGCGGACATGCTTACAGATCTGTTCCTCTGCAAAACATGCGAGAGAT 1980  
Qy 1981 GAATCAGAAATTTCAACATTTGCTTCAACGACGGAACAGAGACTGTTCAAGATGTTTCC 2040  
| | | | |  
Db 1981 GAATCAGAAATTTCAACATTTGCTTCAACGACGGAACAGAGACTGTTCAAGATGTTTCC 2040  
Qy 2041 CGGCGTGTCAAGAAATCTCAACCGGTCGTCAAGAAAGAGACGTAATGGAACCTGTGGCAT 2100  
| | | | |  
Db 2041 CGGCGTGTCAAGAAATCTCAACCGGTCGTCAAGAAAGAGACGTAATGGAACCTGTGGCAT 2100  
Qy 2101 TCATCATCTGCTGGGCGGCGCTCCGAGATTGCTTGTCTCGGCTGTGCAATCTGTCAACGT 2160  
| | | | |  
Db 2101 TCATCATCTGCTGGGCGGCGCTCCGAGATTGCTTGTCTCGGCTGTGCAATCTGTCAACGT 2160  
Qy 2161 GGATCTGATGACTGTGTGTTCTGAGACATAAATGACTTAAACAGATATGGCTCCGATG 2220  
| | | | |  
Db 2161 GGATCTGATGACTGTGTGTTCTGAGACATAAATGACTTAAACAGATATGGCTCCGATG 2220  
Qy 2221 GTTATCTTCCAGATTTGGCTGAGAGCAACCTCTGTAGGGCATTCGGCAGTGGTGGGACT 2280  
| | | | |  
Db 2221 GTTATCTTCCAGATTTGGCTGAGAGCAACCTCTGTAGGGCATTCGGCAGTGGTGGGACT 2280  
Qy 2281 TGAACCTGAGACCCCGGAAACCCAAAGCCAAACAGACAAACAGAGACGACGCGGGGCTC 2340  
| | | | |  
Db 2281 TGAACCTGAGACCCCGGAAACCCAAAGCCAAACAGACAAACAGAGACGACGCGGGGCTC 2340  
Qy 2341 TGTGCTTCTGCTGCTACAGTACTCGGACCTTTCAACGACCTGACACAGGGGAGACCCG 2400  
| | | | |  
Db 2341 TGTGCTTCTGCTGCTACAGTACTCGGACCTTTCAACGACCTGACACAGGGGAGACCCG 2400  
Qy 2401 TCAACGGGCGGAGTGCAGCGGCGCTCGAGACGACAAAGGCTTAAGACACAGAGCTCAAG 2460  
| | | | |  
Db 2401 TCAACGGGCGGAGTGCAGCGGCGCTCGAGACGACAAAGGCTTAAGACACAGAGCTCAAG 2460  
Qy 2461 CGGCTGACCAATCGTACCTGCGGTATTAACACGCGGACGCGGATTTCAAGAGGCTGCG 2520  
| | | | |  
Db 2461 CGGCTGACCAATCGTACCTGCGGTATTAACACGCGGACGCGGATTTCAAGAGGCTGCG 2520  
Qy 2521 AAGAAATACGCTCTTTTGGGGGCAACCTCGGGCGAGGAGTCTTCAGGCGCAAGAGAGG 2580  
| | | | |  
Db 2521 AAGAAATACGCTCTTTTGGGGGCAACCTCGGGCGAGGAGTCTTCAGGCGCAAGAGAGG 2580  
Qy 2581 TTCTCGAACCTTTTGGTGTGTTGAGAGAGTGTCTAAGACGGCTCTCTGAAAGAAAGTGC 2640  
| | | | |  
Db 2581 TTCTCGAACCTTTTGGTGTGTTGAGAGAGTGTCTAAGACGGCTCTCTGAAAGAAAGTGC 2640  
Qy 2641 CGGTAGAGAGTGCSCCAAGAGGACAGACTCTCTCGGGGCAATTGGCAAGACAGGCGCAGC 2700  
| | | | |  
Db 2641 CGGTAGAGAGTGCSCCAAGAGGACAGACTCTCTCGGGGCAATTGGCAAGAGGCGCAGC 2700  
Qy 2701 AGCCCGCTAAAAAGAGACTCAATTTTGTGAGACTGTGCGACTCAGAGTCAAGTCCCAACC 2760  
| | | | |  
Db 2701 AGCCCGCTAAAAAGAGACTCAATTTTGTGAGACTGTGCGACTCAGAGTCAAGTCCCAACC 2760  
Qy 2761 CACAACTCTGTGGGAACCTTCAGCAACCCCGTGTGTGGGACCTTACCTACAAATGGCTT 2820  
| | | | |  
Db 2761 CACAACTCTGTGGGAACCTTCAGCAACCCCGTGTGTGGGACCTTACCTACAAATGGCTT 2820  
Qy 2821 CAGCGGTGGCGCAACCAATGACAGACAAATTAACGAAGCGCGCGACGAGTGGGTAAATGCT 2880  
| | | | |

Dh 2821 CAGCGGTGGCGCA CCAATGGCAGACAATAA GAAAGCGCCGACGAGTGGTAATGCTT 2880  
Qy 2881 CAGGAATTTGGCATTTGGATTCCACATGGCTGGGGGAGACAGAGTATGACCA CCGACACC 2940  
Dh 2881 CAGGAATTTGGCATTTGGATTCCACATGGCTGGGGGAGACAGAGTATGACCA CCGACACC 2940  
Qy 2941 GAACATGGGCTTTGGCCCACTTAACAACA CACTTCAAGCAAAATCTCGATGCTTCA 3000  
Dh 2941 GAACATGGGCTTTGGCCCACTTAACAACA CACTTCAAGCAAAATCTCGATGCTTCA 3000  
Qy 3001 CGGGGGCCAGCAAGACCACTACTTGGCTACAGACCCCTGGGGGTAATTTGATTT 3060  
Dh 3001 CGGGGGCCAGCAAGACCACTACTTGGCTACAGACCCCTGGGGGTAATTTGATTT 3060  
Qy 3061 TCACAGATTCACATGGCATTTCTCACACGTA GGTGGAGGACTCATCAACAATTT 3120  
Dh 3061 TCACAGATTCACATGGCATTTCTCACACGTA GGTGGAGGACTCATCAACAATTT 3120  
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Dh 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAGTCAAGAGGTCA 3180  
Qy 3181 CGACGATGATGGCTGTCAGACCATCGCTTAATACCTTACAGCA CGGTTCAAGTCTTGT 3240  
Dh 3181 CGACGATGATGGCTGTCAGACCATCGCTTAATACCTTACAGCA CGGTTCAAGTCTTGT 3240  
Qy 3241 CGGACTCGGAGTACAGTTCGCTACGTCGTCGCTGCGGACCAAGGGCTGCCCTC 3300  
Dh 3241 CGGACTCGGAGTACAGTTCGCTACGTCGTCGCTGCGGACCAAGGGCTGCCCTC 3300  
Qy 3301 CGTTCGCCGCGAGCGTGTTCATGATTTCCGAGTACGGCTTACCTTA CCGTCAACAATGCA 3360  
Dh 3301 CGTTCGCCGCGAGCGTGTTCATGATTTCCGAGTACGGCTTACCTTA CCGTCAACAATGCA 3360  
Qy 3361 GCCAGAGTGGGAGCGCTCATCTCTTTTACGCTGCGAAATATTTCCATCGCAGATGCTGA 3420  
Dh 3361 GCCAGAGTGGGAGCGCTCATCTCTTTTACGCTGCGAAATATTTCCATCGCAGATGCTGA 3420  
Qy 3421 GAACGGGCAATTAACCTTACCTTCACTACCTTGAAGAGAGTGGCTTTCCACAGCAGCT 3480  
Dh 3421 GAACGGGCAATTAACCTTACCTTCACTACCTTGAAGAGAGTGGCTTTCCACAGCAGCT 3480  
Qy 3481 ACGGCGCAGGCAAGCGCTGAGACCGGCTGATGAATCTCTCATGCA CCAAGTACCTGTAAT 3540  
Dh 3481 ACGGCGCAGGCAAGCGCTGAGACCGGCTGATGAATCTCTCATGCA CCAAGTACCTGTAAT 3540  
Qy 3541 ACCTGGAAGAACTCACAATCAGTCCGGAAGTCCCAAAAACAAGACTTGGCTTTAGCC 3600  
Dh 3541 ACCTGGAAGAACTCACAATCAGTCCGGAAGTCCCAAAAACAAGACTTGGCTTTAGCC 3600  
Qy 3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGAACCTGTTACC 3660  
Dh 3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGAACCTGTTACC 3660  
Qy 3661 GGCAGCAGCGCGTTTCTAAAACAAAAAACAACAACAAGCAACTTTACCTGGAACCTGTTACC 3720  
Dh 3661 GGCAGCAGCGCGTTTCTAAAACAAAAAACAACAACAAGCAACTTTACCTGGAACCTGTTACC 3720  
Qy 3721 GTGCTTCAAAATATTAACCTTAATGGGCGTGAATCTATATCAACCTTGGCACTGTATAGG 3780  
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Dh 3781 CCTCAACAAGAGCAGACAAGTCTTTCCATGAGCGGTGTCATGATTTTGGAA 3840  
Qy 3841 AGGAGAGCGCGGAGCTTCAAACTGATGAGCAATGTATGATCAAGACGAAGAGG 3900  
Dh 3841 AGGAGAGCGCGGAGCTTCAAACTGATGAGCAATGTATGATCAAGACGAAGAGG 3900  
Qy 3901 AAATCAAGCCATTAACCCGCTGGGCAACGAAGATTTGGGACTGTGCACTCATCTCC 3960  
Dh 3901 AAATCAAGCCATTAACCCGCTGGGCAACGAAGATTTGGGACTGTGCACTCATCTCC 3960

Qy 3961 AGACAGCAGACAGACCCCTGCGACCGGAGATGTGATGTTATGGAGCTTACCTGGAA 4020  
Dh 3961 AGACAGCAGACAGACCCCTGCGACCGGAGATGTGATGTTATGGAGCTTACCTGGAA 4020  
Qy 4021 TGGTGTGGCAAGACAGACGTAATACCTGCAAGGCTCTATTGGGCAAAATTCCTACA 4080  
Dh 4021 TGGTGTGGCAAGACAGACGTAATACCTGCAAGGCTCTATTGGGCAAAATTCCTACA 4080  
Qy 4081 CGGATGGAACCTTACACCGCTCTCATAGGCGGCTTTGGAACCTTAACACCCGCTC 4140  
Dh 4081 CGGATGGAACCTTACACCGCTCTCATAGGCGGCTTTGGAACCTTAACACCCGCTC 4140  
Qy 4141 CTCAGATCTCATCAAAAAACGCGCTGTTCTCGAATCCTCCGCGAGATTTTCGCTA 4200  
Dh 4141 CTCAGATCTCATCAAAAAACGCGCTGTTCTCGAATCCTCCGCGAGATTTTCGCTA 4200  
Qy 4201 CAAAGTTTGCTTCAATTCATCAACCAAGTATTCACAGACAAAGTACGATGGAAT 4260  
Dh 4201 CAAAGTTTGCTTCAATTCATCAACCAAGTATTCACAGACAAAGTACGATGGAAT 4260  
Qy 4261 GGGAGCTGCAGAAAGAAAGACGAACGCTGGAATCCCGAAGTGCAGTATACCTACT 4320  
Dh 4261 GGGAGCTGCAGAAAGAAAGACGAACGCTGGAATCCCGAAGTGCAGTATACCTACT 4320  
Qy 4321 ATGCAAAATCTGCCAAGTGTATTTCACTGTGACAAACAATGACTTTATATGAGCTTC 4380  
Dh 4321 ATGCAAAATCTGCCAAGTGTATTTCACTGTGACAAACAATGACTTTATATGAGCTTC 4380  
Qy 4381 GCCCATTTGGACCGCTTACCTCAACCGCTGCCCTGTAATGTGTGTTAATCAATAACCG 4440  
Dh 4381 GCCCATTTGGACCGCTTACCTCAACCGCTGCCCTGTAATGTGTGTTAATCAATAACCG 4440  
Qy 4441 GTTAATTCGATGCAATGTAATTTGATGTCATGCTTATTTATCTTATCTGATCACCATA 4500  
Dh 4441 GTTAATTCGATGCAATGTAATTTGATGTCATGCTTATTTATCTTATCTGATCACCATA 4500  
Qy 4501 GCAACCGGTTACACATTAACCTGTTAGTTGCTTCGCGAATACCCCTAGTATGAGATT 4560  
Dh 4501 GCAACCGGTTACACATTAACCTGTTAGTTGCTTCGCGAATACCCCTAGTATGAGATT 4560  
Qy 4561 GCCCATCTCTTATGCGCGCTGCTGCTGCTGGGCGCGGACAGACAGCTTGGCCG 4620  
Dh 4561 GCCCATCTCTTATGCGCGCTGCTGCTGCTGGGCGCGGACAGACAGCTTGGCCG 4620  
Qy 4621 TCTGCGGACCTTTGGTCCGAGGCGCCACCGAGCGAGCGGCACTAGAGGAGTGGC 4680  
Dh 4621 TCTGCGGACCTTTGGTCCGAGGCGCCACCGAGCGAGCGGCACTAGAGGAGTGGC 4680  
Qy 4681 CAA 4683  
Dh 4681 CAA 4683  
RESULT 3  
ADG39763  
ID ADG39763 standard; DNA; 4683 BP.  
XX  
XX ADG39763;  
XX  
XX 11-MAR-2004 (first entry)  
DE AAV-6 genomic DNA sequence SEQ ID NO:25.  
XX  
XX parvovirus; rep; cap; DNA binding domain; capsid interacting domain;  
KM recombinant hybrid parvovirus particle;  
KM recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;  
gene; ds.  
XX  
XX OS Adeno-associated virus 6.  
XX  
XX FN W02003104392-A2.

PD 18-DEC-2003.  
XX 02-DEC-2002; 2002MO-US038423.  
XX 18-DEC-2001; 2001US-0341919P.  
XX (UNNC-) UNIV NORTH CAROLINA.  
XX Samliski RJ, Rabinowitz JE;  
XX WPI; 2004-062324/06.  
PT New polynucleotides comprising parvovirus rep coding sequences and  
PT parvovirus cap coding sequences, useful in producing higher stocks of  
PT hybrid parvovirus vectors for delivering therapeutic nucleic acids to a  
PT subject.  
XX Disclosure; SEQ ID NO 25; 115bp; English.  
XX  
XX The present invention describes a polynucleotide (1), comprising  
XX parvovirus rep coding sequences and parvovirus cap coding sequences. The  
XX rep coding sequences encodes a DNA binding domain from a first  
XX parvovirus, and a capsid interacting domain from a parvovirus different  
XX from the first parvovirus. The cap coding sequence comprises sequences  
XX from the different parvovirus. Also described: (1) a vector comprising  
XX (1); (2) a cell comprising (1), or parvovirus rep coding sequences and  
XX parvovirus cap coding sequences, where the rep coding sequences encode a  
XX DNA binding domain from a first parvovirus and a capsid interacting  
XX domain from a parvovirus different from the first parvovirus, the cap  
XX coding sequences comprise sequences from the different parvovirus, and  
XX the rep coding sequences are stably integrated into the genome of the  
XX cell; and (3) producing a recombinant hybrid parvovirus particle or adeno  
XX -associated virus (rAAV) particle. (1) can be used in vaccines, and in  
XX gene therapy. The polynucleotide (1) can be used in producing higher  
XX stocks of hybrid parvoviruses or parvovirus vectors, which may be used in  
XX the delivery of nucleic acids having biological effect to treat or  
XX ameliorate the symptoms associated with any disorder related to gene  
XX expression. The polynucleotide may be used to produce a parvovirus vector  
XX to express an immunogenic polypeptide in a subject, e.g. for vaccination.  
XX The parvovirus vector may also be used to provide an antisense nucleic  
XX acid to a cell in vitro or in vivo, or in diagnostic and screening  
XX methods. The present sequence is used in the exemplification of the  
XX present invention.  
XX  
SQ Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;  
Query Match 99.6%; Score 4663.8; DB 12; Length 4683;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 1 TTGGCCACTCCCTCTCTGCGGCTGCTGCTCATGAGCCGGGCGCAAAAGTGGCC 60  
Db 1 TTGGCCACTCCCTCTCTGCGGCTGCTGCTCATGAGCCGGGCGCAAAAGTGGCC 60  
QY 61 CGAGCCCGGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGAGAGAGGAGTG 120  
Db 61 CGAGCCCGGGGCTTGGCCGGGCGGCTCAGTGAAGCGAGCGCGAGAGAGGAGTG 120  
QY 121 GCCAATCTCATCTAGAGGGTCTCTGAGAGGGTGAAGTCTGAACGTGAATTACGTATAG 180  
Db 121 GCCAATCTCATCTAGAGGGTCTCTGAGAGGGTGAAGTCTGAACGTGAATTACGTATAG 180  
QY 181 GGTTAGGAGAGGTCTCTGATTTAGAGTCAAGTGAAGTCTTTGGGACATTTTGGACACAT 240  
Db 181 GGTTAGGAGAGGTCTCTGATTTAGAGTCAAGTGAAGTCTTTGGGACATTTTGGACACAT 240  
QY 241 GTGGTCAGCTGGATTTTAAAGCCGAGTGAAGCAAGAGGCTCTCATTTTGAAGCGGGA 300  
Db 241 GTGGTCAGCTGGATTTTAAAGCCGAGTGAAGCAAGAGGCTCTCATTTTGAAGCGGGA 300  
QY 301 GGTTTGAACGCGACGCGCATATGCGGGGTTTACAGATTGTGATTAAAGTCCCGACGA 360  
Db 301 GGTTTGAACGCGACGCGCATATGCGGGGTTTACAGATTGTGATTAAAGTCCCGACGA 360

QY 361 CTTTGAACGAGATCTGCCCGGCAATTTCTGACAGCTTTTGAACATGGGTTGGCCGAGAAAGA 420  
Db 361 CTTTGAACGAGATCTGCCCGGCAATTTCTGACAGCTTTTGAACATGGGTTGGCCGAGAAAGA 420  
QY 421 ATGGAGATTGGCCGAGATTCTGACATGATCTGATTTGAATTGAGCAGGACCCCTTGAC 480  
Db 421 ATGGAGATTGGCCGAGATTCTGACATGATCTGATTTGAATTGAGCAGGACCCCTTGAC 480  
QY 481 CTGGCCGAGAGAGCTGACGCGCGCACTTCTGTGCTCACTGCGCGCGCTGAGTAAAGCCCC 540  
Db 481 CTGGCCGAGAGAGCTGACGCGCGCACTTCTGTGCTCACTGCGCGCGCTGAGTAAAGCCCC 540  
QY 541 GAGAGCCCTCTTTCTTTGTTGACATTTGAGAGAGGAGGAGTCTTCACTTCCATTTCT 600  
Db 541 GAGAGCCCTCTTTCTTTGTTGACATTTGAGAGAGGAGGAGTCTTCACTTCCATTTCT 600  
QY 601 GGTGAGACACAGGGGGTCAATTCATGATCTGAGGCGCTTCTGAGTCAAGATTAGCGA 660  
Db 601 GGTGAGACACAGGGGGTCAATTCATGATCTGAGGCGCTTCTGAGTCAAGATTAGCGA 660  
QY 661 CAAGCTGTGACAGCATCTACCGCGGATGAGCCGACCTGCCCCAATGTTGCGGT 720  
Db 661 CAAGCTGTGACAGCATCTACCGCGGATGAGCCGACCTGCCCCAATGTTGCGGT 720  
QY 721 GACCAAGCGGTAAATGCGCGCGGAGAGGGGGGAAAGAGTGTGACAGATGCTCATATCC 780  
Db 721 GACCAAGCGGTAAATGCGCGCGGAGAGGGGGGAAAGAGTGTGACAGATGCTCATATCC 780  
QY 781 CAATCACTCTGCGCCAAAGATCTAGCCGAGCTCAGTGAAGGCGTGAATACATGAGAGA 840  
Db 781 CAATCACTCTGCGCCAAAGATCTAGCCGAGCTCAGTGAAGGCGTGAATACATGAGAGA 840  
QY 841 GTATATAAGCGCGTGTAAACCTGCGCGAGCGCAACGCGTGTGCGACGACTGAC 900  
Db 841 GTATATAAGCGCGTGTAAACCTGCGCGAGCGCAACGCGTGTGCGACGACTGAC 900  
QY 901 CCAGCTGACGAGACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
Db 901 CCAGCTGACGAGACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
QY 961 TGTATCGAGTCAAAATCTGCGACGCTACATGAGTGTGAGTGTGAGTGTGAGCCG 1020  
Db 961 TGTATCGAGTCAAAATCTGCGACGCTACATGAGTGTGAGTGTGAGTGTGAGCCG 1020  
QY 1021 GGGATCACTCTCGAAGAGAGTGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
Db 1021 GGGATCACTCTCGAAGAGAGTGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
QY 1081 GCGCGCTCCCAATCTGCGGCTCCAGATCAAGGCGGCTTGAACAATGCGGCAAGATCAT 1140  
Db 1081 GCGCGCTCCCAATCTGCGGCTCCAGATCAAGGCGGCTTGAACAATGCGGCAAGATCAT 1140  
QY 1141 GCGCGCTGCAAAATCTGCGGCTCCAGATCAAGGCGGCTTGAACAATGCGGCAAGATCAT 1200  
Db 1141 GCGCGCTGCAAAATCTGCGGCTCCAGATCAAGGCGGCTTGAACAATGCGGCAAGATCAT 1200  
QY 1201 AACCAACGCAATTTACCGCATCTGAGCTGAACGAGCTGACGCTGCTTACGCGGCTC 1260  
Db 1201 AACCAACGCAATTTACCGCATCTGAGCTGAACGAGCTGACGCTGCTTACGCGGCTC 1260  
QY 1261 GGTCTTTCTGCGGCTGCGGCGGAGAAAGTTCGGAAGAAAGCAACATGCGGCTGTTGG 1320  
Db 1261 GGTCTTTCTGCGGCTGCGGCGGAGAAAGTTCGGAAGAAAGCAACATGCGGCTGTTGG 1320  
QY 1321 GCGCGGCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
Db 1321 GCGCGGCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
QY 1381 GCGCTGCTCACTGAGCAATGAGAACTTCTCTTCAAGATTTGCGTCAAGAGATGCT 1440  
Db 1381 GCGCTGCTCACTGAGCAATGAGAACTTCTCTTCAAGATTTGCGTCAAGAGATGCT 1440



OY	1441	GATCTGCTGGAGAGGAGGCAAGATGACGGCCCAAGTCTGTGAGTCCGACAGGCCATTCT	1500
Db	1441	GATCTGCTGGAGAGGAGGCAAGATGACGGCCCAAGTCTGTGAGTCCGACAGGCCATTCT	1500
OY	1501	CGGCGGACAGCAAGGTGCGCGTGTGACCAAAAGTGCMAAGTCTCCGCGCCAGATCGATCCAC	1560
Db	1501	CGGCGGACAGCAAGGTGCGCGTGTGACCAAAAGTGCMAAGTCTCCGCGCCAGATCGATCCAC	1560
OY	1561	CCCCGTGATCGTCACTTCAACACCAACATGTGCGCGTGTGATGTGACGGGAACAGCACCC	1620
Db	1561	CCCCGTGATCGTCACTTCAACACCAACATGTGCGCGTGTGATGTGACGGGAACAGCACAC	1620
OY	1621	CTTGCAGACCAAGACGCGCTGTGACGACCCGATGTTCAAATTTGAACCTACCGCGCTCT	1680
Db	1621	CTTGCAGACCAAGACGCGCTGTGACGACCCGATGTTCAAATTTGAACCTACCGCGCTCT	1680
OY	1681	GGAGCATGACTTTGGCAGAGTGACAAACAGAGAAAGTCAAAAGGTTCTTCCGCTGGGCGCA	1740
Db	1681	GGAGCATGACTTTGGCAGAGTGACAAACAGAGAAAGTCAAAAGGTTCTTCCGCTGGGCGCA	1740
OY	1741	GGATCACGTGACCGAGGTGGCGCATGATTTCTACGTCAGAAAGGTGAGGCCAACACAG	1800
Db	1741	GGATCACGTGACCGAGGTGGCGCATGATTTCTACGTCAGAAAGGTGAGGCCAACAGAG	1800
OY	1801	ACCGGCCCCCGATGACGCGGATTAAGAGGACCCCAAGCGGCGCTGCCCTCATGTGCGGA	1860
Db	1801	ACCGGCCCCCGATGACGCGGATTAAGAGGACCCCAAGCGGCGCTGCCCTCATGTGCGGA	1860
OY	1861	TCCATCGACGTGACGCGGAAAGAGCTCCGGTGGACTTTGCGCGACAGTACCAAAACAA	1920
Db	1861	TCCATCGACGTGACGCGGAAAGAGCTCCGGTGGACTTTGCGCGACAGTACCAAAACAA	1920
OY	1921	ATGTTCTCGTCAACGCGGGCATGCTTCAAGTCTGTTCCTTGCAAAATGCGAGAGAT	1980
Db	1921	ATGTTCTCGTCAACGCGGGCATGCTTCAAGTCTGTTCCTTGCAAAATGCGAGAGAT	1980
OY	1981	GATCAGAAATTTCAACATTTGCTTCAACCAAGGACCGAAGCTTCAGATGTGTTCCC	2040
Db	1981	GATCAGAAATTTCAACATTTGCTTCAACCAAGGACCGAAGCTTCAGATGTGTTCCC	2040
OY	2041	CGGCGTGCAGAAATGTCAAACCGGTGTGAGAAAGAGAGCTATGAGAAATCTGTGCGAT	2100
Db	2041	CGGCGTGCAGAAATGTCAAACCGGTGTGAGAAAGAGAGCTATGAGAAATCTGTGCGAT	2100
OY	2101	TCATCATCTGCTGGGCGGGCTCCCGAATGTCTTGCGGCTTGCGATCTGTGTCACGCT	2160
Db	2101	TCATCATCTGCTGGGCGGGCTCCCGAATGTCTTGCGGCTTGCGATCTGTGTCACGCT	2160
OY	2161	GGATCTGATGACTGTGTGTTCTGAGCAATTAATGACTTAAACAGAGTATGTCTCCGATG	2220
Db	2161	GGATCTGATGACTGTGTGTTCTGAGCAATTAATGACTTAAACAGAGTATGTCTCCGATG	2220
OY	2221	GTTATCTTCCAGATTGGGCTGAGGACAACTCTGAGGGGATTCGAGAGTGTGGGACT	2280
Db	2221	GTTATCTTCCAGATTGGGCTGAGGACAACTCTCTGAGGGGATTCGAGAGTGTGGGACT	2280
OY	2281	TGAAACCTGAGGCGCCGAAACCCAAAGCCAAACAGCAAAACAGGACGACGCGCGGGCTC	2340
Db	2281	TGAAACCTGAGGCGCCGAAACCCAAAGCCAAACAGCAAAACAGGACGACGCGCGGGCTC	2340
OY	2341	TGCTGCTTCTGCTGACAAATGACCTCGGACCTTCAACGAGCTCGACAAAGGGGAGCCCG	2400
Db	2341	TGCTGCTTCTGCTGACAAATGACCTCGGACCTTCAACGAGCTCGACAAAGGGGAGCCCG	2400
OY	2401	TCAACGCGGCGAGTCAACGCGGCTTCGAGCACGACAAAGGCTTCGACACAGGACGTCAAAG	2460
Db	2401	TCAACGCGGCGAGTCAACGCGGCTTCGAGCACGACAAAGGCTTCGACACAGGACGTCAAAG	2460
OY	2461	CGGCTGACAAATCCGTAACCTGCGGTATTAACACAGCGGACGCGAGTTTCAGGAGCGTCTGC	2520
Db	2461	CGGCTGACAAATCCGTAACCTGCGGTATTAACACAGCGGACGCGAGTTTCAGGAGCGTCTGC	2520
OY	2521	AAGAATATCGTCTTTTGGGGGCAACTTCGGGCGAGCACTTTCAGGCCAAAGAGGG	2580

Db	2521	AAAGAAATACGTCCTTTGGGGGCAACCTGGGCGAGCATGTTCCAGGCCAAGAAAGAGGG	2580
Qy	2581	TTCTCGAACCCTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCTTGAAAGAAAGCTC	2640
Db	2581	TTCTCGAACCCTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCTTGAAAGAAAGCTC	2640
Qy	2641	CGGTAGACAGTCCGCACAAAGCCAGACTCTCTCTGGGGCATTTGGCAAGACAGCCAGC	2700
Db	2641	CGGTAGACAGTCCGCACAAAGCCAGACTCTCTCTGGGGCATTTGGCAAGACAGCCAGC	2700
Qy	2701	AGCCCGCTAAAAAAGAGACTCAATTTTGGTTCAGATGGGGACTCAGAGTCAGTCCCGAGC	2760
Db	2701	AGCCCGCTAAAAAAGAGACTCAATTTTGGTTCAGATGGGGACTCAGAGTCAGTCCCGAGC	2760
Qy	2761	CACAACCTCTCGAGAAACCTTCAGCAACCCCGCTGCTGTGGGACTTACTTAACAATGGCTT	2820
Db	2761	CACAACCTCTCGAGAAACCTTCAGCAACCCCGCTGCTGTGGGACTTACTTAACAATGGCTT	2820
Qy	2821	CAGCGGTGGCGCAACCAATGGCAGCAATTAACGAAGGCGCCAGCGAGTGGGTATGGCT	2880
Db	2821	CAGCGGTGGCGCAACCAATGGCAGCAATTAACGAAGGCGCCAGCGAGTGGGTATGGCT	2880
Qy	2881	CAGGAAATTTGGCATTTGGCATTCACAAGGGCTGGGGCGACAGGTATATACCAACGAGCACCC	2940
Db	2881	CAGGAAATTTGGCATTTGGCATTCACAAGGGCTGGGGCGACAGGTATATACCAACGAGCACCC	2940
Qy	2941	GAACATGGGGCTTGGCCCACTATACAAACAACCACTCTCAAGCAAAATCTCCAGTGCCTTCAA	3000
Db	2941	GAACATGGGGCTTGGCCCACTATACAAACAACCACTCTCAAGCAAAATCTCCAGTGCCTTCAA	3000
Qy	3001	CGGGGGCCAGCAACGACCAACTTCTGGGCTACAGACCCCTGGGGGTATTTTGAAT	3060
Db	3001	CGGGGGCCAGCAACGACCAACTTCTGGGCTACAGACCCCTGGGGGTATTTTGAAT	3060
Qy	3061	TCACACAGTTCACATCGCATTTCTCACACGTGACTGGGACGGACTATGACAACAAT	3120
Db	3061	TCACACAGTTCACATCGCATTTCTCACACGTGACTGGGACGGACTATGACAACAAT	3120
Qy	3121	GGGGATTTCCGGCCCAAGAGACTCAACTTCAAGCTTCTTCAACATCAATCAAGTCAAGAGGTCA	3180
Db	3121	GGGGATTTCCGGCCCAAGAGACTCAACTTCAAGCTTCTTCAACATCAATCAAGTCAAGAGGTCA	3180
Qy	3181	CGACGAATGATGGCGTCAGACCAATCGGTAATACTTTACGACGCGTTCAGTCTTGT	3240
Db	3181	CGACGAATGATGGCGTCAGACCAATCGGTAATACTTTACGACGCGTTCAGTCTTGT	3240
Qy	3241	CGGACTCGGATTAACATTTCCCGTAACGTCTCGGCTCTGGGCAACAGGGCGCTCCCTC	3300
Db	3241	CGGACTCGGATTAACATTTCCCGTAACGTCTCGGCTCTGGGCAACAGGGCGCTCCCTC	3300
Qy	3301	CGTTCCCGGCGAAGCTGTTTCATGATTCGCGAGTACGGCTACCTAACGCTCAACATGGCA	3360
Db	3301	CGTTCCCGGCGAAGCTGTTTCATGATTCGCGAGTACGGCTACCTAACGCTCAACATGGCA	3360
Qy	3361	GCCAGGCAAGTGGAGCGCTCATCTTTTACGTGCTGGAATATTTTCCATTCGCAATGCTGA	3420
Db	3361	GCCAGGCAAGTGGAGCGCTCATCTTTTACGTGCTGGAATATTTTCCATTCGCAATGCTGA	3420
Qy	3421	GAAACGGGCAATTAACCTTTACCTTCAGCTACACCTTCGAGAGAGTGGCTTTTCAACGACGCT	3480
Db	3421	GAAACGGGCAATTAACCTTTACCTTCAGCTACACCTTCGAGAGAGTGGCTTTTCAACGACGCT	3480
Qy	3481	ACGGGCAACGACAGGCGCTGGAACGGGCTGATGAATCTCTTCATGACCAATGACTGTAT	3540
Db	3481	ACGGGCAACGACAGGCGCTGGAACGGGCTGATGAATCTCTTCATGACCAATGACTGTAT	3540
Qy	3541	ACCTGAACAGAACTCACAAATCAGTCCGGAAGTGCCTCAACAGAGCTTGCTGTTTAAACC	3600
Db	3541	ACCTGAACAGAACTCACAAATCAGTCCGGAAGTGCCTCAACAGAGCTTGCTGTTTAAACC	3600
Qy	3601	GTGGGTCTCCAGCTGGGCAATGTTCTGTTACGCCCAAAAATGGCTTACTGGAACCTGTTTACC	3660
Db	3601	GTGGGTCTCCAGCTGGGCAATGTTCTGTTTACGCCCAAAAATGGCTTACTGGAACCTGTTTACC	3660

Db 3601 GGGGGTCTCAGCTGGCATGTCTGTTCAAGCCCAAAAATGCGTACTGGACCTGTACC 3660  
 Qy 3661 GGGGACAGCGGCTTCTAAAAAAGAGACAAACAAGCACTTTACCTGGACTG 3720  
 Db 3661 GGGAGCAGCGGCTTCTAAAAAAGAGACAAACAAGCACTTTACCTGGACTG 3720  
 Qy 3721 GTGCTTCAAAATATATACCTTAATGGGCGTGAATCATATATCAACCTGGCACTGCTATGG 3780  
 Db 3721 GTGCTTCAAAATATATACCTTAATGGGCGTGAATCATATATCAACCTGGCACTGCTATGG 3780  
 Qy 3781 CCTCACACAAAGACGACAAAGACAAGTCTTTCCCATGAGCGGTGCATGATTTTGGAA 3840  
 Db 3781 CCTCACACAAAGACGACAAAGACAAGTCTTTCCCATGAGCGGTGCATGATTTTGGAA 3840  
 Qy 3841 AGGAGAGGCGGAGCTTCAAAACACTGATTTGGACAAATGTATGATCAACAGAGAGG 3900  
 Db 3841 AGGAGAGGCGGAGCTTCAAAACACTGATTTGGACAAATGTATGATCAACAGAGAGG 3900  
 Qy 3901 AAATCAAAAGCCACTAACCCCGTGGCCACCGAAAGATTGGGACTGTGGCAGTCAATCTCC 3960  
 Db 3901 AAATCAAAAGCCACTAACCCCGTGGCCACCGAAAGATTGGGACTGTGGCAGTCAATCTCC 3960  
 Qy 3961 AGAGCAGCAGCAGACAGACCTGCGACCGGAGATGTGCATGTTATGGAGCCTTACCTGGA 4020  
 Db 3961 AGAGCAGCAGCAGACAGACCTGCGACCGGAGATGTGCATGTTATGGAGCCTTACCTGGA 4020  
 Qy 4021 TGGTGTGGCAGACAGACAGTATCTGCGAGGCTCTATTTGGGCCAAATTTCTCTCA 4080  
 Db 4021 TGGTGTGGCAGACAGACAGTATCTGCGAGGCTCTATTTGGGCCAAATTTCTCTCA 4080  
 Qy 4081 CGGATGGAACCTTTACCCGCTCTCATGGGGGGCTTTGGAAGTGAAGCCGGCTC 4140  
 Db 4081 CGGATGGAACCTTTACCCGCTCTCATGGGGGGCTTTGGAAGTGAAGCCGGCTC 4140  
 Qy 4141 CTCAGATCTCTATCAAAAACAGCCTGTCTCTGCGAATCTCCGCGCAGAGTTTTCGCTA 4200  
 Db 4141 CTCAGATCTCTATCAAAAACAGCCTGTCTCTGCGAATCTCCGCGCAGAGTTTTCGCTA 4200  
 Qy 4201 CAAAGTTTGTCTTCAATTCACCCAGTATTCACAGGACAAAGTGAAGCTGAGATTGAAT 4260  
 Db 4201 CAAAGTTTGTCTTCAATTCACCCAGTATTCACAGGACAAAGTGAAGCTGAGATTGAAT 4260  
 Qy 4261 GGGAGCTGCAAGAAAGAAAGAGCAAAAGCTGGAATCCGAAAGTCAATTAATCT 4320  
 Db 4261 GGGAGCTGCAAGAAAGAAAGAGCAAAAGCTGGAATCCGAAAGTCAATTAATCT 4320  
 Qy 4321 ATGCAAAATCTGCCAAGCTTGAATTCATCTGGAACAAATGGAATTAATCTGAGCCTC 4380  
 Db 4321 ATGCAAAATCTGCCAAGCTTGAATTCATCTGGAACAAATGGAATTAATCTGAGCCTC 4380  
 Qy 4381 GCGCCATTGGGACCCGTTACTCACCCGCTCCCTGTAATGTGTTAATCAATTAACCG 4440  
 Db 4381 GCGCCATTGGGACCCGTTACTCACCCGCTCCCTGTAATGTGTTAATCAATTAACCG 4440  
 Qy 4441 GTTAATCGTGCATTTGAACCTTTGCTCATGTCCTAATATCTTAATCTGTCACCATTA 4500  
 Db 4441 GTTAATCGTGCATTTGAACCTTTGCTCATGTCCTAATATCTTAATCTGTCACCATTA 4500  
 Qy 4501 GCAACCGGTTACATTAATGCTTAATGTTGCGCTTCGGAATACCCCTAAGATGAGATT 4560  
 Db 4501 GCAACCGGTTACATTAATGCTTAATGTTGCGCTTCGGAATACCCCTAAGATGAGATT 4560  
 Qy 4561 GCGCACTCCCTCTATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620  
 Db 4561 GCGCACTCCCTCTATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4620  
 Qy 4621 TCTGCGGACCTTTGCTGCGAGGCCCAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4680  
 Db 4621 TCTGCGGACCTTTGCTGCGAGGCCCAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4680  
 Qy 4681 CAA 4683  
 Db 4681 CAA 4683

RESULT 4  
 AAD00772  
 ID AAD00772 standard; DNA; 4718 BP.  
 XX  
 AC AAD00772;  
 XX  
 DT 08-SEP-2000 (first entry)  
 XX  
 DE Adeno-associated virus serotype 1 DNA.  
 XX  
 KW Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;  
 KW cap protein; recombinant viral vector; gene delivery; gene therapy;  
 KW vaccine; transgene; ss.  
 XX  
 OS Adeno associated virus serotype 1.  
 XX  
 FH Key  
 FT repeat\_unit  
 FT 1..143  
 FT /tag= a  
 FT /label= 5'\_ITR  
 FT /note= "Inverted terminal repeat which is capable of  
 FT forming T-shaped hairpin structure"  
 FT 89..110  
 FT /tag= b  
 FT /bound\_moiety= "Rep protein"  
 FT 124..125  
 FT /tag= c  
 FT /note= "Terminal resolve site (TRS)"  
 FT 219..226  
 FT /tag= d  
 FT /bound\_moiety= "USP"  
 FT /note= "E box"  
 FT 236..299  
 FT /tag= e  
 FT /label= p5\_promoter  
 FT 237..245  
 FT /tag= f  
 FT /bound\_moiety= "YY1 factor"  
 FT 270..275  
 FT /tag= g  
 FT /label= p5\_TATA-Box  
 FT 299..306  
 FT /tag= h  
 FT /note= "YY1/p5 RNA"  
 FT 335..2272  
 FT /tag= j  
 FT /product= "Rep 68"  
 FT /function= "regulates replication and integration of AAV  
 FT DNA into host cell's chromosome"  
 FT /note= "The coding region is interrupted by intron"  
 FT 335..2206  
 FT /tag= i  
 FT /product= "Rep 78"  
 FT /function= "regulates replication and integration of AAV  
 FT DNA into host cell's chromosome"  
 FT 857..862  
 FT /tag= 1  
 FT /label= p19\_TATA\_Box  
 FT 882..883  
 FT /tag= m  
 FT /note= "p19 RNA"  
 FT 1007..2272  
 FT /tag= o  
 FT /product= "Rep 40"  
 FT /function= "regulates replication and integration of AAV  
 FT DNA into host cell's chromosome"  
 FT /note= "The coding region is interrupted by intron"  
 FT 1007..2206  
 FT /tag= n  
 FT /product= "Rep 52"  
 FT /function= "regulates replication and integration of AAV

FT	DNA into host cell's chromosome"
FT	1836..1841
FT	/tag= p
FT	/label= P40_TATA-BOX
FT	1875..1876
FT	/tag= q
FT	/note= "P40 RNA"
FT	1924..2220
FT	/tag= k
FT	/note= "This region interrupts the coding sequence of Rep
FT	68 and Rep 40"
FT	2223..4433
FT	/tag= r
FT	/product= "VP1 protein"
FT	/note= "Capsid protein"
FT	2634..4433
FT	/tag= s
FT	/product= "VP2 protein"
FT	/note= "Capsid protein"
FT	/partial
FT	2829..4433
FT	/tag= t
FT	/product= "VP3 protein"
FT	/note= "Capsid protein"
FT	4447..4452
FT	/tag= u
FT	4576..4718
FT	/tag= v
FT	/label= 3_'ITR
FT	/note= "Inverted terminal repeat which is capable of
FT	forming T-shaped hairpin structure"
PD	WO20028061-A2.
PD	18-MAY-2000.
PF	02-NOV-1999; 99WO-US025694.
PR	05-NOV-1998; 98US-0107114P.
PA	(TYPE-) UNIV PENNSYLVANIA.
PI	Wilson JM, Xiao W;
DR	WPI; 2000-376571/32.
DR	P-PDB; AAV71161, AAV71164, AAV71165, AAV71166, AAV71167, AAV71168,
DR	AAV71169.
XX	Novel adeno-associated virus serotype 1 polynucleotide useful for
PT	preparation of medicament for delivery of a transgene to a host.
XX	Claim 1; Fig 1; 108pp; English.
PS	The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA
CC	characterised by two inverted terminal repeats (ITR) and open reading
CC	frames for rep and capsid (cap) proteins. The rep reading frame encodes
CC	four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading
CC	frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1
CC	sequence or its fragments particularly ITRs, rep and cap coding regions,
CC	are useful in production of recombinant viral vectors for gene delivery.
CC	These vectors can be used as gene therapy vectors, vaccine vectors or
CC	antisense delivery vectors. The AAV-1 does not induce the formation of
CC	neutralising antibodies specific to any serotype of AAV hence is useful
CC	for transforming host cells, and in the preparation of a medicament for
CC	the delivery of transgene to a host
XX	
SQ	Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;
Query Match	90.8%; Score 4253.2; DB 3; Length 4718;
Best Local Similarity	94.7%; Freq. No. 0;
Matches 4471; Conservative	0; Mismatches 208; Indels 43; Gaps 5;

Db	1	TTGCCATCTCCCTCTCTGCGCGCTCGCTCGCTGCGTGGGCTCTCGGACCAAGTCCG	60
Qy	61	CGACGCCCGGGCTTTGGCCCGGCGGCTCTCACTGAGCGAGCGAGCGCAGAGGAGTG	120
Db	61	AGAGCGGAGAGCTGCTCTGCTCTGCGGGCCCAACGAGCGAGCGAGCGCAGAGAGGAGTG	120
Qy	121	GCCAACTCCATCATCTAGGGGT-----TCTGAGGGGTGGATCCTGA	163
Db	121	GGCAACTCCATCATCTAGGGGTATATCGAGAGCGCTCCACGCTGCCGCTCACGCTGA	180
Qy	164	CGTGAATTACGTCATAGGGTTAGGGAGGTCCGTGATTAGAGTCACTGAGTG- TTTTGC	222
Db	161	CGTAATTACGTCATAGGG---GAGTGGTCCGTGATTAGCTGATCAGTGAGTCTTTTGC	237
Qy	223	GACATTTTTCGACACCATGTGTGTCACGCTGGGTATTTAAGCCGAGTGAAGCACGAGGT	282
Db	238	GACATTTTTCGACACCACTGTGCCATTATAGGTTATATGCGCAAGTGAAGACAGAT	297
Qy	283	CTCCATTTTGAAGGGGGGTTGTAAGCGGAGCGCCATGCGGGGTTTTCAGAGATTGT	342
Db	288	CTCCATTTTGAACCGGAATTGGAACGAGCAGACCATGCCGGCTTCTACGAGATCGT	357
Qy	343	GATTAAAGTCCCCAGCGACTTGAAGCATCTGCCCGCATTTTCTGAAGCTTTGTGAA	402
Db	358	GATCAAGGTGCGAGCGACTGACAGCAGCATCTCCGGCATTTTCTGATCTGTTGTGAG	417
Qy	403	CTGGGTGGCCGAGAAAGGATGGGAGTTGGCGCCAGATTCTGACATGATCTGATCTGAT	462
Db	418	CTGGGTGGCCGAGAAAGGATGGGAGTGGCCCCCGGATTTCTGACATGATCTGATCTGAT	477
Qy	463	TGAGCAGGACCCCTTGACCCGTGGCCGAGAACTGACAGCGCATCTCTGTCTCACTGGCG	522
Db	478	TGAGCAGGCACTCCGTCGACCTGTGGCCGAGAACTGACAGCGCATCTCTGTCTCACTGGCG	537
Qy	523	CCGCGTAGTAAAGGCCCGGAGGCCCTCTTTTGTTCAGTTTCAAGAAAGGCGAGTCTCTA	582
Db	538	CCGCGTAGTAAAGGCCCGGAGGCCCTCTTTTGTTCAGTTTCAAGAAAGGCGAGTCTCTA	597
Qy	583	CTTCACCTCCATATTCTGTGAGAGACCAAGGGGATCAATCCATGGTGTGGGCGCCTT	642
Db	598	CTTCACCTCCATATTCTGTGAGAGACCAAGGGGATCAATCCATGGTGTGGGCGCCTT	657
Qy	643	CTGAGTCAGATTAGCGAAGAGTGTGTGACAGCATCTACCGCGGATTCGAGCCGACCT	702
Db	658	CCTGAGTCAGATTAGGGACAAGCTGTGTGACAGCATCTACCGCGGATTCGAGCCGACCT	717
Qy	703	GCCCAACTGTGTGCGGTGACCAAGAGCGGTAAAGGGCGGAGGGGGAAACAAGTGT	762
Db	718	GCCCAACTGTGTGCGGTGACCAAGAGCGGTAAAGGGCGGAGGGGGAAACAAGTGT	777
Qy	763	GAGCAGTGTACATCCCAACTACCTCTCTGCCCAAGACTCAGGCCGAGCTGAGTGGG	822
Db	778	GAGCAGTGTACATCCCAACTACCTCTCTGCCCAAGACTCAGGCCGAGCTGAGTGGG	837
Qy	823	GTGACCTTAATGAGAGATATTAAGGCGGTATTAACTGTGCCGAGCGCAACCGCT	882
Db	838	GTGACCTTAATGAGAGATATTAAGGCGGTATTAACTGTGCCGAGCGCAACCGCT	897
Qy	883	CGTGCGCAGCACCTGAGCCCAAGTCAAGCAGCAACCCAGAGCAGAAACAAGAAATCTGAA	942
Db	898	CGTGCGCAGCACCTGAGCCCAAGTCAAGCAGCAACCCAGAGCAGAAACAAGAAATCTGAA	957
Qy	943	CCCCAATTCTGACGCGCTGTATCTCGGTCAAAAACCTCCGACGCTACATGAGCTGT	1002
Db	958	CCCCAATTCTGACGCGCTGTATCTCGGTCAAAAACCTCCGCGCTACATGAGCTGT	1017
Qy	1003	CGGGTGGTGTGAGCGGGGATCACTCCGAGAAAGAGTGAATCCAGAGGACCAAGC	1062
Db	1018	CGGGTGGTGTGAGCGGGGATCACTCCGAGAAAGAGTGAATCCAGAGGACCAAGC	1077
Qy	1063	CTCGATCAATCTCTTCAACGCGGCTCCAATCTCGCGTCCAGATCAAGCGCGCTTGA	1122

D	b	1078	CTCGATCATCTCTCTTCAACGCCGCTTCCAACTCGCGGTCCAGATCAAGCGCGCTCTGGA	1137
Q	y	1123	CAATGCGGCAAGATCATGCGGCTGACCAAAATCCGCGCCGACCTACCTGTGATGCGCCGC	1182
D	b	1138	CAATGCGGCAAGATCATGCGGCTGACCAAAATCCGCGCCGACCTACCTGTGATGCGCCGC	1197
Q	y	1183	TCGCGCCGCAATTAACCAACCGCATTTACCGCATCTCGAGCTGAACGCGTACGA	1242
D	b	1198	TCGCGCCGCAATTAACCAACCGCATCTACCGCATCTCGAGCTGAACGCGTACGA	1257
Q	y	1243	CCCTGCTACGCGCGCTCCGTCTTTCTCGGCTGCGGCCCAAAAAGTTTCGAAAACGCA	1302
D	b	1258	ACCTGCTACGCGCGCTCCGTCTTTCTCGGCTGCGGCCCAAAAAGTTTCGAAAACGCA	1317
Q	y	1303	CACATCTGCGCTTTTGGGCGCGGCCACACGCGGCAAGACCAATCTCGGGAAGCATGCG	1362
D	b	1318	CACATCTGCGCTTTTGGGCGCGGCCACACGCGGCAAGACCAATCTCGGGAAGCATGCG	1377
Q	y	1363	CCAGCGCGTGCCTTCTACGCGCTGCTCAACTGACACATGAGAACTTTCCCTTCAACGA	1422
D	b	1378	CCAGCGCGTGCCTTCTACGCGCTGCTCAACTGACACATGAGAACTTTCCCTTCAATGA	1437
Q	y	1423	TTGCGTGCACAAAGATGTGATCTGTGAGAGAGGCAAGATGACGGCCAAAGTGTGGA	1482
D	b	1438	TTGCGTGCACAAAGATGTGATCTGTGAGAGAGGCAAGATGACGGCCAAAGTGTGGA	1497
Q	y	1483	GTCCGCCAAGGCCATTTCTCGCGCGGACGAAGGTGCGCTGGAACCAAAAGTCAAGTCTC	1542
D	b	1498	GTCCGCCAAGGCCATTTCTCGCGCGGACGAAGGTGCGCTGGAACCAAAAGTCAAGTCTC	1557
Q	y	1543	CGCCAGATCGATCCCAACCCCGGTGATGTCACCTCCAAACCAACATGTGCGCGGTAT	1602
D	b	1558	CGCCAGATCGATCCCAACCCCGGTGATGTCACCTCCAAACCAACATGTGCGCGGTAT	1617
Q	y	1603	TGACGGAAACGACCACTTTCAGACACACAGCCGTTGACGACCGGATGTTCAAAAT	1662
D	b	1618	TGACGGAAACGACCACTTTCAGACACACAGCCGTTGACGACCGGATGTTCAAAAT	1677
Q	y	1663	TGAATCAACCCCGCTCTGAGCATGACTTTGGCAAGGTGACAAAGCAGAAATCAAAAG	1722
D	b	1678	TGAATCAACCCCGCTCTGAGCATGACTTTGGCAAGGTGACAAAGCAGAAATCAAAAG	1737
Q	y	1723	GTTCCTCGGCTGCGGCGCAGATCAAGTACGAGGCTGCGCATGATCTACGTCAGAA	1782
D	b	1738	GTTCCTCGGCTGCGGCGCAGATCAAGTACGAGGCTGCGCATGATCTACGTCAGAA	1797
Q	y	1783	GGGTGAGCCAAACAGACCCCGCCGATGACGCGGATAAACGCAAGCCCAAGCGGC	1842
D	b	1798	GGGTGAGCCAAACAGACCCCGCCGATGACGCGGATAAACGCAAGCCCAAGCGGC	1857
Q	y	1843	CTGCGCCCTCACTCCGCGATTCATGACGTCAAGCGCGAAGAGCTCCGGTGAATTTGC	1902
D	b	1858	CTGCGCCCTCACTCCGCGATTCATGACGTCAAGCGCGAAGAGCTCCGGTGAATTTGC	1917
Q	y	1903	CGACAGGTACCAAAACAAATGTTCTGTCACGCGGACGCTTTCAGATGCTTTCCCTG	1962
D	b	1918	CGACAGGTACCAAAACAAATGTTCTGTCACGCGGACGCTTTCAGATGCTTTCCCTG	1977
Q	y	1963	CAAAATGCGAGAGATGAATCAAGATTTTCAACATTTGCTTCAACGCAAGGACACAGA	2022
D	b	1978	CAAAATGCGAGAGATGAATCAAGATTTTCAACATTTGCTTCAACGCAAGGACACAGA	2037
Q	y	2023	CTGTTTCAAGATTTTCCCGCGGTGTCAAGATCTCAACCGGTCTGACAAAGAGAGCTA	2082
D	b	2038	CTGTTTCAAGATTTTCCCGCGGTGTCAAGATCTCAACCGGTCTGACAAAGAGAGCTA	2097
Q	y	2083	TCGGAATCTGTGCTCAATTCATCTGCTGGGCGGGCTCCGAGATTTGCTTGCCTGCG	2142
D	b	2098	TCGGAATCTGTGCTCAATTCATCTGCTGGGCGGGCTCCGAGATTTGCTTGCCTGCG	2157
Q	y	2143	CTGCGATCTGATCAACGTGATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAAC	2202
D	b	2158	CTGCGATCTGATCAACGTGATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAAC	2217

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Q	y	2203	CAGGATGCTGCCGATGTTATCTTCCAGATTGGCTGAGAGACAACTCTTGAGGGA	2262
D	b	2218	CAGGATGCTGCCGATGTTATCTTCCAGATTGGCTGAGAGACAACTCTTGAGGGA	2277
Q	y	2263	TTCCGCAATGTTGGGACTTGAACCTTGAGGCCGCAAAACCCAAAGCCAAAGC	2322
D	b	2278	TTCCGCAATGTTGGGACTTGAACCTTGAGGCCGCAAAACCCAAAGCCAAAGC	2337
Q	y	2323	AGACGACGCGCGGGGTCTGCTCTTCTGCTCAAGTACCTTGAGACCTTTCAACGAC	2382
D	b	2338	AGACGACGCGCGGGGTCTGCTCTTCTGCTCAAGTACCTTGAGACCTTTCAACGAC	2397
Q	y	2383	TCGACAGGGGAGCCGCTCAACCGCGGATGACGCGGCCCTTGAGACGACAAAGGCT	2442
D	b	2398	TCGACAGGGGAGCCGCTCAACCGCGGATGACGCGGCCCTTGAGACGACAAAGGCT	2457
Q	y	2443	ACGACGACGACTCAAAAGCGGGTGAATCCGTAACCTGCGGTATTAACACCGCCGACG	2502
D	b	2458	ACGACGACGACTCAAAAGCGGGTGAATCCGTAACCTGCGGTATTAACACCGCCGACG	2517
Q	y	2503	AGTTTCAGGAGCGTCTGCAAGAAATACGTCCTTTTGGGGCAACCTCGGCGACGCT	2562
D	b	2518	AGTTTCAGGAGCGTCTGCAAGAAATACGTCCTTTTGGGGCAACCTCGGCGACGCT	2577
Q	y	2563	TTCCAGGCCAAGAGGTTCTGCAACCTTTTGGTCTGTGTGAGAGAGTCTTAAGAG	2622
D	b	2578	TTCCAGGCCAAGAGGTTCTGCAACCTTTTGGTCTGTGTGAGAGAGTCTTAAGAG	2637
Q	y	2623	CTCCTGGAAGAAAGTCCCGGTAGAGAGTGCACCAAGACCGACCTCTCGGCA	2682
D	b	2638	CTCCTGGAAGAAAGTCCCGGTAGAGAGTGCACCAAGACCGACCTCTCGGCA	2697
Q	y	2683	TTGSCAAGACAGGCCAGACCGCGCTAAAAAGACCTCAATTTTGTGAGCTGCGACT	2742
D	b	2698	TTGSCAAGACAGGCCAGACCGCGCTAAAAAGACCTCAATTTTGTGAGCTGCGACT	2757
Q	y	2743	CAGAGTCACTCCCGACCCCAACCTCTCGAGAACTCCACGACAAACCCCGCTCTG	2802
D	b	2758	CAGAGTCACTCCCGACCCCAACCTCTCGAGAACTCCACGACAAACCCCGCTCTG	2817
Q	y	2803	GACCTACTCAATGCTTTCAGAGCGGTGCGGACCAATGCGCAGACATTAACGAAGCGCG	2862
D	b	2818	GACCTACTCAATGCTTTCAGAGCGGTGCGGACCAATGCGCAGACATTAACGAAGCGCG	2877
Q	y	2863	ACGAGTGGGTATGCTTCAGGAAATTGGCATTTGCCAATGCTGCGGCGACAGAG	2922
D	b	2878	ACGAGTGGGTATGCTTCAGGAAATTGGCATTTGCCAATGCTGCGGCGACAGAG	2937
Q	y	2923	TCATCACACCAAGACCCGAAACATGGGCTTTGCCCACTTATTAACAACCTCTTAACAG	2982
D	b	2938	TCATCACACCAAGACCCGAAACATGGGCTTTGCCCACTTATTAACAACCTCTTAACAG	2997
Q	y	2983	AAATCTCAAGTCTTCAACGGGGGCGACGAACGACCACTTTCGCTGACAGACCC	3042
D	b	2998	AAATCTCAAGTCTTCAACGGGGGCGACGAACGACCACTTTCGCTGACAGACCC	3057
Q	y	3043	CTTGGGGGTATTTTGAATTTCAACAGATTCACCTGCAATTTCTCAACAGTACGCGAGC	3102
D	b	3058	CTTGGGGGTATTTTGAATTTCAACAGATTCACCTGCAATTTCTCAACAGTACGCGAGC	3117
Q	y	3103	GACTCATCAACAAATTTGGGGGATTCGCGGCCCAAGAGACATCACTTCAAGCTTCAACA	3162
D	b	3118	GACTCATCAACAAATTTGGGGGATTCGCGGCCCAAGAGACATCACTTCAAGCTTCAACA	3177
Q	y	3163	TTCAAGTCAAGAGGTGACGACGATGATGCGGTCAAGACCATGCTTAATTAACCTTACA	3222
D	b	3178	TTCAAGTCAAGAGGTGACGACGATGATGCGGTCAAGACCATGCTTAATTAACCTTACA	3237
Q	y	3223	GCACGTTCAAGTCTTGTGAGCTCGGAGTACCAATTCCTGACGCTCTGCGCTCTGCG	3282
D	b	3238	GCACGTTCAAGTCTTGTGAGCTCGGAGTACCAATTCCTGACGCTCTGCGCTCTGCG	3297

QY 3283 ACCAGGGCTGCTCCCTCCGTTCCGGGGAACGNTTCATGATTCGGCAGTACGGCTACCC 3342  
 DB 3298 ACCAGGGCTGCTCCCTCCGTTCCGGGGAACGNTTCATGATTCGGCAGTACGGCTACCC 3357  
 QY 3343 TAAAGCTCAACAATGGAGCAGGAGCAGTGGAGCCGTACCTTTTACTGCTGGAAATATTT 3402  
 DB 3358 TGAAGCTCAACAATGGAGCAGGAGCAGTGGAGCCGTACCTTTTACTGCTGGAAATATTT 3417  
 QY 3403 TCCCATGCAAGATCTGAGAAACGGGCAATTAATTTACTTCACTGATCACTTTCAGAGACG 3462  
 DB 3418 TCCCTTCTCAGATCTGAGAAACGGGCAATTAATTTACTTCACTGATCACTTTCAGAGACG 3477  
 QY 3463 TGCCCTTCCACAGAGCTACGCGACAAGCAGAGCTGGACCGGCTGATGATGATCTCTCA 3522  
 DB 3478 TGCCCTTCCACAGAGCTACGCGACAAGCAGAGCTGGACCGGCTGATGATGATCTCTCA 3537  
 QY 3523 TCGACCAATACCTGTATTTACTCTGAACAGAACTCAAACTCACTCCGGAAGTCCCAAAACA 3582  
 DB 3538 TCGACCAATACCTGTATTTACTCTGAACAGAACTCAAACTCACTCCGGAAGTCCCAAAACA 3597  
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 DB 3598 AGGACTTGTCTTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTCAAGCCCAAAACTGGC 3657  
 QY 3643 TACCTGGAACCTGTATTCACGAGCAGCGCGCTTTTAAACAAAACAGACAACAACA 3702  
 DB 3658 TACCTGGAACCTGTATTCACGAGCAGCGCGCTTTTAAACAAAACAGACAACAACA 3717  
 QY 3703 GCAACTTTACCTGAGCTGTGCTTCAAAATTAACCTTTAATGGCGTGAATCTAATATCA 3762  
 DB 3718 GCAACTTTACCTGAGCTGTGCTTCAAAATTAACCTTTAATGGCGTGAATCTAATATCA 3777  
 QY 3763 ACCCTGGACCTGCTATGAGCCCTCAACAAGACGACAAAGAAATTTTCCCATGAGCG 3822  
 DB 3778 ACCCTGGACCTGCTATGAGCCCTCAACAAGACGACAAAGAAATTTTCCCATGAGCG 3837  
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 DB 3838 GTGTCATGATTTTGGAAAGAGAGCGCCGAGCTTCAAAACATGCAATTTGGACAATGTCA 3897  
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 DB 3898 TGATTAACAAGAGAGAAATTAAGCACTAAACCCCGTGGCCAGCCGAAAGATTTGGGA 3957  
 QY 3943 CTGTGGCAGTCAATCTCCAGAGCAGACAGACCCCTGCGACCGGAGATTTGCATGTA 4002  
 DB 3958 CCGTGGCAGTCAATTTCCAGAGCAGACAGACCCCTGCGACCGGAGATTTGCATGTA 4017  
 QY 4003 TGGAGCCTTACCTGGAATGCTGTGGCAAGACAGAGCTATTAATCTGAGAGGTCTTAATTT 4062  
 DB 4018 TGGAGCCTTACCTGGAATGCTGTGGCAAGATTAAGAGCTTAATCTGAGAGGTCTTAATTT 4077  
 QY 4063 GGGGCAAAATTCCTCAACGAGATGACAATTTCAACCCGCTCTCTCTCAATGGGCGGCTTTG 4122  
 DB 4078 GGGGCAAAATTCCTCAACGAGATGACAATTTCAACCCGCTCTCTCTCAATGGGCGGCTTTG 4137  
 QY 4123 GACTTAAGCAACCCGCTCTCTCAATCTCAATCAAAACACGCGCTTCTCTGCGAATCTCTC 4182  
 DB 4138 GACTTAAGCAACCCGCTCTCTCAATCTCAATCAAAACACGCGCTTCTCTGCGAATCTCTC 4197  
 QY 4183 CGGAGAGTTTTCGGCTACAAAGTTTGTTCATTCATCAACCAATATTCACAGAGACAG 4242  
 DB 4198 CGGAGAGTTTTCGGCTACAAAGTTTGTTCATTCATCAACCAATATTCACAGAGACAG 4257  
 QY 4243 TGAGCGTGAAGATTTGAGAGCTGCAAGAAAGAAACAGCAAAACGCTGGAATCCGAG 4302  
 DB 4258 TGAGCGTGAAGATTTGAGAGCTGCAAGAAAGAAACAGCAAAACGCTGGAATCCGAG 4317  
 QY 4303 TGGAGTATACCTAATCAATGCAAAATTCGCAACGTTGATTTTCACTGTGAGCAACAATG 4352  
 DB 4318 TGGAGTATACCTAATCAATGCAAAATTCGCAACGTTGATTTTCACTGTGAGCAACAATG 4377  
 QY 4363 GACTTTTACTAGCCTTGCCCAATGGCACCCGTTACCTCAACCCGTTCCCTGTAAATGT 4422

DB 4378 GACTTTATATGAGCCTCGGCCCATTTGGACCCGTTTACCTTACCCGCTGTAAATTAAC 4437  
 QY 4423 GTGTAAATCAATTAACCGGTTAAATTTGTGTCAGTTGAATTTGTCTCATGTCTTAATTA 4482  
 DB 4438 GTGTAAATCAATTAACCGGTTAAATTTGTGTCAGTTGAATTTGTCTCATGTCTTAATTA 4497  
 QY 4483 TCTTATCTGTGTCACATAGCAACCGGTTACATTAATGCTAGTTGAGCTTGGCGA-- 4540  
 DB 4498 TCTTATC-GGTATACATGTTATAGCTTACATTAATCTCTGTTGGCTTCGGATA 4556  
 QY 4541 -----ATACCCCTAGTATGATGAGTTGCGCACTTCCTTATGCGCGC 4581  
 DB 4557 AAGACTTACGTATGATGGGTTTACCCCTAGTATGAGAGTTGCCACATCCCTCTGCGCGC 4616  
 QY 4582 TCGCTGCTGTGTGGGGCCGCGAGACAGAGCTCTGCTGTCGGAACCTTTGTCCGCA 4641  
 DB 4617 TCGCTGCTGTGTGGGGCCCTGCGACCAAGGTCGCGACAGCGCAAGAGCTCTGCTGCC 4676  
 QY 4642 GGGCCCAACGAGGAGCGGACGCGCATPAGAGGAGTGGCCAA 4683  
 DB 4677 GGGCCCAACGAGGAGCGGACGCGCATPAGAGGAGTGGCCAA 4718  
 RESULT 5  
 ADE76507  
 ID ADE76507 standard; DNA; 4718 BP.  
 AC ADE76507;  
 XX 29-JAN-2004 (first entry)  
 DT XX  
 DE Adeno-associated virus (AAV) related DNA, SEQ ID NO 6.  
 XX  
 KM adeno-associated virus; AAV; cytosolic; antiposoriatic; antirheumatic;  
 KM antiarthritic; neuroprotective; antidiabetic; antihydrid;  
 KM dermatological; antinflammatory; gene therapy; vaccine;  
 KM hyperproliferative; cancer; psoriasis; autoimmune disease;  
 KM rheumatoid arthritis; multiple sclerosis; diabetes;  
 KM autoimmune thyroiditis; scleroderma; Crohn's disease; gene; de.  
 OS Adeno-associated virus 1.  
 XX  
 PN BPJ31057L-A2.  
 XX  
 PD 14-MAY-2003.  
 XX  
 PF 12-NOV-2002; 2002BP-00257826.  
 XX  
 PR 13-NOV-2001; 2001US-0350607P.  
 PR 17-DEC-2001; 2001US-0341117P.  
 PR 01-MAY-2002; 2002US-0377066P.  
 PR 05-JUN-2002; 2002US-0386675P.  
 XX  
 PA (TYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Gao G, Wilson JM, Alvira M;  
 XX WPI; 2003-450984/43.  
 DR  
 PT Detecting adeno-associated virus sequences in a sample, useful for e.g.  
 PT preventing or treating hyperproliferative or autoimmune diseases,  
 PT comprising subjecting a sample having a DNA to amplification via  
 PT polymerase chain reaction.  
 XX  
 PS Claim 14; SEQ ID NO 6; 419pp; English.  
 XX  
 CC The invention relates to a novel method for detecting adeno-associated  
 CC virus (AAV) sequences in a sample, which comprises subjecting a sample  
 CC containing a DNA to amplification via a polymerase chain reaction (PCR).  
 CC The AAV sequence have the following activities: cytosolic,  
 CC antiposoriatic, antirheumatic, antidiabetic, neuroprotective,  
 CC antidiabetic, antihydrid, dermatological, and antinflammatory. The AAV

CC sequence can be used in gene therapy or as part of a vaccine to treat  
CC disorders. The method is useful in detecting and/or identifying AAV  
CC sequences and isolating novel sequences that are identified. The  
CC sequences may be used e.g. for preventing or treating hyperproliferative  
CC conditions such as cancers and psoriasis, and other autoimmune diseases  
CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune  
CC chrydroids, scleroderma or Crohn's disease. This polynucleotide sequence  
CC represents an AAV related DNA sequence of the invention.  
XX

SQ Sequence 4718 BP, 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Query Match 90.8%; Score 4253.2; DB 10; Length 4718;  
Best Local Similarity 94.7%; Pred. No. 0;

Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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QY 1 TTGGCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGCGCGGCAACAAAGTCCGC 60
DB 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTGAGGGGCTCGCGCAAAAGTCCGC 60
QY 61 CGAGCGCGGCGCTTGGCGCGGCGCTCAGTGAAGCGAGCGCGGCGAGAGGAGTG 120
DB 61 AGACGCGCAGAGCTCTGCTCTGCGCGCCCAACGAGCGAGCGCGAGAGGAGTG 120
QY 121 GCCAATCTCATCTAGGAGGCT-----TCTGAGAGGGGTGAGTCTGGA 163
DB 121 GGCACATCTCATCTAGGAGGTAATGCGAGCGGCTCCCAACGCTCCCGCTGAG 180
QY 164 CGTGAATTAAGTCAATAGGAGTTCCTGTAATTAAGAGTCACTGAGTG-TTTTGC 222
DB 181 CGTAAATTAAGTCAATAGGAGTTCCTGTAATTAAGAGTCACTGAGTGCTTTTGC 237
QY 223 GACATTTTGGCAACCATGAGTGTGACGCTGGGTATTTAAGCCCGAGTGAAGCAGAGGT 282
DB 238 GACATTTTGGCAACCATGAGTGTGACGCTGGGTATTTAAGCCCGAGTGAAGCAGAGGT 297
QY 283 CTCATTTTGAAGCGGAGGTTTGAACGCGAGCGCATGCGGGGTTTTCAGAGTTGT 342
DB 298 CTCATTTTGAACGCGGAAATTTGAACGAGCAGCAGCATGCGGGCTTCTAGAGATGCT 357
QY 343 GATTAAAGTCCCGACGCACTTTGACGAGCATCTGCCGCAATTTTGAACGCTTTGAA 402
DB 358 GATCAAGGTGCGGAGCGACCTGAGCAGACCATCGCGGCAATTTCTGACTGTTTGTAG 417
QY 403 CTGGGTGGCGGAGAGGATGGAGTTGCGCGCAGATCTGACATGATCTGAATCTGAT 462
DB 418 CTGGGTGGCGGAGAGGATGGAGTTGCGCGCAGATCTGACATGATCTGAATCTGAT 477
QY 463 TGACGAGGCAACCCCTGACCGTGGCGAGAGACTGCAAGCGCATTTCTGATCTGAGCG 522
DB 478 TGACGAGGCAACCCCTGACCGTGGCGGAGAGACTGCAAGCGCATTTCTGATCTGAGCG 537
QY 523 CGCGGTGAGTAAGGCGCGGAGCGCTCTTCTTTGTTCAATTGAGAAAGGCGAGTCTTA 582
DB 538 CGCGGTGAGTAAGGCGCGGAGCGCGCTCTTCTTTGTTCAATTGAGAAAGGCGAGTCTTA 597
QY 583 CTTCACCTCCATATTTCTGTGTGAGACCAACGCGGGGTCAATCCATGCTGTGGCGGCTT 642
DB 598 CTTCACCTCCATATTTCTGTGTGAGACCAACGCGGGGTCAATCCATGCTGTGGCGGCTT 657
QY 643 CTTGAGTCAAGTTCGAGCAAGCTGTGACAGCATCTACCGCGGAGTTCGAGCGCACCT 702
DB 658 CTTGAGTCAAGTTCGAGCAAGCTGTGACAGCATCTACCGCGGAGTTCGAGCGCACCT 717
QY 703 GCCCAACTGTTTCCGCGGTGACCAAGACGCTGAATGCGCGCGAGAGGGGAAACAAGTGT 762
DB 718 GCCCAACTGTTTCCGCGGTGACCAAGACGCTGAATGCGCGCGAGAGGGGAAACAAGTGT 777
QY 763 GGACGAGTGTACATCCCAACTACCTCTGCGCCCAAGCTGAGCCGAGCTGAGTGGGC 822
DB 778 GGACGAGTGTACATCCCAACTACCTCTGCGCCCAAGCTGAGCCGAGCTGAGTGGGC 837
QY 823 GTGACATAACATGAGAGATATATAGCGCGTGTTTAAACTGTGCGGAGCGCAACGCGCT 882
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DB 838 GTGACATAACATGAGAGATATATAGCGCGCTGTTTGAACCTGCGCGAGCGCAACGCGCT 897
QY 883 CTGCGCGCAACACTGACCCACGTCAGCCAGACCCAGAGAGCAAGAACAGAGATCTGAA 942
DB 898 CGTGGCGGAGACCTGACCCACGTCAGCCAGACCCAGAGAGCAAGAACAGAGATCTGAA 957
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DB 958 CCCCAATTCTAGAGGCGGCTGATCCCGGTCAAAAACCTCCGCGGCTTCATGAGACTGCT 1017
QY 1003 CGGTGAGTGTGAGACCGGGGCAATCACTCCGAGAGAGTGAATCCAGAGAGCACAGGC 1062
DB 1018 CGGTGAGTGTGAGACCGGGGCAATCACTCCGAGAGAGTGAATCCAGAGAGCACAGGC 1077
QY 1063 CTCTGATCTCTCTTCAACGCGCGCTCCAATCTCGGGTCCCAATCAAGGCGCTTGA 1122
DB 1078 CTCTGATCTCTCTTCAACGCGCGCTCCAATCTCGGGTCCCAATCAAGGCGCGCTTGA 1137
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DB 1138 CAATGCGCGCAAGATCAATGAGGCTGACCAATCCGCGCGGACCTAACCTGTGAGCGCGCG 1197
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DB 1198 TCCGCGCGCGCAATTAACCAACCGCATTTACCGCATCTTGAAGCTGAACGCGTACGA 1257
QY 1243 CCTGCTGATCGCGGCTCGTCTTTCTCGGCTGCGGCCCAAGAAAGTTTGGAAACGCA 1302
DB 1258 ACTGCTGATCGCGGCTCGTCTTTCTCGGCTGCGGCCCAAGAAAGTTTGGAAACGCGCA 1317
QY 1303 CACCATGAGTGTGAGGCGCGGCAACAGGGGGAAGCAACATCGCGGGAAGCATGCG 1362
DB 1318 CACCATGAGTGTGAGGCGCGGCAACAGGGGGAAGCAACATCGCGGGAAGCATGCG 1377
QY 1363 CCAGCGCGTGCCTTCTTACAGGCTGCTCACTGACACATGAGCAATCTTCCCTTCAACGA 1422
DB 1378 CCAGCGCGTGCCTTCTTACAGGCTGCTGCTCACTGACACATGAGCAATCTTCCCTTCAACGA 1437
QY 1423 TTGCGTGAACAAGTGTGATCTGTGTGAGAGAGGCAAGTGAACGCGCAAGTGTGGA 1482
DB 1438 TTGCGTGAACAAGTGTGATCTGTGTGAGAGAGGCAAGTGAACGCGCAAGTGTGGA 1497
QY 1483 GTCCGCAAGGCGCATTTCCGCGGCGGACAGAGTGCCTGTGACCAAAAGTCAAGTGCCTC 1542
DB 1498 GTCCGCAAGGCGCATTTCCGCGGCGGACAGAGTGCCTGTGACCAAAAGTCAAGTGCCTC 1557
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DB 1558 CGCCCAATCGATCCCAACCCCGGTGATGCTCACTTCAACCAACCAATGTCGCGGTGAT 1617
QY 1603 TGACGAGAAACAGACCACTTTCAGACACACAGACCGGTTGACAGGACCGGATGTTCAATT 1662
DB 1618 TGACGAGAAACAGACCACTTTCAGACACACAGACCGGTTGACAGGACCGGATGTTCAATT 1677
QY 1663 TGAACCTACCCGCGTGTGAGACATGACTTTTGGAAAGTGAACAAAGAGAAAGTCAAGA 1722
DB 1678 TGAACCTACCCGCGTGTGAGACATGACTTTTGGAAAGTGAACAAAGAGAAAGTCAAGA 1737
QY 1723 GTTCTTCGCTGGCGGAGATCACTGACCGAGTGGCGCATGATTCTACGTCAGAAA 1782
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DB 1858 CTGCGCCCTCAGTGGCGGATCATGAGTCAAGCGGGAAGGAGCTCGGAGGACTTTGC 1917
QY 1903 CGACAGGTACCAAAACAATGTTCTGTCACGCGGCGATCTTCAGATGCTGTTTCCCTG 1962
DB 1918 CGACAGGTACCAAAACAATGTTCTGTCACGCGGCGATCTTCAGATGCTGTTTCCCTG 1977
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QY 1963 CAAAACATGCGAGATGATGATCAGAAATTTCAACATTTGCTTACGACGGGACCAAGAGA 2022  
DB 1978 CAAGACATGCGAGAGATGATGATCAGAAATTTCAACATTTGCTTACGACGGGACCAAGAGA 2037  
QY 2023 CTGTTCAAGATGTTTTCCCGGCGGTGTCAGAAATCTTCAACCGGTGCTCAGAAAAGAGACGTA 2082  
DB 2038 CTGTTCAAGATGTTTTCCCGGCGGTGTCAGAAATCTTCAACCGGTGCTCAGAAAAGAGACGTA 2097  
QY 2083 TTGGAAATCTGTCGATTCATTCATCTGTCGGGGCGGGCTCCGAGATTTGCTTGCGGC 2142  
DB 2098 TTGGAAATCTGTCGATTCATTCATCTGTCGGGGCGGGCTCCGAGATTTGCTTGCGGC 2157  
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DB 2338 AGGACGACGCGCGGGGTCTGCTGCTTCTGCTACAAATGATCCTCGAACCTTTCACACGAC 2397  
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DB 2398 TCGACAAAGGGGAGCCGCTCAACCGCGGCGGACGCGCCCTCGAGGACGACAAAGGCTT 2457  
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DB 2938 TCATACCAACCAAGCAACCGGACCTTGGCCACTTATTAACAACCTCTTAACAGC 2997  
QY 2983 AAATCTCAGTGTTCACAGGGGGCGACAGCAACCACTACTTGGCTACAGCAACC 3042  
DB 2998 AAATCTCAGTGTTCACAGGGGGCGACAGCAACCACTACTTGGCTACAGCAACC 3057

QY 3043 CTTGGGGGATATTTGATTTCAACAGATTCACACTGCCATTTCTGACACGATGCTGGACG 3102  
DB 3058 CTTGGGGGATATTTGATTTCAACAGATTCACACTGCCATTTCTGACACGATGCTGGACG 3117  
QY 3103 GACTCATCAACCAATTTGGGATTTCCGGCCCAAGAGCTCAACTTAAGCTTTCAACA 3162  
DB 3118 GACTCATCAACCAATTTGGGATTTCCGGCCCAAGAGCTCAACTTAAGCTTTCAACA 3177  
QY 3163 TCCAAATCAAGAGGATGACGACGAATGATGGCGCTCACGACATCGCTTAATACCTTACA 3222  
DB 3178 TCCAAATCAAGAGGATGACGACGAATGATGGCGCTCACGACATCGCTTAATACCTTACA 3237  
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DB 3238 GCAAGGTTCAAGCTTTGTCGAACTTCGAGATTCAGAGTTCCGTAAGTCTCGGCTTGGC 3297  
QY 3283 ACCAGGCTGCTCCCTCCGTTCCCGGCGGACGTTTATGATTTCCGCAATAGGCTAAC 3342  
DB 3298 ACCAGGCTGCTCCCTCCGTTCCCGGCGGACGTTTATGATTTCCGCAATAGGCTAAC 3357  
QY 3343 TAAAGCTCAACAAATGGCAGGCGAGGTCAGGCTCATCTTTTACTGCTGGAATATT 3402  
DB 3358 TAAAGCTCAACAAATGGCAGGCGAGGTCAGGCTCATCTTTTACTGCTGGAATATT 3417  
QY 3403 TCCCATGCAAGATGCTGAGAACGGGCAATTAATTTTACCTTACCTTACCTTCAAGACG 3462  
DB 3418 TCCCATGCAAGATGCTGAGAACGGGCAATTAATTTTACCTTACCTTACCTTCAAGACG 3477  
QY 3463 TGCCTTTTCCACAGAGCTTAAGCCGACAGCCAGAGCTTGGACCGGCTGATGTAATCTCTCA 3522  
DB 3478 TGCCTTTTCCACAGAGCTTAAGCCGACAGCCAGAGCTTGGACCGGCTGATGTAATCTCTCA 3537  
QY 3523 TCGACCGATGCTGATTTTACCTGAAACGAATCTCAATCTGATCCGGAAGTCCCAAAACA 3582  
DB 3538 TCGACCGATGCTGATTTTACCTGAAACGAATCTCAATCTGATCCGGAAGTCCCAAAACA 3597  
QY 3583 AGGACTTGTGTTAGCGGCTGCTTCAAGCTGGCATGCTGTTTCAAGCCCAAAACTGGC 3642  
DB 3598 AGGACTTGTGTTAGCGGCTGCTTCAAGCTGGCATGCTGTTTCAAGCCCAAAACTGGC 3657  
QY 3643 TACTGGAACCTGTTACCGGACAGCGGCTTTCTAAACAAAACGAAACAAACAA 3702  
DB 3658 TACTGGAACCTGTTATCCGACAGCGGCTTTCTAAACAAAACGAAACAAACAA 3717  
QY 3703 GCAACTTACCTGGACTGCTGCTTCAAAATATTAACCTTAATGGCGGATTTATATCA 3762  
DB 3718 GCAACTTACCTGGACTGCTGCTTCAAAATATTAACCTTAATGGCGGATTTATATCA 3777  
QY 3763 ACCCTGGACTGCTAGTGGCTTCAACAAAGACGACAAAGCAAGTTCTTCCATGAGCG 3822  
DB 3778 ACCCTGGACTGCTAGTGGCTTCAACAAAGACGACAAAGCAAGTTCTTCCATGAGCG 3837  
QY 3823 GTGTCATGATTTTGGAAAGAGAGCGCCGAGCTTCAACACTGCAATGGCAATGTCA 3882  
DB 3838 GTGTCATGATTTTGGAAAGAGAGCGCCGAGCTTCAACACTGCAATGGCAATGTCA 3897  
QY 3883 TGATCAAGACGAAGAGAAATTAAGCCACTTAACCTGTGGCCACCGAAGATTTGGGA 3942  
DB 3898 TGATCAAGACGAAGAGAAATTAAGCCACTTAACCTGTGGCCACCGAAGATTTGGGA 3957  
QY 3943 CTGTGGAGTCAATCTTCAAGAGCAGACAGACCTGTGACCCGAGATGTGCATGTTA 4002  
DB 3958 CTGTGGAGTCAATCTTCAAGAGCAGACAGACCTGTGACCCGAGATGTGCATGTTA 4017  
QY 4003 TGGAGGCTTAACTTGGAAATGTTGGGCAACAGAGCGTAACTCTGACAGGCTTAAATT 4062  
DB 4018 TGGAGGATTAACCTGGATGTTGGGCAACAGAGCGTAACTCTGACAGGCTTAAATT 4077  
QY 4063 GGGCAAAATTTCTTCAACAGGATGGAACATTTACCGCTCTCTTCAATGGGCGCTTTG 4122  
DB 4078 GGGCAAAATTTCTTCAACAGGATGGAACATTTACCGCTCTCTTCAATGGGCGCTTTG 4137  
QY 4123 GACTTAAGACCCGCTCTCAAGTCTCATCAAAAAACGCGCTGTTCTTGGCAATCTTC 4182



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Db 4138 GACTCAGAAACCGGCTCCTCAGATCCTCATCAAAACAGCGCTGTCTCGGAATCCGC 4197
Qy 4183 CGGACAGTTTGGCTACAAAGTTTGTCTTATCATCCCAAGTATTCAGAGACAG 4242
Db 4198 CGGCGAGTTTCACTACAAAGTTTGTCTTATCATCAACCAATCTCCAGAGACAG 4257
Qy 4243 TGAGCGTGAATTAATGAGAGCTGACAGAAAGAAACAGAAAGCTGGAATCCGAG 4302
Db 4258 TGAAGTGTGAATTAATGAGAGCTGACAGAAAGAAACAGAGCGCTGGAATCCGAG 4317
Qy 4303 TGACATTAATCACTAATGCAAAATCTGCCAAGTTGATTCATCTGACAAACAATG 4362
Db 4318 TGACATTAATCACTAATGCAAAATCTGCCAAGTTGATTCATCTGACAAACAATG 4377
Qy 4383 GACTTATTAATCACTGCTGCGCCCATTTGGACACCCGTTACCTCCCTCTGTAATGT 4422
Db 4378 GACTTATTAATCACTGCTGCGCCCATTTGGACACCCGTTACCTCCCTCTGTAATGT 4437
Qy 4423 GTGTTAATCAATTAACCGGTTAATCGTGTGAGTTGAACCTTGTGATGCTTATTA 4482
Db 4438 GTGTTAATCAATTAACCGGTTAATCGTGTGAGTTGAACCTTGTGATGCTTATTA 4497
Qy 4483 TCTTATCTGTGACCAATGCAACCGGTTACACATTAACTGCTTAACTTGGCTTCCGA-- 4540
Db 4498 TCTTATCTGTGACCAATGCAACCGGTTACACATTAACTGCTTAACTTGGCTTCCGA 4556
Qy 4541 -----ATACCCCTAGTATGAGTTGAGTTGCCACTCCCTCTATGCGGCG 4581
Db 4557 AAGAATTACATCGATCGGGTTACCCCTAGTATGAGTTGCCACTCCCTCTATGCGGCG 4616
Qy 4582 TCGCTCGCTCGGTGGGGCGGACAGAGCTCTGCGGAGCCTTGGTGGCGCA 4641
Db 4617 TCGCTCGCTCGGTGGGGCGGACAGAGCTCTGCGGAGCCTTGGTGGCGCA 4676
Qy 4642 GGGCCACCGAGCGAGCGAGCGGATAGAGGAGTGGCCAA 4683
Db 4677 GGGCCACCGAGCGAGCGAGCGGATAGAGGAGTGGCCAA 4718

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RESULT 6
ADL3984 standard; DNA; 4718 BP.
XX ADL3984;
AC ADL3984;
XX 06-MAY-2004 (first entry)
DT 06-MAY-2004 (first entry)
XX Adeno-associated virus serotype 1 complete DNA.
DE Adeno-associated virus serotype 1 complete DNA.
XX ss; cytosolic; neuroprotective; antiinflammatory; gene therapy;
KW expression construct; adeno-associated virus;
KW integration efficiency element; inverted terminal repeat; integration;
KW chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma;
KW retinoblastoma; inflammatory disease; arthritis;
KW neurodegenerative disease.
XX Adeno-associated virus 1.
OS Adeno-associated virus 1.
XX WO2003087334-A2.
XX 23-OCT-2003.
PD 09-APR-2003; 2003WO-US011191.
PF 09-APR-2003; 2003WO-US011191.
XX 09-APR-2002; 2002US-0371044P.
PR (CORR ) CORNELL RES FOUND INC.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Falck-Pedersen BS, Philipott N;
XX WPI; 2003-833723/77.
XX

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PT New expression construct comprising a nucleic acid sequence encoding an  
PT adeno-associated virus integration efficiency element; useful for  
PT treating cancer e.g. lung cancer or colon cancer or inflammatory disease  
PT e.g. arthritis.

PS Disclosure; SEQ ID NO 3; 62bp; English.

XX

CC The invention relates to an expression construct comprising a nucleic  
CC acid sequence encoding an adeno-associated virus integration efficiency  
CC element (AAV IRE), which is devoid of AAV inverted terminal repeats (AAV  
CC ITRs) and site-specifically integrates into a host cell chromosome when  
CC provided to the host cell in conjunction with an AAV Rep protein. The  
CC expression construct can be used as a therapeutic factor for treating a  
CC mammal for a pathologic state which is cancer, including lung cancer,  
CC colon cancer, renal cancer, anal cancer, bile duct cancer, bladder  
CC cancer, bone cancer, brain cancer, spinal chord cancer, breast cancer,  
CC cervical cancer, lymphoma, endometrial cancer, esophageal cancer,  
CC gallbladder cancer, gastrointestinal cancer, laryngeal cancer, leukemia,  
CC liver cancer, multiple myeloma, neuroblastoma, ovarian cancer, pancreatic  
CC cancer, prostatic cancer, retinoblastoma, skin cancer, stomach cancer,  
CC testicular cancer, thymus cancer or thyroid cancer. Other pathologic  
CC states include inflammatory disease (arthritis), neurodegenerative  
CC disease, a disease of an organ attributed to the presence of increased or  
CC decreased level of a particular gene product(s). This sequence  
CC corresponds to the AAV serotype 1 complete DNA including the IRE  
CC sequence.

SO Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Query Match 90.8%; Score 4253.2; DB 10; Length 4718;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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Qy 1 TTGGCCACTCCCTCTCTGCGGCTTGGCTGCTCACTGAGCCGCGGACCAAGTGGCC 60
Db 1 TTGGCCACTCCCTCTCTGCGGCTTGGCTGCTCACTGAGCCGCGGACCAAGTGGCC 60
Qy 61 CGAGCCCGGGGCTTGGCGCGGCGGCTCACTGAGCGAGCGAGCGCGAGAGGAGATG 120
Db 61 AGACGCGAGAGCTCTGCTCTCCGCGCCACCGAGCGAGCGAGCGAGAGGAGATG 120
Qy 121 GCCAATCTCATCTAGAGGT-----TCTGAGAGGGGTGAGTCTGA 163
Db 121 GGCAACTCATCTAGAGGTGATTCGGAACCGGCTCCCAAGCTGCGCGTCAAGGCTGA 180
Qy 164 CGTGAATTAATCTATGAGGTGTTAGAGGTCTGTATTAAGAGTCACTGAGTG--TTTGGC 222
Db 181 CGTAAATTAATCTATGAGGTGTTAGAGGTCTGTATTAAGAGTCACTGAGTGCTTTTGGC 237
Qy 223 GACATTTTGGAGCAACCAATGAGTCAAGCTGCTATTTAAAGCCGAGAGAGCAACGAGGT 282
Db 238 GACATTTTGGAGCAACCAATGAGTCAAGCTGCTATTTAAAGCCGAGAGAGCAACGAGGT 297
Qy 283 CTTCATTTTGAAGCGGAGGTTTGAACGCGAGCGCATGCGGGGTTTACGAGATTGT 342
Db 298 CTTCATTTTGAAGCGGAGGTTTGAACGCGAGCGCATGCGGGGTTTACGAGATTGT 357
Qy 343 GATTAGGTCCCGACGCACTTGAACGAGCATCTGCGCGGCAATTTCTGACACTTTTGAA 402
Db 358 GATCAAGGTGCGAGCGCACTGAGAGCACTGCGGGCAATTTCTGACTGTTTGTGAG 417
Qy 403 CTGGGTGCGGAGAGAAAGAGTGGAGTTGGCCGCGAATTTGACATGATCTGAATCTGAT 462
Db 418 CTGGGTGCGGAGAGAAAGAGTGGAGTGGCCCGGAGTTTGAACATGATCTGAATCTGAT 477
Qy 463 TGACGAGCAACCTCTGACCGTGGCCGAGAAAGCTGACGCGACTCTGCTGCTCACTGGCG 522
Db 478 TGACGAGCAACCTCTGACCGTGGCCGAGAAAGCTGACGCGACTCTGCTGCTCACTGGCG 537
Qy 523 CCGCGTGAATAGGCCCCCGAGGCGCTCTTTTGTTCAGTTGCAAGAAAGGCGAGTCTTA 582
Db 538 CCGCGTGAATAGGCCCCCGAGGCGCTCTTTTGTTCAGTTGCAAGAAAGGCGAGTCTTA 597

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QY 583 CTTCCACCTCCATATTTCTGTGAGAGACCGGGGTCAAAATCCATGCTGTGGCCGCTT 642  
Db 598 CTTCCACCTCCATATTTCTGTGAGAGACCGGGGTCAAAATCCATGCTGTGGCCGCTT 657  
QY 643 CTTGAGTCAAGTATGAGCAAGCTGTGTGACCAATCTTACCGGGGATCGAGCCGCT 702  
Db 658 CTTGAGTCAAGTATGAGCAAGCTGTGTGACCAATCTTACCGGGGATCGAGCCGCT 717  
QY 703 GCCCAATCGTTTCCGGGTGACCAAGACGGTATATGCGCGGAGGGGGGAAACAAGTGT 762  
Db 718 GCCCAATCGTTTCCGGGTGACCAAGACGGTATATGCGCGGAGGGGGGAAACAAGTGT 777  
QY 763 GGAAGAGTGTACATCCCAACTACTCTGCGCAAGACTAGCGCCGAGCTGCACTGGGC 822  
Db 778 GGAAGAGTGTACATCCCAACTACTCTGCGCAAGACTAGCGCCGAGCTGCACTGGGC 837  
QY 823 GTGACATPACATGAGAGATATATAGCGCGTGTATTAACCTGTGCGGAGCCAAACGGCT 882  
Db 838 GTGACATPACATGAGAGATATATAGCGCGTGTATTAACCTGTGCGGAGCCAAACGGCT 897  
QY 883 CGTGGCGACGACCTGACCCGACGTCAGCCAGACCCAGAGAGAGAAACAAGAGATCTTGA 942  
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QY 943 CCCCATTCTGACCGCGCTGTATCCGGTCAAAAACTCCGACGCTTACATGAGACTGGT 1002  
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QY 1003 CGGGTGTGTGTGACCGGGGATTCATCTCGAGAGAGATGTATCCAGAGAGACAGGC 1062  
Db 1018 CGGGTGTGTGTGACCGGGGATTCATCTCGAGAGAGATGTATCCAGAGAGACAGGC 1077  
QY 1063 CTGCGATCTCTCTTCAACGCGCGCTCCAACTCGCGGTGCCAGATCAAGGCGCTGTGGA 1122  
Db 1078 CTGCGATCTCTCTTCAACGCGCGCTCCAACTCGCGGTGCCAGATCAAGGCGCTGTGGA 1137  
QY 1123 CAATGCGGCAAGATCATGAGCGCTGACCAAAATCCGCGCCGACTTACCTGTAGGCCCGC 1182  
Db 1138 CAATGCGGCAAGATCATGAGCGCTGACCAAAATCCGCGCCGACTTACCTGTAGGCCCGC 1197  
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Db 1198 TCCGCGCGGCGACATTTAAACCAACCGCATTTTCCGACTCTGAGACTGAAACGGCTACGA 1257  
QY 1243 CCGTGCCTTACGCGGCGCTCGCTTTCTGCGCTGGGCGCCAGAAAAAGTTCCGAAAAACGCA 1302  
Db 1258 ACCTGCTTACGCGCGCTCGCTTTCTGCGCTGGGCGCCAGAAAAAGTTCCGAAAAACGCA 1317  
QY 1303 CACCATGTGCTGTTTGGGCGGCGCACCAAGGCAAGACCAACATCCGAGAAAGCATGCGC 1362  
Db 1318 CACCATGTGCTGTTTGGGCGGCGCACCAAGGCAAGACCAACATCCGAGAAAGCATGCGC 1377  
QY 1363 CCAGCGCGTCCCTTTCTAGCGCTGCTCAACTGGAACCAATGAGAACTTTCCCTTCAACGA 1422  
Db 1378 CCAGCGCGTCCCTTTCTAGCGCTGCTCAACTGGAACCAATGAGAACTTTCCCTTCAATGA 1437  
QY 1423 TTGCGTGCACAAGATGTGATCTGGTGGAGAGAGGGCAAGATGACGCGCAAGGCTGTGGA 1482  
Db 1438 TTGCGTGCACAAGATGTGATCTGGTGGAGAGAGGGCAAGATGACGCGCAAGGCTGTGGA 1497  
QY 1483 GTCCGCGCAAGGCAATCTTCGCGGCGAGCAAGGTGCGCTGAGCCAAAAGTCAAGTCGTC 1542  
Db 1498 GTCCGCGCAAGGCAATCTTCGCGGCGAGCAAGGTGCGCTGAGCCAAAAGTCAAGTCGTC 1557  
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Db 1558 CGCCCAATTCGATCCCAACCCCGGTGATGTGTCACTTCCAAACCAACATGTGCGCGTGTAT 1617  
QY 1603 TGAAGGAAACAGACCACTTCAGACACACAGACCGCTTGGAGAGACCGGATGTTCAAAAT 1662  
Db 1618 TGAAGGAAACAGACCACTTCAGACACACAGACCGCTTGGAGAGACCGGATGTTCAAAAT 1677  
QY 1663 TGAACCTCACCGCGCTGTGAGACATGACTTTTGGCAAGGTGACAAAGCAGAAAGTCAAGA 1722

Db 1678 TGAACCTCACCGCGCTGTGAGACATGACTTTGGCAAGGTGACAAAGCAGAAAGTCAAGA 1737  
QY 1723 GTTCTTCCGCTGGGCGGAGATCACCGTACCGAGGTGGCCCAAGATTCTACGTCAGAAA 1782  
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QY 1783 GGGTGAAGCAACAACAGACCCGCCCGGATGACGCGGATTAAGCGAGCCCAAGCGGGC 1842  
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QY 1843 CTGCCCCCTCAGTGGCGGATTCATGACGTGACAGCGGAAAGAGCTCCGTTGACTTTGC 1902  
Db 1858 CTGCCCCCTCAGTGGCGGATTCATGACGTGACAGCGGAAAGAGCTCCGTTGACTTTGC 1917  
QY 1903 CGACAGTACCAAAAACAATGTTCTGCTCAGCGGGGCAATGCTTCAATGCTGTTCCCTG 1962  
Db 1918 CGACAGTACCAAAAACAATGTTCTGCTCAGCGGGGCAATGCTTCAATGCTGTTCCCTG 1977  
QY 1963 CAAAACATGCGAGAGATGATCAAGATTTCAACATTTGCTTACGCAACGCGGACAGAGA 2022  
Db 1978 CAAACATGCGAGAGATGATCAAGATTTCAACATTTGCTTACGCAACGCGGACAGAGA 2037  
QY 2023 CTGTTCAGAATGTTTCCCGCGCTGTCAAACTTCAAACCGGTGTCAAAAAGAGAGTA 2082  
Db 2038 CTGTTCAGAATGTTTCCCGCGCTGTCAAACTTCAAACCGGTGTCAAAAAGAGAGTA 2097  
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QY 2143 CTGCGATCTGATCAACCTGATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAC 2202  
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QY 2203 CAGGTATGCTGCCGATGTTATCTTCAGATTGGCTCGAGACCAACTTCTGAGGGCA 2262  
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QY 2263 TTGCGAGTGTGGGACTTGAACCTGGAGCCCGGAAACCAAGCCCAACAGCAAAAGC 2322  
Db 2278 TTGCGAGTGTGGGACTTGAACCTGGAGCCCGGAAACCAAGCCCAACAGCAAAAGC 2337  
QY 2323 AGAGCAGCGGCGGGGCTGTGGCTTCTGTGCTTACAAGTACTTCGACCTTCAACGAGC 2382  
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QY 2383 TCGACAAAGGGAGACCCGCTCAAGCGGCGGATGCAAGCGGCTTCGAGACAGCAAGGCT 2442  
Db 2398 TCGACAAAGGGAGACCCGCTCAAGCGGCGGATGCAAGCGGCTTCGAGACAGCAAGGCT 2457  
QY 2443 ACGACAGCAGCTCAAAAGCGGGTGAACAATCGTACCTGGGTATTAACCAAGCGGACGCG 2502  
Db 2458 ACGACAGCAGCTCAAAAGCGGGTGAACAATCGTACCTGGGTATTAACCAAGCGGACGCG 2517  
QY 2503 AGTTTCAGAGCGCTCTGCAAGAGATACGCTTTTGGGGCAACCTCGGCGAGCAGCT 2562  
Db 2518 AGTTTCAGAGCGCTCTGCAAGAGATACGCTTTTGGGGCAACCTCGGCGAGCAGCT 2577  
QY 2563 TCCAGGCCAAGAGGGGTTCTGAACTTTTGGTCTGTGTTGAGGAAAGTGTCTAAGCGG 2622  
Db 2578 TCCAGGCCAAGAGGGGTTCTGAACTTTTGGTCTGTGTTGAGGAAAGGCTCTAAGCGG 2637  
QY 2623 CTGCTGGAAGAAACGTCGGGTGAGCAGTCGCAACAAGACCAAGACTCTCTCGGGCA 2682  
Db 2638 CTGCTGGAAGAAACGTCGGGTGAGCAGTCGCAACAAGACCAAGACTCTCTCGGGCA 2697  
QY 2683 TTGCGAAGACAGGCAAGCCCGCTTAAAGAAGCTCAATTTTGTGACACTTGGCGACT 2742  
Db 2698 TCGGCAAGACAGGCAAGCCCGCTTAAAGAAGCTCAATTTTGTGACACTTGGCGACT 2757  
QY 2743 CAGAGTCACTCCCGACCCCAACTTCCGAGAACTTCAAGCAACCCCGCTGTGTGG 2802

Db 2758 CAGAGTCAGTCCCGATCCAAACCTCTGAGAACTCCAGAACCCCGCTGCTGTGG 2817  
Qy 2803 GACCTACTCAATGAGCTTCAGGGGGTGGCGACCAATGGCAGACATTAAGAAAGGCGCG 2862  
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Qy 2923 TCATCAACCAACGACACCCGGAACATGGGCTTGGCCCACTTAATAACAACCTCTCAAGC 2982  
Db 2938 TCATCAACCAACGACACCCGGAACATGGGCTTGGCCCACTTAATAACAACCTCTCAAGC 2997  
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Qy 3103 GACTCATCAACAACAATTGGGGATTTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACA 3162  
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Qy 3703 GCAACTTAACTGACCTGAGTGGTCTTCAAAATTAATTAATTAATGAGGCTGTAATCTATCA 3762  
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Qy 3763 ACCCTGGCAGCTGTAATGAGCTCACAAAGACGACAAAGCAAGTCTTTTCCCATGAGCG 3822  
Db 3778 ACCCTGGCAGCTGTAATGAGCTCACAAAGACGACAAAGCAAGTCTTTTCCCATGAGCG 3837  
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Qy 3883 TGATCAGACGAGAGGAGAAATCAAAAGCCATTAACCCCGTGGCCACCGAAAGATTTGGGA 3942  
Db 3898 TGATTAACAGAGAGAGAGAAATTAAGCCATTAACCTGTGGCCACCGAAAGATTTGGGA 3957  
Qy 3943 CTGTGGCAGTCAATCTCCAGAGCAGACAGACACCTTCGACACCGAGATGTCATGTTA 4002  
Db 3958 CCGTGGCAGTCAATTTCCAGAGCAGACAGACAGACCTTCGACACCGAGATGTCATGTTA 4017  
Qy 4003 TGGAGCCTTAACCTGGAATGAGTGTGGCAAGACAGAGCGTATTAATCTGAGGAGTCTATTT 4062  
Db 4018 TGGAGCCTTAACCTGGAATGAGTGTGGCAAGATGAGAGCGTATTAATCTGAGGAGTCTATTT 4077  
Qy 4063 GGGCCCAAAATTCCTACACGAGATGAGACCTTTACCCGCTCTCTCAATGGGCGGCTTTG 4122  
Db 4078 GGGCCCAAAATTCCTACACGAGATGAGACCTTTACCCGCTCTCTCAATGGGCGGCTTTG 4137  
Qy 4123 GACTTAAGCACCCGCTCTCAGATCCATCAAAACACGCGCTGTTCTCGAATCTTC 4182  
Db 4138 GACTTAAGCACCCGCTCTCAGATCCATCAAAACACGCGCTGTTCTCGAATCTTC 4197  
Qy 4183 CGGCAAGTCTTTCGAGTCAAAAGTTTGGCTTCAATCAACCCAGATTTCAACAGACAG 4242  
Db 4198 CGGCAAGTCTTTCGAGTCAAAAGTTTGGCTTCAATCAACCCAGATTTCAACAGACAG 4257  
Qy 4243 TGAGCTGGAGATTAATGAGAGCTGCGAAGAAAGAAACAGAAACGCTGGAATCCGAAAG 4302  
Db 4258 TGAGCTGGAGATTAATGAGAGCTGCGAAGAAAGAAACAGAAACGCTGGAATCCGAAAG 4317  
Qy 4303 TGCAGTATACATCTTAATCAATCTGCAACAGTGTGATTTCACTGTGGACAAACAATG 4362  
Db 4318 TGCAGTATACATCTTAATCAATCTGCAACAGTGTGATTTCACTGTGGACAAACAATG 4377  
Qy 4363 GACTTATACATGAGCTTGTGCGCCCATGAGCAACCGGTTACCTGACCCGCTGTAATTTG 4422  
Db 4378 GACTTATACATGAGCTTGTGCGCCCATGAGCAACCGGTTACCTGACCCGCTGTAATTTG 4437  
Qy 4423 GTTATTAATCAATAACCGGTTAATGCTGTCAATGTAATTTGATTCATATCTTATTA 4482  
Db 4438 GTTATTAATCAATAACCGGTTAATGCTGTCAATGTAATTTGATTCATATCTTATTA 4497  
Qy 4483 TCTTATCTGATCAGCATAGCAACCGGTTAATGCTGTCAATGTAATTTGATTCATATCTTATTA 4540  
Db 4498 TCTTATCTGATCAGCATAGCAACCGGTTAATGCTGTCAATGTAATTTGATTCATATCTTATTA 4556  
Qy 4541 -----ATACCCCTAATGATGAGTGGCCACTCCCTTATGCGCGC 4581  
Db 4557 AAAGACTTAAGTCAATCGGTTTACCCCTAATGATGAGTGGCCACTCCCTTATGCGCGC 4616  
Qy 4582 TCGCTCGCTGGTGGGGCCGCGAGACAGACTTGCCTGTGCGACCTTTGGTCCGCA 4641  
Db 4617 TCGCTCGCTGGTGGGGCCGCGAGACAGACTTGCCTGTGCGACCTTTGGTCCGCA 4676  
Qy 4642 GGCCCAACGAGCGAGCGGCGCATAGAGGGAGTGGCCAA 4683  
Db 4677 GGCCCAACGAGCGAGCGGCGCATAGAGGGAGTGGCCAA 4718

RESULT 7  
ADG39758  
ID ADG39758 standard; DNA; 4718 BP.  
XX  
AC ADG39758;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE AAV-1 genomic DNA sequence SHQ ID NO:20.  
XX  
KM parvovirus; rep; cap; DNA binding domain; capsid interacting domain;  
KM recombinant hybrid parvovirus particle;  
KM recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;  
KM gene; ds.  
XX

OS Adeno-associated virus 1.  
XX MO2003104392-A2.  
XX 18-DEC-2003.  
XX 02-DEC-2002; 2002MO-US038423.  
XX 18-DEC-2001; 2001US-0341919P.  
XX (UTNC-) UNIV NORTH CAROLINA.  
XX Samuleki RJ, Rabinowitz JE;  
XX WPI; 2004-062324/06.  
XX  
XX New polynucleotides comprising parvovirus rep coding sequences and  
PT parvovirus cap coding sequences, useful in producing higher stocks of  
PT hybrid parvovirus vectors for delivering therapeutic nucleic acids to a  
PT subject.  
XX  
XX Disclosure; SEQ ID NO 20; 115pp; English.  
XX  
XX The present invention describes a polynucleotide (I), comprising  
CC parvovirus rep coding sequences and parvovirus cap coding sequences. The  
CC rep coding sequences encodes a DNA binding domain from a first  
CC parvovirus, and a capsid interacting domain from a parvovirus different  
CC from the first parvovirus. The cap coding sequence comprises sequences  
CC from the different parvovirus. Also described: (1) a vector comprising  
CC (1); (2) a cell comprising (1), or parvovirus rep coding sequences and  
CC parvovirus cap coding sequences, where the rep coding sequences encode a  
CC DNA binding domain from a first parvovirus and a capsid interacting  
CC domain from a parvovirus different from the first parvovirus, the cap  
CC coding sequences comprise sequences from the different parvovirus, and  
CC the rep coding sequences are stably integrated into the genome of the  
CC cell; and (3) producing a recombinant hybrid parvovirus particle or adeno  
CC associated virus (rAAV) particle. (1) can be used in vaccines, and in  
CC gene therapy. The polynucleotide (I) can be used in producing higher  
CC stocks of hybrid parvoviruses or parvovirus vectors, which may be used in  
CC the delivery of nucleic acids having biological effect to treat or  
CC ameliorate the symptoms associated with any disorder related to gene  
CC expression. The polynucleotide may be used to produce a parvovirus vector  
CC to express an immunogenic polypeptide in a subject, e.g. for vaccination.  
CC The parvovirus vector may also be used to provide an antisense nucleic  
CC acid to a cell in vitro or in vivo, or in diagnostic and screening  
CC methods. The present sequence is used in the exemplification of the  
CC present invention.  
XX  
XX Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;  
SQ  
Query Match 90.8%; Score 4253.2; DB 12; Length 4718;  
Best Local Similarity 94.7%; Pred. No. 0;  
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;  
QY 1 TTGGCCACTCCCTCTGCGGCTGCTGCTCACTGAGCGCGGCGAACCAAGGTGCGC 60  
DB 1 TTGGCCACTCCCTCTGCGGCTGCTGCTCACTGAGCGCGGCGAACCAAGGTGCGC 60  
QY 61 CGAGCGCCCGGCGCTTTGCCCGGCGCTCACTGAGCGGCGGCGGAGAGAGAGT 120  
DB 61 AGAGCGGAGAGCTGCTGCTGCTGCGGCCCAACGAGCGAGCGCGGAGAGAGAGT 120  
QY 121 GCGAAGCTCATCACTAGAGGT-----TCTGAGAGGGGTGAGTGGCGA 163  
DB 121 GCGAAGCTCATCACTAGAGGTATCGCGAAGCGCTCCCAAGCTGCGCGTCAAGCGCTGA 180  
QY 164 CGTGAATTACGTCAATAGGGTTAGGAGGTCTGTATTAAGATCACTGAGTGT-TTTTGC 222  
DB 181 CGTAAATTAATCAATAGG---GAGTGTCTGTATTAATGCTGACGTAAGTGTGCTTTTGC 237  
QY 223 GACATTTTGGCAGACACATGTGTCACTGCTGGGTATTTAAGCCGAGTGAAGACGAGGCT 282  
DB 238 GACATTTTGGCAGACACATGTGTCACTTAAAGGTATATATGCGAGTGAAGACGAGCAT 297

QY 283 CTCATTTTGAAGGGAGGTTTGAACGCGCAGCGCATGCGCGGCTTTTACGAGATTGT 342  
DB 298 CTCATTTTGAAGCGCAAAATTTGAACGAGACGAGCATTCGCGGCTTACGAGATCGT 357  
QY 343 GATTAAAGTCCCGACGCACTTGAAGCATGTGCCCGGATTTTGAACGCTTTGTGA 402  
DB 358 GATCAAGTCCGAGCGCACTTGAACGAGCATGTGCCCGGATTTTGAACGCTTTGTGA 417  
QY 403 CTGGGTGCGCGAAGAAATGGAGTTGGCCGCGAATTCAGATGGATGTGATCGAT 462  
DB 418 CTGGGTGCGCGAAGAAATGGAGTTGGCCGCGAATTCAGATGGATGTGATCGAT 477  
QY 463 TGAAGAGCACCCCTGACCGTGGCCGAGAAAGTGCAGCGGCACTTCGTGTCCACTGCGC 522  
DB 478 TGAAGAGCACCCCTGACCGTGGCCGAGAAAGTGCAGCGGCACTTCGTGTCCAAATGGCG 537  
QY 523 CCGGTGAGTAAAGGCCCGGAGGCCCTCTTCTTTGTTCACTTGAAGAGGCGAGTCTTA 562  
DB 538 CCGGTGAGTAAAGGCCCGGAGGCCCTCTTCTTTGTTCACTTGAAGAGGCGAGTCTTA 597  
QY 583 CTTCCACCTCAATTTCTGTGAGACCAAGGGGTCAATTCATGCTGTGGCCGCTT 642  
DB 598 CTTCCACCTCAATTTCTGTGAGACCAAGGGGTCAATTCATGCTGTGGCCGCTT 657  
QY 643 CTGAGTCAATTAAGCAGCAAGCTGTGACAGACCATCTACCGCGGATCGAGCCGACCT 702  
DB 658 CTGAGTCAATTAAGCAGCAAGCTGTGACAGACCATCTACCGCGGATCGAGCCGACCT 717  
QY 703 GCCCACTGTTGCGGCTGACCAAGACGCGTAATGCGCCGAGGGGGCAAGTGTGT 762  
DB 718 GCCCACTGTTGCGGCTGACCAAGACGCGTAATGCGCGGAGGGGGCAAGTGTGT 777  
QY 763 GAGCAGTGTATATCCCAATACCTCTGCCCAAGACTCAGCCGAGCTGAGTGGGC 822  
DB 778 GAGCAGTGTATATCCCAATACCTCTGCCCAAGACTCAGCCGAGCTGAGTGGGC 837  
QY 823 GTGACATTAATGAGAGATATTAAGCGGCTTTTAACTTGGCCGAGCGCAACGCGCT 882  
DB 838 GTGACATTAATGAGAGATATTAAGCGGCTTTTAACTTGGCCGAGCGCAACGCGCT 897  
QY 883 GTGCGCGACGACCTGACCGTCAAGCCAGACCCAGAGCAGAACAGGAATCTGAA 942  
DB 898 GTGCGCGACGACCTGACCGTCAAGCCAGACCCAGAGCAGAACAGGAATCTGAA 957  
QY 943 CCCCAATTGAGCGCGCTCATTCGCGTCAAAAACCTCCGACGCTACATGAGCGTGT 1002  
DB 958 CCCCAATTGAGCGCGCTCATTCGCGTCAAAAACCTCCGCGGCTACATGAGCGTGT 1017  
QY 1003 CGGCTGCTGTGAGACCGGGGCAATCACTCCGAGAAAGCACTGATCCAGAGGACAGGC 1062  
DB 1018 CGGCTGCTGTGAGACCGGGGCAATCACTCCGAGAAAGCACTGATCCAGAGGACAGGC 1077  
QY 1063 CTGTACATCTCTTCAAGCGCGCTTCAACTGCGGCTCCCAATCAAGCGCGCTTGA 1122  
DB 1078 CTGTACATCTCTTCAAGCGCGCTTCAACTGCGGCTCCCAATCAAGCGCGCTTGA 1137  
QY 1123 CAATGCGGCAAGATCAATGCGGCTGACCAATCCGCGCCGACATCTCGGTAGGCCCGC 1182  
DB 1138 CAATGCGGCAAGATCAATGCGGCTGACCAATCCGCGCCGACATCTCGGTAGGCCCGC 1197  
QY 1183 TCGCGCCGCGCAATTAACCAACCGCATTTACCGCATCTGAGCTGAACCGCTTACGA 1242  
DB 1198 TCGCGCCGCGCAATTAACCAACCGCATCTGAGCTGAGCTGAACCGCTTACGA 1257  
QY 1243 CCTGTCTACGCGGCTCGCTCTTTTCTGCGCTGCGGCCAGAAAAAGTTCCGAAAAACGCA 1302  
DB 1258 ACCTGTCTACGCGGCTCGCTCTTTTCTGCGCTGCGGCCAGAAAAAGTTCCGAAAAACGCA 1317  
QY 1303 CACCATCTGCTGTTGGGCGCGGCAACCAAGGCAAGAACATGCGGAGGCAAGCATGCG 1362  
DB 1318 CACCATCTGCTGTTGGGCGCGGCAACCAAGGCAAGAACATGCGGAGGCAAGCATGCG 1377

QY 1363 CCACGCGTGCCTTCTACGCGTGCATCAATGACCAATGAGAACTTTCCCTTCAAGA 1422  
| | | | |  
Db 1378 CCACGCGTGCCTTCTACGCGTGCATCAATGACCAATGAGAACTTTCCCTTCAAGA 1437  
| | | | |  
QY 1423 TTGCGTCGACAAAGATGATGATCTGGTGGAGAGGAGCAAGATGACGGCCAAAGTGTGGA 1482  
| | | | |  
Db 1438 TTGCGTCGACAAAGATGATGATCTGGTGGAGAGGAGCAAGATGACGGCCAAAGTGTGGA 1497  
| | | | |  
QY 1483 GTCCGCGCAAGGCGCAATTCCTGGCGGAGACAGAGTGGCGGTGACCAAAATGCAATCGTC 1542  
| | | | |  
Db 1498 GTCCGCGCAAGGCGCAATTCCTGGCGGAGACAGAGTGGCGGTGACCAAAATGCAATCGTC 1557  
| | | | |  
QY 1543 CGCCAGATTCGATCCCAACCCCGATGATGATCACTTCCAAACCAATGATGGCGCGTAT 1602  
| | | | |  
Db 1558 CGCCAGATTCGATCCCAACCCCGATGATGATCACTTCCAAACCAATGATGGCGCGTAT 1617  
| | | | |  
QY 1603 TGACGGGAACAGCACACCTTTCAGACACACAGACCGTTTGACAGACCGGATGTTCAATT 1662  
| | | | |  
Db 1618 TGACGGGAACAGCACACCTTTCAGACACACAGACCGTTTGACAGACCGGATGTTCAATT 1677  
| | | | |  
QY 1663 TGAATCTACCCGCGCTCTGAGACATGACTTTGGCAAGTGAAGCAAGAGTCAAGA 1722  
| | | | |  
Db 1678 TGAATCTACCCGCGCTCTGAGACATGACTTTGGCAAGTGAAGCAAGAGTCAAGA 1737  
| | | | |  
QY 1723 GTTCTTCGCTGGGCGAGATCAGTGAACGAGGTGGCGCATGAGTTCTACGTCAAGA 1782  
| | | | |  
Db 1738 GTTCTTCGCTGGGCGAGATCAGTGAACGAGGTGGCGCATGAGTTCTACGTCAAGA 1797  
| | | | |  
QY 1783 GGGTGGAGCCAAACAAGACCCGCCAGATGACCGGATAAAGCGAGCCCAAGCGGCG 1842  
| | | | |  
Db 1798 GGGTGGAGCCAAACAAGACCCGCCAGATGACCGGATAAAGCGAGCCCAAGCGGCG 1857  
| | | | |  
QY 1843 CTGCGCTCAGTCCGCGATCCATGCACTGACAGCGGGAAGAGCTCCGCTGAGCTTTGC 1902  
| | | | |  
Db 1858 CTGCGCTCAGTCCGCGATCCATGCACTGACAGCGGGAAGAGCTCCGCTGAGCTTTGC 1917  
| | | | |  
QY 1903 CGACAGATCAACAAATGTTCTGCTCAAGCGGCGCATGCTTCAGATGCTGTTCCCTG 1962  
| | | | |  
Db 1918 CGACAGATCAACAAATGTTCTGCTCAAGCGGCGCATGCTTCAGATGCTGTTCCCTG 1977  
| | | | |  
QY 1963 CAAACATGCAAGAGATGAATCAAGATTTTCAACATTTGCTTCAAGCAAGGACCAAGA 2022  
| | | | |  
Db 1978 CAAACATGCAAGAGATGAATGAATTTTCAACATTTGCTTCAAGCAAGGACCAAGA 2037  
| | | | |  
QY 2023 CTGTTCAAGATGTTTCCCGCGCTGCAAGATCTCAACCGGCTGCTCAAGAAAGAGAGTA 2082  
| | | | |  
Db 2038 CTGTTCAAGATGTTTCCCGCGCTGCAAGATCTCAACCGGCTGCTCAAGAAAGAGAGTA 2097  
| | | | |  
QY 2083 TCGGAACTGTGTCATTCATCATCTGCTGGGCGGAGCTCCGAGATTGCTGCGGC 2142  
| | | | |  
Db 2098 TCGGAACTGTGTCATTCATCATCTGCTGGGCGGAGCTCCGAGATTGCTGCGGC 2157  
| | | | |  
QY 2143 CTGCGATCTGATCAACGTGATCTGAGTACTGTTCTGAGCAATTAATGACTTAAC 2202  
| | | | |  
Db 2158 CTGCGATCTGATCAACGTGATCTGAGTACTGTTCTGAGCAATTAATGACTTAAC 2217  
| | | | |  
QY 2203 CAGGATGCTGCGGATGTTATCTTCAAGATGGCTTGAAGACAACTCTCTGAAGGCA 2262  
| | | | |  
Db 2218 CAGGATGCTGCGGATGTTATCTTCAAGATGGCTTGAAGACAACTCTCTGAAGGCA 2277  
| | | | |  
QY 2263 TTCCGCAATGGTGGGACTTGAACCTGAGGCCGGAACCCAAAGCCAAACAGCAAAAGC 2322  
| | | | |  
Db 2278 TTCCGCAATGGTGGGACTTGAACCTGAGGCCGGAACCCAAAGCCAAACAGCAAAAGC 2337  
| | | | |  
QY 2323 AGAGCAGCGGCGGCTGCTGCTTCTGCTCAAGATCACTTCGACCTTTCACAGGAC 2382  
| | | | |  
Db 2338 AGAGCAGCGGCGGCTGCTGCTTCTGCTCAAGATCACTTCGACCTTTCACAGGAC 2397  
| | | | |  
QY 2383 TCGACAAAGGGAGGCGCTGCAACGCGGCGGATGACGCGGCTTCAAGACAGCAAGGCT 2442  
| | | | |  
Db 2398 TCGACAAAGGGAGGCGCTGCAACGCGGCGGATGACGCGGCTTCAAGACAGCAAGGCT 2457  
| | | | |  
QY 2443 ACGACAGCAGCTCAAGCGGAGTGACAACTCGTACCTCGGATTAACACAGCCGAGCGG 2502  
| | | | |

Db 2458 ACGACAGCAGCTCAAGCGGAGTGACAACTCGTACCTCGGATTAACACAGCCGACGCG 2517  
| | | | |  
QY 2503 AGTTCAAGAGCGTCTGACAGAAATACGTTTGGGGGCAACCTCGGCGAGACGCT 2562  
| | | | |  
Db 2518 AGTTCAAGAGCGTCTGACAGAAATACGTTTGGGGGCAACCTCGGCGAGACGCT 2577  
| | | | |  
QY 2563 TCCAGGCGCAAGAGGCTCTGAACTTTGGTCTGGTGAAGGAGTGTGAAGAGC 2622  
| | | | |  
Db 2578 TCCAGGCGCAAGAGGCTCTGAACTTTGGTCTGGTGAAGGAGTGTGAAGAGC 2637  
| | | | |  
QY 2623 CTCTGGAAGAAAGCGTCCGCTAGAGAGTGCACCAAGAGCCAGACTCTCTCGGCA 2682  
| | | | |  
Db 2638 CTCTGGAAGAAAGCGTCCGCTAGAGAGTGCACCAAGAGCCAGACTCTCTCGGCA 2697  
| | | | |  
QY 2683 TTGCAAGACAGGCGCAGACCGCTTAAGAAAGACTCAATTTTGTGACACTGCGACT 2742  
| | | | |  
Db 2698 TTGCAAGACAGGCGCAGACCGCTTAAGAAAGACTCAATTTTGTGACACTGCGACT 2757  
| | | | |  
QY 2743 CAGAGTCAATCCCGACCCCAACCTCTCGGAGAACTTCCAGCAACCCCGCTGCTGG 2802  
| | | | |  
Db 2758 CAGAGTCAATCCCGACCCCAACCTCTCGGAGAACTTCCAGCAACCCCGCTGCTGG 2817  
| | | | |  
QY 2803 GACCTACTAATGAGCTTCAAGCGGCGGACCAATGGCAGACATTAACGAAGCGCG 2862  
| | | | |  
Db 2818 GACCTACTAATGAGCTTCAAGCGGCGGACCAATGGCAGACATTAACGAAGCGCG 2877  
| | | | |  
QY 2863 ACGAGTGGATATGCTCAGAGAAATTTGGCATTTGCGATTCGATGCTGGCGACAGAG 2922  
| | | | |  
Db 2878 ACGAGTGGATATGCTCAGAGAAATTTGGCATTTGCGATTCGATGCTGGCGACAGAG 2937  
| | | | |  
QY 2923 TCAATCAACCAAGCAACCCGAACATGGGCTTTGGCCACTTAACAAACCTTCAAGC 2982  
| | | | |  
Db 2938 TCAATCAACCAAGCAACCCGAACATGGGCTTTGGCCACTTAACAAACCTTCAAGC 2997  
| | | | |  
QY 2983 AAATCTCAAGTCTTCAACGGGGGCGCAGCAACGAACCACTTCCGCTCAAGACCC 3042  
| | | | |  
Db 2998 AAATCTCAAGTCTTCAACGGGGGCGCAGCAACGAACCACTTCCGCTCAAGACCC 3057  
| | | | |  
QY 3043 CTTGGGGATTTTGAATTTCAACAGATTCACCTCCATTTCTCAACAGTACGCGAGC 3102  
| | | | |  
Db 3058 CTTGGGGATTTTGAATTTCAACAGATTCACCTCCATTTCTCAACAGTACGCGAGC 3117  
| | | | |  
QY 3103 GACTCATCAACAAATTTGGGAGATTTCCGGCCAGAGACCTCAAGTCAAGCTTCAACA 3162  
| | | | |  
Db 3118 GACTCATCAACAAATTTGGGAGATTTCCGGCCAGAGACCTCAAGTCAAGCTTCAACA 3177  
| | | | |  
QY 3163 TCCAAATCAAGGAGGTCAAGCAAGATGAGCGTCAAGACCATGCTAATTAACCTTACA 3222  
| | | | |  
Db 3178 TCCAAATCAAGGAGGTCAAGCAAGATGAGCGTCAAGACCATGCTAATTAACCTTACA 3237  
| | | | |  
QY 3223 GCACGGTTCAAGTCTTGTGAGACTCGAGATCAAGTTCGCGTACGTCCTCGGCTCTGCGC 3282  
| | | | |  
Db 3238 GCACGGTTCAAGTCTTGTGAGACTCGAGATCAAGTTCGCGTACGTCCTCGGCTCTGCGC 3297  
| | | | |  
QY 3283 ACAGGCGTGCCTCCCTCCGTTCCCGGCGACGTTTCATGATTTCCGCAAGTACGCGTACC 3342  
| | | | |  
Db 3298 ACAGGCGTGCCTCCCTCCGTTCCCGGCGACGTTTCATGATTTCCGCAAGTACGCGTACC 3357  
| | | | |  
QY 3343 TAAAGCTCAACAAATGGGAGCGAGGAGATGGGAGCGCTATCTTTTACGCTGGAATAT 3402  
| | | | |  
Db 3358 TAAAGCTCAACAAATGGGAGCGAGGAGATGGGAGCGCTATCTTTTACGCTGGAATAT 3417  
| | | | |  
QY 3403 TCCCATGCAAGATCTGAAGAACGGGCAATTAATTTTACCTTCAAGTCAACCTTCAAGAGC 3462  
| | | | |  
Db 3418 TCCCATGCAAGATCTGAAGAACGGGCAATTAATTTTACCTTCAAGTCAACCTTCAAGAGC 3477  
| | | | |  
QY 3463 TGCCTTTCACAGAGCTTACCGGACAGCAGAGGCTGAGACCGGCTGATGAATCTCTCA 3522  
| | | | |  
Db 3478 TGCCTTTCACAGAGCTTACCGGACAGCAGAGGCTGAGACCGGCTGATGAATCTCTCA 3537  
| | | | |  
QY 3523 TCGACAGTACTGTATTTAATCTGAACGAATCTCAATTCAGTCCGGAAGTCCCAAAACA 3582  
| | | | |

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Dh 3538 TCGACCAATACCTGATATTACTGTAACAGAACTCAAAATCAATCCGGAAGTCCCAACAA 3597
Qy 3583 AGGACTTGCTGTTTAAAGCCGTGGTCTCCAGCTGGAGATGTCTGTTACAGCCAAAAACTGGC 3642
Dh 3598 AGGACTTGCTGTTTAAAGCCGTGGTCTCCAGCTGGAGATGTCTGTTACAGCCAAAAACTGGC 3657
Qy 3643 TACCTGGAACCTGTTTAAAGCCGTGGTCTCCAGCTGGAGATGTCTGTTTAAAGCCAAAACTG 3702
Dh 3658 TACCTGGAACCTGTTTAAAGCCGTGGTCTCCAGCTGGAGATGTCTGTTTAAAGCCAAAACTG 3717
Qy 3703 GCAACTTTACTGAGACTGTGTCTTCAAAATATTAACCTTAATGGGCGGTAACTCTATATCA 3762
Dh 3718 GCAATTTTAACTGAGCTGTGTCTTCAAAATATTAACCTTAATGGGCGGTAACTCTATATCA 3777
Qy 3763 ACCCTGGACATGCTATGGCTCTCAACAAGAGCAAAAGACAAGTTCTTCTCCATGGAGCG 3822
Dh 3778 ACCCTGGACATGCTATGGCTCTCAACAAGAGCAAAAGACAAGTTCTTCTCCATGGAGCG 3837
Qy 3823 GTGTCAATGTTTTGGAAGAAGAGCCCGAGCTTCAAAACACTGCATTTGGACAATGTCA 3882
Dh 3838 GTGTCAATGTTTTGGAAGAAGAGCCCGAGCTTCAAAACACTGCATTTGGACAATGTCA 3897
Qy 3883 TGATCAACAGAGAGAGAGAAATCAAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3942
Dh 3898 TGATTTACAGAGAGAGAGAAATTAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3957
Qy 3943 CTGTGGCAGTCAATCTCCAGAGCAGCAGACAGACCTGCGACCGAGATGTGCATGTTA 4002
Dh 3958 CCGTGGCAGTCAATTTCCAGAGCAGCAGACAGACCTGCGACCGAGATGTGCATGTTA 4017
Qy 4003 TGGAGACCTTACCTGGAATGTTGTGGCAAGAACAAGACGTAATACCTGAGGGTCTCATATT 4062
Dh 4018 TGGAGACATTAACCTGGAATGTTGTGGCAAGATAGAGATAGAGATGCTGAGGGTCCCATATT 4077
Qy 4063 GGGCCAAAATCTCCAGACOGATGAGACCTTCAACCCGTCTCTCTCATTTGGCGGCTTTG 4122
Dh 4078 GGGCCAAAATCTCCAGACOGATGAGACCTTCAACCCGTCTCTCTCATTTGGCGGCTTTG 4137
Qy 4123 GACTTAAGCACCCGCTCCTCAGATCTCATCAAAACACCCGTGTCTCTCGAATCTCTC 4182
Dh 4138 GACTCAAGAACCCGCTCCTCAGATCTCATCAAAACACCCGTGTCTCTCGAATCTCTC 4197
Qy 4183 CGGAGAGTTTTGCGCTACAAAGTTTGCTTCAATTCATCAACCCAGTATTTCAACAGACAAG 4242
Dh 4198 CGGAGAGTTTTGCGCTACAAAGTTTGCTTCAATTCATCAACCCAGTATTTCAACAGACAAG 4257
Qy 4243 TGAGGTGGAGATTTGAATGGAGCTCGAGAAAGAAACAGCAACGCTGGAATCCCGAAG 4302
Dh 4258 TGAGGTGGAAATTTGAATGGAGCTCGAGAAAGAAACAGCAACGCTGGAATCCCGAAG 4317
Qy 4303 TGCAGTATACATCTTAATGCAAAATCTGCCAAAGCTTGATTTCACTGTGACAACAATG 4362
Dh 4318 TGCAGTATACATCTTAATGCAAAATCTGCCAAAGCTTGATTTCACTGTGACAACAATG 4377
Qy 4363 GACTTATATGAGCTTCCGCCATTTGGCACCCGTTTACCTCAACCCGTCCTCTGTAATGT 4422
Dh 4378 GACTTATATGAGCTTCCGCCATTTGGCACCCGTTTACCTCAACCCGTCCTCTGTAATG 4437
Qy 4423 GTGTTAATCAATAAACCGGTTAATCTGTGCTGAGTTGAACCTTGGCTCATATCTCTATTA 4482
Dh 4438 GTGTTAATCAATAAACCGGTTAATCTGTGCTGAGTTGAACCTTGGCTCATATCTCTATTA 4497
Qy 4483 TCTTATCTGTACCATGACAACCGGTTAATCAATTAACCTGTAATGTCGCTGCGCA-- 4540
Dh 4498 TCTTATCT-GTTCACATGTTATAGCTTAACATTAACCTGTAATGTCGCTGCGCAATA 4556
Qy 4541 -----ATACCTTAATGATGAGTTGCCACTCCCTCTATGCGCGC 4581
Dh 4557 AAAAGACTTACGTATCGGGTTAACCCCTAGATGATGAGTTGCCACTCCCTCTGCGCGC 4616
Qy 4582 TCGCTCGCTCGGTGGGGCGGAGAGAGAGAGCTGCGCGTCTGCGGACCTTTGGTCCGA 4641
Dh 4617 TCGCTCGCTCGGTGGGGCGTGGAGACAAAGGTCCGAGAGAGAGCTGCTGCTGCC 4676
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Qy 4642 GGCCCCACGAGGAGCGGAGCGGCAATGAGGAGTGGCCAA 4683
Dh 4677 GGCCCCACGAGGAGCGGAGCGGCAATGAGGAGTGGCCAA 4718

RESULT 8
ADM39402
ID ADM39402 standard; DNA; 4239 BP.
XX
AC ADM39402;
XX
DT 24-MAR-2005 (first entry)
XX
DE Adeno-associated virus 2 (AAV2) rep-AAV1 cap fusion DNA - SEQ ID 5.
XX
KM genetically engineered microorganism; vector; rep; cap; ds.
XX
OS Adeno-associated virus 2.
OS Chimeric.
OS Unidentified.
XX
PN CN1461805-A.
XX
PD 17-DEC-2003.
XX
PF 27-MAY-2002; 2002CN-00117965.
XX
PR 27-MAY-2002; 2002CN-00117965.
XX
PA (BENY-) BENYUAN ZHENGYANG GENETIC TECHNOLOGY CO.
XX
PI Wu X, Cao H, Dong X;
XX
DR WPI; 2004-248658/24.
XX
FT Structure of a recombinant herpes simplex virus and its use.
XX
PS Claim 5; SEQ ID NO 5; 102pp; Chinese.
XX
CC The invention relates to a novel recombinant herpes simplex virus (rHSV)
CC whose genome is respectively inserted by the Adeno-associated virus (AAV)
CC rep gene and cap gene. The AAV genes may be derived from viruses AAV1,
CC AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be
CC useful for generating recombinant vectors with high efficiency and no
CC need of reconfiguration. The current sequence is that of the Adeno-
CC associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
CC DNA (SEQ ID 5) of the invention.
XX
SQ Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;

Query Match 81.8%; Score 3831.4; DB 13; Length 4239;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 3997; Conservative 0; Mismatches 236; Indels 4; Gaps 2;

Qy 191 GTCTGTATTAGAGTGCATGATGATTTTTCGACATTTTTCGACACCATGTGTCACGC 250
Dh 6 GTCTGTATTAGAGTGCATGATGATTTTTCGACATTTTTCGACACCATGTGTCACGC 65
Qy 251 TGGGTATTTTAAGCCCGAGTGAAGCAGCAGAGGTCTCCATTTTGAAGGGGAGTTTGAACG 310
Dh 66 TGGGTATTTTAAGCCCGAGTGAAGCAGCAGAGGTCTCCATTTTGAAGGGGAGTTTGAACG 125
Qy 311 CGCAG-CGCCATGCGGGGTTTTCAGAGATTGATTAAGTCCCGACGACCTTGAACA 369
Dh 126 CGCAGCCGCATGCGGGGTTTTCAGAGATTGATTAAGTCCCGACGACCTTGAACG 185
Qy 370 GCATTCGCCCGGCAATTTCTGACAGCTTTGTGAACCTGGTGGCGGAGAAATGGAGATT 429
Dh 186 GCATTCGCCCGGCAATTTCTGACAGCTTTGTGAACCTGGTGGCGGAGAAATGGAGATT 245
Qy 430 GCGCCGATTTTCACATGATCTGAATCTGAATCTGAATTGAGCAGGACCCCTGACCGTGGCGGA 489
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Db 246 GCCGCGAATTCGACATGATCTGAACTGATTGACGAGCACCCTGATCCGTGACCGA 305  
Qy 490 GAAGCTGACGCGGCACTTCTGTGTCACCTGAGCGCGGAGTAAGAGCCCGGAGGCCCT 549  
Db 306 GAAGCTGACGCGGCACTTCTGTGTCACCTGAGCGCGGAGTAAGAGCCCGGAGGCCCT 365  
Qy 550 CTTCTTTGTTGCAAGTTCGAGAAAGGCGAGTCTTACTTCCACTTCAATATTTCTGTGAGAC 609  
Db 366 TTTCTTTGTTGCAAGTTCGAGAAAGGCGAGTCTTACTTCCACTGCAAGTCTGTGTGAAAC 425  
Qy 610 CACGGGGGTCAAAATCAGTGTGCTGAGCGCGCTTCTTGAAGTCAAGTATTAAGCAAGCTGAT 669  
Db 426 CACCGGGGTCAAAATCAGTGTGCTGAGCGCGCTTCTTGAAGTCAAGTATTAAGCAAGCTGAT 485  
Qy 670 GCAGCACTTACCGCGGGATGAGCGGACCCCTGCGCAACCTGTTTCGCGGTACCAAGAC 729  
Db 486 TCAGGAATTTACCGCGGGATGAGCGGACCCCTGCGCAACCTGTTTCGCGGTACCAAGAC 545  
Qy 730 GCGTATGCGCGCGAGGGGGGAGCAAGGTGTGACGAGTCTACATCTCCCACTACT 789  
Db 546 CAGAAATGGCGCGAGGGGGGAGCAAGGTGTGAGTGTGATCTACATCTCCCACTACT 605  
Qy 790 CTTGCTCCCAAGTCAAGCCCGAGCTGACGTGCGGTGACCTAAATGAGAGAGTATATAAG 849  
Db 606 GCTCCCAAAACCCAGCTGAGCTCAGTGGCGGTGACCTAATATGAAACAGTATTTAAG 665  
Qy 850 GCGGTGTTTAAACCTGGCGAGCGGAAACGCTCGTGGCGGACGACCTGACCCAGCTGAC 909  
Db 666 GCGCTGTTGAAATCTCAGGAGCGGTAAACGTTGTGGCGGACGACCTGACCCAGCTGTC 725  
Qy 910 CCAGACCCAGAGAGCAAGAGAGAACTGAAACCCCAATTTCTGACGCGCTGTATCCG 969  
Db 726 GCAAGCGAGAGAGCAAGAGAGAACTGAAATCCCAATTTCTGATGGCGGTGATCAG 785  
Qy 970 GTCAAAAACCTTCGCAAGCTTATGAGAGCTGTGGTGTGCTGTGGAACGGGGCATAC 1029  
Db 786 ATCAAAAACCTTCAGCAAGTATCATGAGCTGTGGTGTGCTGTGGAACGGGGCATAC 845  
Qy 130 CTCCGAGAGAGAGTGGATCCAGAGAGACGAGGCTCGTACATCTCTTCAACCGGCTTC 1089  
Db 846 CTCCGAGAGAGAGTGGATCCAGAGAGACGAGGCTCGTACATCTCTTCAACCGGCTTC 905  
Qy 1090 CAACCTCGCGCTCCAGATCAAGGCGCTCTGGAACAATCCCGCAAGATCATGCGCTGAC 1149  
Db 906 CAACCTCGCGCTCCAGATCAAGGCGCTCTGGAACAATCCCGCAAGATCATGCGCTGAC 965  
Qy 1150 CAATTCGCGCGCGCACTACTGTGAGCGCGCTCGCGCGCGCAATTAACCAACCG 1209  
Db 966 TAAAAACCGCGCGCACTACTGTGAGCGCGCTCGCGCGCGCAATTAACCAACCG 1025  
Qy 1210 CATTTACCGCATCTCTGAGCTGAAAGGCTACGACCTTACGCGGCTCCGTCTTCT 1269  
Db 1026 GATTATTAATAATTTTGAATCAAAAGGATGATCCCAATATGCGGCTTCCGTCTTCT 1085  
Qy 1270 CGGCTGGGCGCAGAAAAGTTTCGGAACAACCACTTGTGCTTTGGCGCGGAC 1329  
Db 1086 GGGATGGGCGCAGAAAAGTTTCGGAACAACCACTTGTGCTTTGGCGCGGAC 1145  
Qy 1330 CACGGGCAAGCAATCGCGGAAGCCATGCGCGCGCGCTTCTACGCTGCGT 1389  
Db 1146 TACCGGGAAGCAACATCGCGGAAGCCATGCGCGCGCTTCTACGCTGCGT 1205  
Qy 1390 CAACCTGACCAATGAGAACTTCTCTTCAAGATTGCGTGCACAAAGATGATCTGTG 1449  
Db 1206 AAACCTGACCAATGAGAACTTCTCTTCAAGATTGCGTGCACAAAGATGATCTGTG 1265  
Qy 1450 GGAGAGGGCAAGATGAGCGGCAAGGTGTGAGTCCGCAAGGCAATTTCTCGCGGAG 1509  
Db 1266 GGAAGAGGGCAAGATGAGCGGCAAGGTGTGAGTCCGCAAGGCAATTTCTCGGAGAG 1325  
Qy 1510 CAAGTGTGCGTGCACAAAAGTGCNAAGTGTGCGCGCGCAATCCATCCCGGTAT 1569  
Db 1326 CAAGTGTGCGTGCACAAAAGTGCNAAGTGTGCGCGCGCAATCCCGGTAT 1385

Qy 1570 GGTCACTCCAAACCAACATGTGCGCGGTATGAGGGGAAACAGCACACCTTGAGCA 1629  
Db 1386 GGTCACTCCAAACCAACATGTGCGCGGTATGAGGGGAACTCAAGACCTTGAGCA 1445  
Qy 1630 CCAGCAGCGGTTCAGAGACCGGATGTTCAAAATTTGAATCAACCCGCGCTGAGACATGA 1689  
Db 1446 CCAGCAGCGGTTCAGAGACCGGATGTTCAAAATTTGAATCAACCCGCGCTGAGACATGA 1505  
Qy 1690 CTTTGGCAAGGTGACAAAGCAAGAGTCTTCCGCTGGGCGCAGATCACGT 1749  
Db 1506 CTTTGGGAAGGTGACAAAGCAAGAGTCTTCCGCTGGGCGCAGAGATCACGT 1565  
Qy 1750 GACGAGGTGCGCATGAGTCTACGTACGAAAGGTGAGACCAACACAGCCGCGCC 1809  
Db 1566 GATTGAGGTGAGCATGAAATTCACGTCAAAAAGGTGAGACCAAAAAGCCGCGCC 1625  
Qy 1810 CGATGACCGGATTAAGAGCGAGCCCAAGCGGCGCTGACAGTCCGAGATCCATCGAC 1869  
Db 1626 CAGTGAACGCAATATTAAGTGAAGCCCAAGCGGCTGCGAGTCAAGTCCGAGATCGAC 1685  
Qy 1870 GTCAAGCGCGAAGAGTCCGCTGAGACTTTCGCAAGTACCAAAACAATGTTCTCG 1929  
Db 1686 GTCAAGCGCGAAGAGTCCGCTGAGACTTTCGCAAGTACCAAAACAATGTTCTCG 1742  
Qy 1930 TCAGCGGCGCATGCTTCAGATGCTGTTCCCTGCAAAAACAGCGAGAGAAATGAGAA 1989  
Db 1743 TCAGCGGCGCATGCTTCAGATGCTGTTCCCTGCAAAAACAGCGAGAGAAATGAGAA 1802  
Qy 1990 TTTCAACATTTGCTTCAACGAGCGGACAGAGACTGTTCAAGATGTTTCCCGCGGTGC 2049  
Db 1803 TTTCAACATTTGCTTCAACGAGCGGACAGAGACTGTTCAAGATGTTTCCCGCGGTGC 1862  
Qy 2050 AGAATCTCAACCGGTGCTCAGAAAGAGAGCTATCGGAACTCTGTGCAATCATCT 2109  
Db 1863 AGAATCTCAACCGGTGCTCAGAAAGAGAGCTATCGGAACTCTGTGCAATCATCT 1922  
Qy 2110 GCTGGGGCGGCTCCGAGATGCTGCTGGCGCGGATGTGTCAAACGAGATCTGGA 2169  
Db 1923 GCTGGGGCGGCTCCGAGATGCTGCTGGCGCGGATGTGTCAAACGAGATCTGGA 1982  
Qy 2170 TGACTGTGTTCTGAGCAATTAATGACTTAACCAAGTATGCTGCGATGTTATCTTC 2229  
Db 1983 TGACTGTGTTCTGAGCAATTAATGACTTAACCAAGTATGCTGCGATGTTATCTTC 2042  
Qy 2230 CAGATTGGCTGAGAGCAACTCTCTGAGGCAATTCGCAAGTGTGGAATTGAACCTG 2289  
Db 2043 CAGATTGGCTGAGAGCAACTCTCTGAGGCAATTCGCAAGTGTGGAATTGAACCTG 2102  
Qy 2290 GAGCGCGGAAACCCAAAGCCCAACAGCAAAAGCAAGAGCGCGGGGTCTGGTCTTC 2349  
Db 2103 GAGCGCGGAAACCCAAAGCCCAACAGCAAAAGCAAGAGCGCGGGGTCTGGTCTTC 2162  
Qy 2350 CTGGCTCAAGTACTCTGAGACCTTCAACGGACTCGCAAGGGGAGACCCGTCACCGG 2409  
Db 2163 CTGGCTCAAGTACTCTGAGACCTTCAACGGACTCGCAAGGGGAGACCCGTCACCGG 2222  
Qy 2410 CGAGTGAAGGGCCCTTGAGACGACAAAGCTTACGACAGAGCTCAAAAGCGGTGACA 2469  
Db 2223 CGAGTGAAGGGCCCTTGAGACGACAAAGCTTACGACAGAGCTCAAAAGCGGTGACA 2282  
Qy 2470 ATCCGTACTGCGGTATTAACAGCGGACGCGGATTTCAAGGAGCGTCTCAAGAAATA 2529  
Db 2283 ATCCGTACTGCGGTATTAACAGCGGACGCGGATTTCAAGGAGCGTCTCAAGAAATA 2342  
Qy 2530 GGTCTTTTGGGGCAACCTCGGGGAGCAGTCTTCAAGGCGCAAGAGAGTCTCGAAC 2589  
Db 2243 GGTCTTTTGGGGCAACCTCGGGGAGCAGTCTTCAAGGCGCAAGAGAGTCTCGAAC 2402  
Qy 2590 CTTTGTGTGTGAGAGAGGTCTTAAGACGCTCTGTGAAAGAAACGTCGGTACAGC 2649  
Db 2403 CTTTGTGTGTGAGAGAGGTCTTAAGACGCTCTGTGAAAGAAACGTCGGTACAGC 2462



QY 2650 AGTGGCCACAGAGCAGACTCTCTCGGGCAATTGGCAGACAGGCCAGCCCGCTA 2709  
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Db 2463 AGTGGCCACAGAGCAGACTCTCTCGGGCAATTGGCAGACAGGCCAGCCCGCTA 2522  
QY 2710 AAAAGAGCTCAATTTTGGTCTGAGACTGGCGACTCAGAGTCAGTCCCGACCCACAACTC 2769  
|||  
Db 2523 AAAAGAGCTCAATTTTGGTCTGAGACTGGCGACTCAGAGTCAGTCCCGACCCACAACTC 2582  
QY 2770 TCGGAGAACTTCGAGCAACCCCGCTGCTGAGGACCTCAATGAGCTTCAGGCGGTG 2829  
|||  
Db 2583 TCGGAGAACTTCGAGCAACCCCGCTGCTGAGGACCTCAATGAGCTTCAGGCGGTG 2642  
QY 2830 GCGCAGCAATGCGAGACATTAACGAAAGCGCGCAGAGAGTGGTAATGCTCAGGAAATT 2889  
2643 GCGCAGCAATGCGAGACATTAACGAAAGCGCGCAGAGAGTGGTAATGCTCAGGAAATT 2702  
QY 2890 GGCATTGGGATTCCACATGCTGGGCGACAGAGTCATCAACAACGACCCGAAATGCG 2949  
|||  
Db 2703 GGCATTGGGATTCCACATGCTGGGCGACAGAGTCATCAACAACGACCCGAAATGCG 2762  
QY 2950 CCTTGGCCCACTATTAACAACCACTCTCAAGCAAAATCTCAGTGTCTCAAGGGGGCGA 3009  
|||  
Db 2763 CCTTGGCCCACTATTAACAACCACTCTCAAGCAAAATCTCAGTGTCTCAAGGGGGCGA 2822  
QY 3010 GCAAAGCAACCACTACTTGGCTTACAGCAGCCCTCGGGGGTAATTTGATTTCACAGAT 3069  
2823 GCAAAGCAACCACTACTTGGCTTACAGCAGCCCTCGGGGGTAATTTGATTTCACAGAT 2882  
QY 3070 TCCACTGCTATTTCTCACACAGTGACTGGCAGCGACTCATCAACAATTGGGGATTCC 3129  
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Db 2883 TCCACTGCTATTTCTCACACAGTGACTGGCAGCGACTCATCAACAATTGGGGATTCC 2942  
QY 3130 GGGCCCAAGAGCTCAACTTCAAGCTCTCAACATCAAGTCAAGAGGTGACAGCAATG 3189  
2943 GGGCCCAAGAGCTCAACTTCAAGCTCTCAACATCAAGTCAAGAGGTGACAGCAATG 3002  
QY 3190 ATGGGCTCAGCAGCATCGCTATTAACCTTACAGCAGCGGTTCAGTCTTCTCGGACTCG 3249  
3003 ATGGGCTCAGCAGCATCGCTATTAACCTTACAGCAGCGGTTCAGTCTTCTCGGACTCG 3062  
QY 3250 AGTACAGTTCCCGTACGTCTCGGCTTGGCAGCAGGGCTGCTCCCTCCGTTCCGG 3309  
|||  
Db 3063 AGTACAGTTCCCGTACGTCTCGGCTTGGCAGCAGGGCTGCTCCCTCCGTTCCGG 3122  
QY 3310 CGGAGCTTCATGATTCGAGTACGGCTACCTTAAGCTCAACAATGGCAGCGAG 3369  
3123 CGGAGCTTCATGATTCGAGTACGGCTACCTTAAGCTCAACAATGGCAGCGAG 3182  
QY 3370 TGGGACGCTCATCTTTTACTGCTGGAATATTTCCATCGCAGATGCTGAACGGGCA 3429  
|||  
Db 3183 TGGGACGCTCATCTTTTACTGCTGGAATATTTCCATCGCAGATGCTGAACGGGCA 3242  
QY 3430 ATTAATTACCTTCAGCTACACCTTCAGAGAGTGCCTTTCCACAGCAGCTACCGGCA 3489  
|||  
Db 3243 ATTAATTACCTTCAGCTACACCTTCAGAGAGTGCCTTTCCACAGCAGCTACCGGCA 3302  
QY 3490 GCCGAGGCTGAGACCGGCTGATGAATCTCTCATGACAGAGCTGATTAACGGAACA 3549  
3303 GCCGAGGCTGAGACCGGCTGATGAATCTCTCATGACAGAGCTGATTAACGGAACA 3362  
QY 3550 GAACTCACAATCAGTCCGGAAGTGCCTCAAAACAGAGCTTGTGTTAGCCGTGGGTCTC 3609  
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Db 3363 GAACTCACAATCAGTCCGGAAGTGCCTCAAAACAGAGCTTGTGTTAGCCGTGGGTCTC 3422  
QY 3610 CAGCTGGCATGTCTGTTCAAGCCCAAAAATGCGTACCTGAGACCTGTTACCGGAGCAGC 3669  
|||  
Db 3423 CAGCTGGCATGTCTGTTCAAGCCCAAAAATGCGTACCTGAGACCTGTTACCGGAGCAGC 3482  
QY 3670 GCGTTTCAAAAACAAAAACAGACAAACAGCAACCTTTACCTGAGCTGTTGTTCAA 3729  
|||  
Db 3483 GCGTTTCAAAAACAAAAACAGACAAACAGCAACCTTTACCTGAGCTGTTGTTCAA 3542  
QY 3730 AATATTAACCTTAATGAGGCGTGAATCTATTAATCAACCTGGGACGTGACTCACA 3789

Db 3543 AATATTAACCTTAATGAGGCGTGAATCTATTAATCAACCTGGGACGTGACTGCTCACA 3602  
QY 3790 AAGACGAAAGACAGTCTTTCCATGAGCGGTGTCAATGATTTTGGAAAGAGAGCG 3849  
|||  
Db 3603 AAGACGAAAGACAGTCTTTCCATGAGCGGTGTCAATGATTTTGGAAAGAGAGCG 3662  
QY 3850 CCGAGCTTCAACACTGATGAGCAATGTCAATGATCAAGACAGAGAGGAATCAAG 3909  
3663 CCGAGCTTCAACACTGATGAGCAATGTCAATGATCAAGAGAGGAATCAAG 3722  
QY 3910 CCACTAACCCGTGGCCACCGAAAGATTGGGACTGTGCACTGATCTCAAGACAGCA 3969  
3723 CCACTAACCCGTGGCCACCGAAAGATTGGGACTGTGCACTGATCTCAAGACAGCA 3782  
QY 3970 GCACAGACCCCTGGACCGGAGATGTGATGTTATGGAAGCTTAACCTGGAATGGTGGC 4029  
3783 GCACAGACCCCTGGACCGGAGATGTGATGTTATGGAAGCTTAACCTGGAATGGTGGC 3842  
QY 4030 AAGACAGAGAGTATACCTGACAGGTCCTATTGGGCAAAATTTCTCACAGGATGAG 4089  
3843 AAGACAGAGAGTATACCTGACAGGTCCTATTGGGCAAAATTTCTCACAGGATGAG 3902  
QY 4090 ACTTTACCCGCTCTCTCATGAGGCGGCTTTGAGACTTAAACAACCGCTCTCAATCC 4149  
3903 ACTTTACCCGCTCTCTCATGAGGCGGCTTTGAGACTTAAACAACCGCTCTCAATCC 3962  
QY 4150 TCAATCAAAAACAGCCGCTTCTGAGAACTCTCGGAGAGTTTGGGCTACAAAGTTTG 4209  
3963 TCAATCAAAAACAGCCGCTTCTGAGAACTCTCGGAGAGTTTGGGCTACAAAGTTTG 4022  
QY 4210 CTTCATTCATCACCCAGTATTTCCACAGACAGCAAGTGAAGCTGAGATTGAGAGTGC 4269  
4023 CTTCATTCATCACCCAGTATTTCCACAGACAGCAAGTGAAGCTGAGATTGAGAGTGC 4082  
Db 4083 AGAAAGAAACAGCAAAACGCTGAATCCGAAAGTGCAGTATCATCTAATGCAAAAT 4142  
QY 4270 AGAAAGAAACAGCAAAACGCTGAATCCGAAAGTGCAGTATCATCTAATGCAAAAT 4329  
4330 CTGCGAACGTTGATTTCACTGTGAGACAAATGGAACCTTATGAGCCCTGCGCCCAATG 4389  
Db 4143 CTGCGAACGTTGATTTCACTGTGAGACAAATGGAACCTTATGAGCCCTGCGCCCAATG 4202  
QY 4390 GCACCCGTTACCTACCCGCTGCCCTGTAATGTGTGT 4426  
4203 GCACCCGTTACCTACCCGCTGCCCTGTAATGTGTGT 4239  
Db

RESULT 9  
AD246598  
ID AD246598 standard; DNA; 4239 BP.  
XX  
AC AD246598;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE HSV-AAV sequence rep2cap6 for AAV/HSV vectors.  
XX  
KW Genetic engineering; gene therapy; vector; cancer; neoplasm; cytostatic;  
KW respiratory disease; respiratory-gen.; neurological disease;  
KW neuroprotective; ds.  
XX  
OS Adeno-associated virus.  
OS Human herpesvirus 1.  
XX  
PN W02005035743-A1.  
PD 21-APR-2005.  
XX  
PF 15-OCT-2003; 2003W0-CN000861.  
XX  
PR 15-OCT-2003; 2003W0-CN000861.  
XX

PA (AGTC-) AGTC GENE TECHNOLOGY CO LTD.  
 XX Mu X, Cao H, Dong X;  
 XX WPI; 2005-296279/30.  
 XX Large-scale production, isolation and purification of serotype adeno-  
 PT associated virus vectors by infecting cells with recombinant herpes  
 PT simplex virus vectors, for use in gene therapy of e.g. cancer and  
 PT respiratory diseases.  
 XX Claim 1; SEQ ID NO 5; 79pp; Chinese.  
 PS  
 XX The invention relates to a recombinant herpes simplex virus (HSV)  
 CC characterized in that its genome is inserted with a DNA sequence selected  
 CC from nucleotide sequences of AD246594-AD246598 or their homologous  
 CC sequences. Also included are preparing the recombinant HSV (comprising  
 CC the construction of DNA fragments that contain sequences AD246594-  
 CC AD246598, and respectively inserting these 5 DNA fragments into genome of  
 CC HSV by applying genetic engineering to give the recombinant HSV, large-  
 CC scale production of 5 serotype recombinant adeno-associated viruses (AAV)  
 CC 1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-  
 CC strain vector cell 1.e. recombinant AAV vector cell-line, infecting the  
 CC corresponding vector cell-line with the 5 recombinant HSV, producing  
 CC recombinant AAV under the infective effect of the 5 recombinant HSV in  
 CC the vector cell-line, separating and purifying the 5 serotype recombinant  
 CC AAV after lysing the AAV-containing cells and culture liquor to give a  
 CC crude lysate and further purification of rAAV by density-gradient  
 CC centrifugation or affinity chromatography) and a recombinant vector  
 CC plasmid pSNAV-NX (containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV  
 CC -5 or AAV-6 genome, with immediate-early enhancer and promoter of  
 CC cytomegalovirus, and a polyclonal site and a polyA signal, respectively,  
 CC between the ITR (inverted terminal repeat), and neomycin-resistance gene-  
 CC expressing cassette at outer edge of ITR). The DNA sequence is inserted  
 CC into XbaI site in UI2 or UI44 gene in HSV genome. The DNA sequence of  
 CC sequence AD246594-AD246598 can also be inserted into other non-essential  
 CC gene regions in HSV genome. The recombinant HSV is optionally inserted  
 CC with other DNA sequences homologous with the already-specified fragments.  
 CC The vectors are for use in gene therapy of e.g. cancer, respiratory  
 CC diseases and neural diseases. The virus vectors are safe, with long  
 CC expression time and wide-spectrum of cell infection, even non-cleaved  
 CC cells and reverse axonal conduction through the incorporated HSV vectors,  
 CC and high transfer efficiently. The present sequence is the HSV-AAV  
 CC sequence repcap6 for the AAV/HSV vectors of the invention.  
 XX  
 SQ Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;  
 Query Match 81.8%; Score 3831.4; DB 14; Length 4239;  
 Best Local Similarity 94.3%; Pred. No. 0;  
 Matches 3997; Conservative 0; Mismatches 236; Indels 4; Gaps 2;

Db 306 GAAGCTGACGCGACATTTCGACGGAATGGCGCGGTGTAGTAAGCCCGGAGGCCCT 365  
 Qy 550 CTTCTTTGTTCAAGTTCCAGAAAGGCGAGCTCTACTTCCACTCCATATTTCTGTGAGAC 609  
 Db 366 TTTCTTTGTGCAATTTTGAAAGGAGAGAGCTACTTCCATGACGCTGCTGTGAAAC 425  
 Qy 610 CACGGGGGTCAAAATCCATGTGTGTGGCGCGCTCTCTGTAGTACAGATTACGCAAGCTGCT 669  
 Db 426 CACCGGGGTGAATTCATGTGTTTGGAGCTTTTCTGTAGTACAGATTTCGCAAAAATCTAT 485  
 Qy 670 GCAGACCATCTACCGCGGGATCGAGCGGACCTCGCCCACTGTCTCGCGTGAACCAAGAC 729  
 Db 486 TCAGAGAAATTTACCGCGGGATCGAGCGGACCTTTCGCAAACTGTCTCGCGTGAACCAAGAC 545  
 Qy 730 GCGTAATGCGCCCGGAGGGGAAACAGGTGTGTGACAGTGTCTATCTCCCACTACTCT 789  
 Db 546 CAGAAATGCGCCCGGAGCGGAAACAGGTGTGTGAGTGTACATCTCCCAATTAATCTT 605  
 Qy 790 CCGCGCCAAAGCTACGCGCGAGCTGACGTGGCGGTGACTAACTGAGAGATATATAG 849  
 Db 606 GCTCCCAAAACCAAGCTTGAAGCTTCACTGAGGCGGTGACTAACTGAGAGATATATAG 665  
 Qy 850 CGCGTGTAAACCTGCGCGAGCGCAACCGCTGTGCGCAGACCTGACCACTGTCAG 909  
 Db 666 CGCTGTTGAATCTCAACGAGCGTAAACGTTGTGTGCGCAGACATCTGACGCAAGTGTCT 725  
 Qy 910 CCAAGCCAGAGACAAACAAAGGAATCTGAATCCCAATTTCTGACGCGCTGTCTATCCG 969  
 Db 726 GCACACGAGAGAGAAACAAAGGAATCCCAATTTCTATGTGCGCGGTGATCTAG 785  
 Qy 970 GTCAAAAACCTCGCAGCTCATATGAGCTGTGTGGGTGTGTGAGCGGGGATCTAC 1029  
 Db 786 ATCAAAAACCTTCACGACGATTCATGAGCTGTGTGGGTGTGTGAGCGGGGATCTAC 845  
 Qy 1030 CTCGAGAGAGAGATTCACGAGAGACAGGCTCTGTACATCTCTTCAACGCGCGCTTC 1089  
 Db 846 CTCGAGAGAGAGATTCACGAGAGACAGGCTCTGTACATCTCTTCAATGCGCGCTTC 905  
 Qy 1090 CAATCTCGCGTCCCAATCAAGGCGCTGTGGAACATATGCGGCAAGATCATGGCGCTGAC 1149  
 Db 906 CAATCTCGCGTCCCAATCAAGGCGCTGTGGAACATATGCGGCAAGATCATGGCGCTGAC 965  
 Qy 1150 CAATCTCGCGTCCCAATCAAGGCGCTGTGGAACATATGCGGCAAGATCATGGCGCTGAC 1209  
 Db 966 TAAAACGCGCGCGATCTCTGTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1025  
 Qy 1210 CATTTACCGCATCTCTGTGAGCTGAACGCGCTGACGCTGCTGACGCGCGCTGCTTCTTCT 1269  
 Db 1026 GATTTATAAATTTTGGAACTAAACGCGGTACGATCCCAATATGCGGCTTCTGCTTCTCT 1085  
 Qy 1270 CGGCTGGGCGCAAAAAGTTTCGAAAAACGCAACCATCTGTGTTTGGGCGCGCGCAC 1329  
 Db 1086 GGAATGCGCGCGCAAAAAGTTTCGAAAAACGCAACCATCTGTGTTTGGGCGCGCGCAC 1145  
 Qy 1330 CACGGGCAAGACCAACATGCGGGAAGCATGCGCCACGCGCTGCTTCTGACGCTGCGT 1389  
 Db 1146 TACCGGAAGACCAACATGCGGGAAGCATGCGCCACGCTGCTTCTGACGCTGCGT 1205  
 Qy 1390 CAATGGAACCAATGGAATCTTCCCTTCAACGATGTGCTGACAAATGTGTATCTGTGTG 1449  
 Db 1206 AAATCTGACCAATGGAATCTTCCCTTCAACGATGTGCTGACAAATGTGTATCTGTGTG 1265  
 Qy 1450 GGAAGAGGCAAAATGACGCGCAAGGTGTGTGAGTCCGCGCAAGGCAATTTCTGCGCGCAG 1509  
 Db 1266 GGAAGAGGCAAAATGACGCGCAAGGTGTGTGAGTCCGCGCAAGGCAATTTCTGCGCGCAG 1365  
 Qy 1510 CAAAGTGCGGTGACCAAAAGTGTGCAAGTGTGCGCGCAAGTGTGCAATCTCCACCGCGGTAT 1569  
 Db 1326 CAAAGTGCGGTGACCAAAAGTGTGCAAGTGTGCGCGCAAGTGTGCAATCTCCACCGCGGTAT 1385  
 Qy 1570 GGTGACCTTCAACCAACATGTGTGCGCGGTGATTTGACGGGAACGACCACTTTGAGCA 1629  
 Db 1386 GGTGACCTTCAACCAACATGTGTGCGCGGTGATTTGACGGGAACGACCACTTTGAGCA 1445

QY	1630	CCAGCAGCCGTTTGCAGGACCCGAGTGTCAAATTTGAATCAACCCGCGCTGTGAGACATGA	1689
Dp	1446	CCAGCAGCCGTTTGCAGGACCCGAGTGTCAAATTTGAATCAACCCGCGCTGTGAGATCA	1505
QY	1690	CTTTGGCAGAGGTGACAAAGCAGAAAGTCAAAAGATCTTCCGCTGGGCGCAGGATCACTG	1749
Dp	1506	CTTTGGAGAGGTCAACCAAGCAGAAAGTCAAAAGATCTTTCGCTGGGCGCAGGATCACTG	1555
QY	1750	GACCGAGGTGCGCATGAGTTCTACGTCAAGAAAGGTGGAGCCAAACAGACCCGCC	1809
Dp	1566	GGTTGAGGTGAGCATGAAATCTACGTCAAAAAGGTGGAGCCAAAGAAAACCCGCC	1625
QY	1810	CGATGACGCGGATATAAAGCGAGCCCAACGGGCGTCCCGCTCAGTGGGATTCATCGAC	1865
Dp	1626	CAGTGACCAAGATATATAGTGAAGCCCAACGGGTGCGCAGTCAAGTTGGCAGCCATCGAC	1685
QY	1870	GTCAGACCGCGAGAGAGCTCCGCTGGAATTTCGCCACAGTACCAAAACAATGTTCTCG	1929
Dp	1686	GTCAGACCGCGA---AGCTTGATCAACTAGCAGACAGATACCAAAACAATGTTCTCG	1742
QY	1930	TCAGCGGGGCATGCTTCAGATGCTGTTCCCTGCAAAATGCGCAGAGATGATCAGAA	1989
Dp	1743	TCAGCGGGGCATGCTTCAGATGCTGTTCCCTGCAAAATGCGCAGAGATGATCAGAA	1802
QY	1990	TTTCAACATTGTGCTTACGACACGGGACCAAGACTGTTCAGAAATGTTTCCCGCGCTGC	2049
Dp	1803	TTTCAACATTGTGCTTACGACACGGGACCAAGAGACTGTTCAGAAATGTTTCCCGCGCTGC	1863
QY	2050	AGAACTTCAACCGGCTGTCAGAAAGAGACGATATCGAAACTCTGTGCATTCATCATCT	2109
Dp	1863	AGAACTTCAACCGGCTGTCAGAAAGAGACGATATCGAAACTCTGTGCATTCATCATCT	1922
QY	2110	GCTGGGGGGGGGCTCCCGAGATTGCTGCTCGGCGCTGCAGCTGCTGCAACGTGGATCTGGA	2169
Dp	1923	GCTGGGGGGGGGCTCCCGAGATTGCTGCTCGGCTGCTGCAACGTGGATCTGGA	1982
QY	2170	TGACTGTGTTTCTGAGCAATAAATGACTTAAACCAAGATATGATGCTGCTCGATGTTATCTTC	2229
Dp	1983	TGACTGTGTTTCTGAGCAATAAATGACTTAAACCAAGATATGATGCTGCTCGATGTTATCTTC	2042
QY	2230	CAGATTTGGCTCGAGGACAACTCTCTGAGGGCATTCGCGCATGCTGTGGGACTTTGAAACCTG	2288
Dp	2043	CAGATTTGGCTCGAGGACAACTCTCTGAGGGCATTCGCGCATGCTGTGGGACTTTGAAACCTG	2102
QY	2290	GAGCCCCCAAAACCCAAAGCCAAACAGCAAAAGCAGAGACGACGGCGGTCTGGTGCCTTC	2349
Dp	2103	GAGCCCCCAAAACCCAAAGCCAAACAGCAAAAGCAGAGACGACGGCGGTCTGGTGCCTTC	2163
QY	2350	CTGGCTACAGATACCTCGGACCTTCAAACGACCTGACACAGGGGGAGCCCTGCAACCGCG	2409
Dp	2163	CTGGCTACAGATACCTCGGACCTTCAAACGACCTGACACAGGGGGAGCCCTGCAACCGCG	2222
QY	2410	CGGATGACGCGGCGCTCGAGACACGACAGGCGCTACACAGAGGTCAAAACGGGTGACA	2465
Dp	2223	CGGATGACGCGGCGCTCGAGACACGACAGGCGCTACACAGAGGTCAAAACGGGTGACA	2282
QY	2470	ATCCGTACCTCGGATATACACACGCGCGACGCGCAATTTCAAGAGCGTCTGCAAGAGATA	2529
Dp	2283	ATCCGTACCTCGGATATACACACGCGCGACGCGCAATTTCAAGAGCGTCTGCAAGAGATA	2342
QY	2530	CGTCTTTTGGGGGCAACTCGGGCGAGACATTTCCAGGCGCAAGAAAGGGTTCCTCGAAC	2588
Dp	2343	CGTCTTTTGGGGGCAACTCGGGCGAGACATTTCCAGGCGCAAGAAAGGGTTCCTCGAAC	2402
QY	2590	CTTTTGTGCTGTTAGAGAGGTGCTTAAGACGGCTCTCGAAAGAAACGTCCGGTAGAGC	2649
Dp	2403	CTTTTGTGCTGTTAGAGAGGTGCTTAAGACGGCTCTCGAAAGAAACGTCCGGTAGAGC	2463
QY	2650	AGTGGCCAAAGACCAAGCTTCTCTCTCGGCAATTTGCAAGACAGGCCAGACCCCGCTA	2709
Dp	2463	AGTGGCCCAAGAGCAAGACTCTCTCGGGCATTTGGCAAGACAGGCCAGACCCCGCTA	2522

QY	2710	AAAAGAGCTCAATTTTGGTCTACAGCTGGCGCATCTAGAGTCAAGTCCCGGACCCCAACACTC	2769
Db	2523	AAAAGAGACTCAATTTTGGTCTACAGCTGGCGCATCTAGAGTCAAGTCCCGGACCCCAACACTC	2582
QY	2770	TCGGAGAACTCCGACAAACCCCGCTCTGTGGGACCTACTCAACATGGCTTTCAGGCGGTG	2829
Db	2583	TCGGAGAACTCCGACAAACCCCGCTCTGTGGGACCTACTCAACATGGCTTTCAGGCGGTG	2642
QY	2830	GCGCACCAATGGCAGACATATACGAGAGCGCCGACGGAGTGGGGTAATGCTTCAGGAAATT	2889
Db	2643	GCGCACCAATGGCAGACATATACGAGAGCGCCGACGGAGTGGGGTAATGCTTCAGGAAATT	2702
QY	2890	GGCAATTCGAAATTCACATGGCTGGGCGCAGAGTCATACCAACAGGACCCGAAATCTGGG	2949
Db	2703	GGCAATTCGAAATTCACATGGCTGGGCGCAGAGTCATACCAACAGGACCCGAAATCTGGG	2762
QY	2950	CCTTGCCCACTTAATACCAACCACTCTTCAACAGCAAAATCTCCAGTGTCTTCAACGGGGCCA	3009
Db	2763	CCTTGCCCACTTAATACCAACCACTCTTCAACAGCAAAATCTCCAGTGTCTTCAACGGGGCCA	2822
QY	3010	GCAACGACCAACCACTACTTGGGCTACAGACCCCGTGGGGTAATTTGATTTTCAACGAT	3069
Db	2823	GCAACGACCAACCACTACTTGGGCTACAGACCCCGTGGGGTAATTTGATTTTCAACGAT	2882
QY	3070	TCCACTCCCAATTTCTCACACGTCAGCTGGGAGCGCACTCATCAACAAATTTGGGGATTCC	3129
Db	2883	TCCACTCCCAATTTCTCACACGTCAGCTGGGAGCGCACTCATCAACAAATTTGGGGATTCC	2942
QY	3130	GGCCCAAGAGACTCAACTTCAAGCTCTTTCACATCTCAAGTCAAGAGAGTCAACGACGATG	3189
Db	2943	GGCCCAAGAGACTCAACTTCAAGCTCTTTCACATCTCAAGTCAAGAGAGTCAACGACGATG	3002
QY	3190	ATGCGCTCACGACCATCGCTAATTAACCTTACACGACGCTTCAAGTCTTGTGGACTCGG	3249
Db	3003	ATGCGCTCACGACCATCGCTAATTAACCTTACACGACGCTTCAAGTCTTGTGGACTCGG	3062
QY	3250	AGTACCAATTCGCGTACGTCCTCGGCTCTGGCGCACAGGCGTGCCTCCCTCCGTTCCCGG	3309
Db	3063	AGTACCAATTCGCGTACGTCCTCGGCTCTGGCGCACAGGCGTGCCTCCCTCCGTTCCCGG	3122
QY	3310	CGGACGGTTCATGATTTCCGAGTACGGGCTAACCTTAAGGCTCAACAATGGGACCGACGACG	3369
Db	3123	CGGACGGTTCATGATTTCCGAGTACGGGCTAACCTTAAGGCTCAACAATGGGACCGACGACG	3182
QY	3370	TGGGACGCTCATCTCTTTCATCTGCTCGTGAATATTTCCCATCGCAGATCTGAGAAACGGGCA	3429
Db	3183	TGGGACGCTCATCTCTTTCATCTGCTCGTGAATATTTCCCATCGCAGATCTGAGAAACGGGCA	3242
QY	3430	ATAACTTTTAACTTTCAGGCTACACCTTTCGAGGACGTCCTTTCACAGGACGTAACGCGACA	3489
Db	3243	ATAACTTTTAACTTTCAGGCTACACCTTTCGAGGACGTCCTTTCACAGGACGTAACGCGACA	3302
QY	3490	GCCAGAGCGTGGACCGGCTGATGATCTCTCATCTGACACAGTACCTTATTTACTCTGAAACA	3549
Db	3303	GCCAGAGCGTGGACCGGCTGATGATCTCTCATCTGACACAGTACCTTATTTACTCTGAAACA	3362
QY	3550	GAACCTCAACATCAGTCCGGAAGTCCCAAAACAAAGACCTTGCTGTTTAAAGCCGTGGTCTC	3609
Db	3363	GAACCTCAACATCAGTCCGGAAGTCCCAAAACAAAGACCTTGCTGTTTAAAGCCGTGGTCTC	3422
QY	3610	CAGCTGCAGTCTGTTTCAAGCCCAAAAACCTGGACTCGGACCCCTGTTTACCCGAGACGAC	3669
Db	3423	CAGCTGCAGTCTGTTTCAAGCCCAAAAACCTGGACTCGGACCCCTGTTTACCCGAGACGAC	3482
QY	3670	GCGTTTCTAAAAACAAAAACAGACAAACAACAGCAACTTACCTGGACTGTGCTTCAA	3729
Db	3483	GCGTTTCTAAAAACAAAAACAGACAAACAACAGCAACTTACCTGGACTGTGCTTCAA	3542
QY	3730	AATATTAACCTTAATGGGCGTGAATCTATTAATCAACCTCTGGACCTGCTAATGGCCCTACACA	3789
Db	3543	AATATTAACCTTAATGGGCGTGAATCTATTAATCAACCTCTGGACCTGCTAATGGCCCTACACA	3602
QY	3790	AAGACGACAAAGACAAATGTTCTTTTCCCATGTAGCGGTGCATGATTTTGGAAAGAGACGCG	3849

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Db 3603 AAGAGCAAGAGAGAGTTCTTTCCATGAGCGGTGTATGATTTTGGAAAGAGACG 3662
Qy 3850 CCGGAGCTTCAAACTGTCATTTGACAAATGTCATATCAACAGACGAAGAAATCAAAAG 3909
Db 3863 CCGGAGCTTCAAACTGTCATTTGACAAATGTCATATCAACAGACGAAGAAATCAAAAG 3722
Qy 3910 CCACTAACCCGCTGCGCCAGAAAGATTGGACCTGTCAGTCAATCTCCAGACACCA 3969
Db 3723 CCACTAACCCGCTGCGCCAGAAAGATTGGACCTGTCAGTCAATCTCCAGACACCA 3782
Qy 3970 GCACAGACCTGTCGACCGGAGATGTCATGTTATGGAGCCTTACCTGAAATGCTGAC 4029
Db 3783 GCACAGACCTGTCGACCGGAGATGTCATGTTATGGAGCCTTACCTGAAATGCTGAC 3842
Qy 4030 AAGACAGAGAGTATACCTGACAGGGTCTTATTTGGGCCAAATTTCTCAACAGATGAC 4089
Db 3843 AAGACAGAGAGTATACCTGACAGGGTCTTATTTGGGCCAAATTTCTCAACAGATGAC 3902
Qy 4090 ACTTCAACCCGCTGTCATGAGGCGCTTTGACCTTAAAGACCCGCGCTCTCAGATCC 4149
Db 3903 ACTTCAACCCGCTGTCATGAGGCGCTTTGACCTTAAAGACCCGCGCTCTCAGATCC 3962
Qy 4150 TCATCAAAAACAGCGCTGTCGAGATCCCTCGGACAGATTTTGGCTACAAAGTTG 4209
Db 3963 TCATCAAAAACAGCGCTGTCGAGATCCCTCGGACAGATTTTGGCTACAAAGTTG 4022
Qy 4210 CTTCATTCATCAACCGATTTTCACAGACAAAGTACGCTGAGATTGAATGGAGCTGC 4269
Db 4023 CTTCATTCATCAACCGATTTTCACAGACAAAGTACGCTGAGATTGAATGGAGCTGC 4082
Qy 4270 AGAAAGAAACAGAGAAAGCTGAGATCCCGAAGTCAATATCACTAATGAAAT 4329
Db 4083 AGAAAGAAACAGAGAAAGCTGAGATCCCGAAGTCAATATCACTAATGAAAT 4142
Qy 4330 CTGCAACGTTGATTTCACTGTGACAAACAAATGACCTTATACCTGAGCCTGCCCATTTG 4389
Db 4143 CTGCAACGTTGATTTCACTGTGACAAACAAATGACCTTATACCTGAGCCTGCCCATTTG 4202
Qy 4390 GCACCCGTTACCTCACCCGCTCCCTGTAATGTTGTGT 4426
Db 4203 GCACCCGTTACCTCACCCGCTCCCTGTAATGTTGTGT 4239

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RESULT 10
ADM39398
ID ADM39398 standard; DNA; 4347 BP.
XX
XX ADM39398;
XX
XX 24-MAR-2005 (first entry)
DT
DE Adeno-associated virus 2 (AAV2) rep-AAV1 cap fusion DNA - SEQ ID 1.
XX
XX KM genetically engineered microorganism; vector; rep; cap; ds.
XX
XX OS Adeno-associated virus 2.
XX
XX OS Chimeric.
XX
XX OS Unidentified.
XX
XX CN1461805-A.
XX
XX PD 17-DEC-2003.
XX
XX PF 27-MAY-2002; 2002CN-00117965.
XX
XX PR 27-MAY-2002; 2002CN-00117965.
XX
XX (BENNY-) BENYUAN ZHENG YANG GENETIC TECHNOLOGY CO.
XX
XX PI Wu X, Cao H, Dong X;
XX
XX WPI; 2004-248658/24.

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XX Structure of a recombinant herpes simplex virus and its use.
PT
XX Claim 1; SEQ ID NO 1; 102bp; Chinese.
PS
XX The invention relates to a novel recombinant herpes simplex virus (rHSV)
XX whose genome is respectively inserted by the Adeno-associated virus (AAV)
XX rep gene and cap gene. The AAV genes may be derived from viruses AAV1,
XX AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be
XX useful for generating recombinant vectors with high efficiency and no
XX need of reconfiguration. The current sequence is that of the Adeno-
XX associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
XX DNA (SEQ ID 1) of the invention.
SQ
XX Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;
XX
XX Query Match 81.2%; Score 3802; DB 13; Length 4347;
XX Best Local Similarity 92.6%; Pred. No. 0;
XX Matches 4026; Conservative 0; Mismatches 315; Indels 5; Gaps 3;
Qy 191 GTCTGTTATTAAGAGTCACTGATGTTTTCGACATTTTCGACACCATATGTCACGC 250
Db 6 GTCTGTTATTAAGAGTCACTGATGTTTTCGACATTTTCGACACCATATGTCACGC 65
Qy 251 TGGGATTTTAAGCCGAGTGAAGCAAGCAGGGTCTCCATTTTGAAGCGGAGTTGAACG 310
Db 66 TGGGATTTTAAGCCGAGTGAAGCAAGCAGGGTCTCCATTTTGAAGCGGAGTTGAACG 125
Qy 311 CGCAG-CGCCATGCGGGGTTTACGAGATTGTATTAAGTCCCAAGCCTTTGACGA 369
Db 126 CGCAGCGGCATGCGGGGTTTACGAGATTGTATTAAGTCCCAAGCCTTTGACGC 185
Qy 370 GCATCTGCGCGCATTTTTCGACAGCTTTGTAACTGCTGCGCGCAAGAAATGAGATT 429
Db 186 GCATCTGCGCGCATTTTTCGACAGCTTTGTAACTGCTGCGCGCAAGAAATGAGATT 245
Qy 430 GCCGCAAGATTCTACATATGATCTGAATCTGAATTGAGAGGACCCCTGAGCGCA 489
Db 246 GCCGCAAGATTCTACATATGATCTGAATCTGAATTGAGAGGACCCCTGAGCGCA 305
Qy 490 GAACTGACGCGCATTTCTGATCACTGACGCGCGCGTGAATGAAGCCCGGAGCCCT 549
Db 306 GAACTGACGCGCATTTCTGATCACTGACGCGCGCGTGAATGAAGCCCGGAGCCCT 365
Qy 550 CTTCCTTTGTTAGTTTCAAGAAAGGCGGAGTCTTACTTCCATATTTCTGTGAGAC 609
Db 366 TTTCTTTTGTGCAATTTGAAGAGGAGAGAGTCTTCCATGACGTCCTGTGAAAC 425
Qy 610 CACGGGGGTCAATTCATATGATGCTGGGCGCTTCTGAGTGAATTAAGCGCAAGCTGCT 669
Db 426 CACGGGGGTCAATTCATATGATGCTGGGCGCTTCTGAGTGAATTAAGCGCAAGCTGAT 485
Qy 670 GCAGACATCTACCGCGGATTCAGACGACCTCCCACTGTTGCGGTGACCAAGAC 729
Db 486 TCAAGAAATTTACCGCGGATTCAGACGACCTTCCCAACTGTTGCGGTGACCAAGAC 545
Qy 730 GCGTATGCGCGCGAGGCGGGAACAAAGTGTGAGAGTGTCAATCCCACTACT 789
Db 546 CAGAAATGCGCGCGAGGCGGGAACAAAGTGTGAGAGTGTCAATCCCACTACT 605
Qy 790 CTTGCCCAAGACTAGCCCGGAGTGAAGTGGGCGTGAATTAAGAGAGTATTAAG 849
Db 606 GCTCCCAAAACCAAGCTTAGCTTCCAGTGGGCGTGAATTAAGAGAGTATTAAG 665
Qy 850 CGCGTGTTTAACTGCGCGAGCGCAACCGCTGCGCGGACGACCTGACCAAGCTGAC 909
Db 666 CGCGTGTTTAACTGCGCGAGCGTAACCGTGTGCGGACGACCTGACCAAGCTGAC 725
Qy 910 CCAAGCCAGAGACGAACAAAGGAGATGTGAATCCCAATTTCTAGCGCTGTCAATCCG 969
Db 726 GCAGACGAGAGAGCAACAAAGGAGATGTGAATCCCAATTTCTAGCGCGGTGATGAG 785
Qy 970 GTCAAAAACCTCCGACGCTCATGAGAGTGTGCGGCTGCTGAGACCGGCGCATCAC 1029

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Db	786	ATCAAAAACCTTAGCCAGGTAACATGAGACTGGTCCGGTGGCTCGTGGCAAAAGGGAATTAC	845
Qy	1030	CTCCGAGAGCAGTGAATCCAGAGAGACCAAGCCCTGTAACATCTCTTCAACGCCGCTC	1089
Db	846	CTCGGAGAGCAGTGAATCCAGAGAGACCAAGCCCTCATACATCTCTTCAATGCGGCTC	905
Qy	1090	CAACTCCGGGTCCCGAGTCAAGGCCCGCTCTGGAACAATCCGCGAAGATCATGCGCTGAC	1149
Db	906	CAACTCCGGGTCCCGAATCAAGGCTGCGCTTGGAACATCCGGGAAAGATTATGAGCTTAC	965
Qy	1150	CAAAATCCGCGCCGACTACTGTTAGGCGCCGCTCCGCGCGCGCATTAACCAACCG	1209
Db	966	TAAACCGCCCCGACTACCTGTGTGGGCAAGAGCCGTTGAGAGACATTTCCAGAACATCG	1025
Qy	1210	CATTTACCGCATCTCTGAGCTGAACGGCTAGACCTGTGCTTACCGCGGCTCCGCTTTCT	1268
Db	1026	GATTTATTAATTTTGGAACTTAACGGGATACGATCCCAATATGAGGCTTCGCTTCTCT	1085
Qy	1270	CGGCTGGGCCCCAGAAAAGGTTCCGAAAAACGCAACCAATCTGCTGTTGGGCGGGCAC	1329
Db	1086	GGGATGGGCGACGAAAAAGTTCCGCAAGAGAACCAATCTGCTGTTGGGCTGCAAC	1145
Qy	1330	CACGGGCAAGACCAACATCGCGGAAGCCATCGCCACGCGCGCTTCTTACCGCTGCGT	1389
Db	1146	TACCGGGAAGACCAACATCGCGGAAGCCATAGCCACACTGCGCTTCTTACCGGCTGCGT	1205
Qy	1390	CAACTGGACCAATGAGACTTTCCTTCAACGATGGCGTCCACAAAGATGATCTGGTG	1449
Db	1206	AAACTGGACCAATGAACTTTCCTTCAACGACTGTGTCCACAAAGATGATGATGATG	1265
Qy	1450	GGAGGAGGCAAGATGACGGGCCAAGGTCGTGGAGTCCGCGCAAGGCCATTTCTCGCGGAG	1509
Db	1266	GAGGAGGGAAGATGACCGCCAAAGTGTGGAGTCCGCGCAAGGCCATTTCTGGAGGAG	1325
Qy	1510	CAAGTGGCGCTGGACCAAAAAGTCAATGCTGTCCGCGCCAGATCCATCCACCCCGTAT	1568
Db	1326	CAAGTGGCGCTGGACCAAAAAGTCAATGCTGTCCGCGCCAGATGACCCGATCCCGTAT	1385
Qy	1570	CGTCACTCCCAACCAACATGTGGCGCGTGTATTAACGGAACAGACCACTTCGAGACA	1629
Db	1386	CGTCACTCCCAACCAACATGTGGCGCGTGTATTAACGGAACCTCAAGACTTCGAGACA	1445
Qy	1630	CCAGCAGCCGTTGCAGACCCGATGTTCAATTGAACTCAACCGCGCTTGGAGCATGA	1689
Db	1446	CCAGCAGCCGTTGCAGACCCGATGTTCAATTGAACTCAACCGCGCTTGGAGCATGA	1505
Qy	1690	CTTTGGCAAGGTCAAAAGCAAGGAAGTCAAAAGTCTTCGCTGGGCGCGAGATCAAGT	1749
Db	1506	CTTTGGGAAAGTCAACCAAGCAAGGAAGTCAAAAGCTTTTTCGCTGGGCAAAAGATCAAGT	1565
Qy	1750	GACCGAGGTGGCGCATGAATTTCTACGTCAAGAAAGGTGGAGCCCAACAGACCCGCC	1809
Db	1566	GATTGAGGTGGAGCATGAATTTCTACGTCAAAAGGTTGAGCCAAAGAAAGCCGCC	1625
Qy	1810	CGATGACCGCGATTAAGCGAGCCCAAGCGGCGCTGCCCTCACTGCGGATCCATCGAC	1868
Db	1626	CAGTACCGCAATTAAGTGAAGCCCAACGGGTGGCGAGTCAAGTGGCGACCATTCAC	1685
Qy	1870	GTCAGACCGCGAAGAGCTCCGCTGGACTTTGGCCACAGAGTACCAAAACAATGTTCTCG	1929
Db	1686	GTCAGACCGCGA--AGCTTGATCAACTACGACAGACAGGATCCAAAACAATGTTCTCG	1742
Qy	1930	TCAGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGATGAATCAGAA	1989
Db	1743	TCAGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGATGAATCAGAA	1802
Qy	1990	TTTCAACATTTGCTTCAGGACCGGGAACAGAGACTGTTCAAGATTTTCCCGGGGTGTC	2049
Db	1803	TTTCAACATTTGCTTCAGGACCGGGAACAGAGACTGTTCAAGATTTTCCCGGGGTGTC	1862
Qy	2050	AGAACTTCAACCGGTCTCAGAAAGAGACGATATGAAACTGTGCTATTCATCATCT	2109

Db	1863	AGATCTCAACCGGTCTGTCAGAAAGAGACGTATCGGAAACTGTGTCCATTCACTACTCT	1922
Oy	2110	GCTGGGGGGGGCTCCCGAGATTGCTTGCTCTGGCTCGCATCTGGTCAACGTGGATCTTGGAA	2169
Db	1923	GCTGGGGGGGGCTCCCGAGATTGCTTGCTCTGGCTCGCATCTGGTCAACGTGGACCTTGGAA	1982
Oy	2170	TGACTGTGTTCTTAGGCAATTAATAGACTTTAAACCAAGGTATGGCTGCGCATGGTATCTTC	2229
Db	1983	TGACTGTGTTCTTAGGCAATTAATAGACTTTAAACCAAGGTATGGCTGCGCATGGTATCTTC	2042
Oy	2230	CAGATTGGCTTGAGAGCAACCTCTCTAGGGGCAATTCGGCAGTGTGGACTTGAACCTTG	2289
Db	2043	CAGATTGGCTTGAGAGCAACCTCTCTAGGGGCAATTCGGCAGTGTGTGGACTTGAACCTTG	2102
Oy	2290	GAGCCCCGAAACCCAAAGCCCAACGAGAAAGAGAGACGACGCGCGGGGGTCTGGTGTCTC	2349
Db	2103	GAGCCCCGAAACCCAAAGCCCAACGAGAAAGAGAGACGACGCGCGGGGGTCTGGTGTCTTC	2162
Oy	2350	CTGGCTCAAGATACCTCGGACCTCTTCAACGGACTCGACAAAGGGGAGCCCGTCACCCGG	2409
Db	2163	CTGGCTCAAGATACCTCGGACCTCTTCAACGGACTCGACAAAGGGGAGCCCGTCACCGGG	2222
Oy	2410	CGGATGCAAGCGGCGCTCTGAGCACGACAAAGGCTTACACACAGACTCAAAAGCGGGTACAA	2469
Db	2223	CGGACGACGCGGCGCTCTGAGCACGACAAAGGCTTACACACAGACTCAAAAGCGGGTACAA	2282
Oy	2470	ATCCGTCACCTGCGGTATTAACACGCCGACGCCGAGTTTCAGAGACGCTCTCAAGAAAGATA	2529
Db	2283	ATCCGTCACCTGCGGTATTAACACGCCGACGCCGAGTTTCAGAGACGCTCTCAAGAAAGATA	2342
Oy	2530	CGTCTTTTGGGGGCAACCTTGCGGCGAGCAGTCTTCCAGGCCCAAGAGAGGGTCTCGAAC	2589
Db	2343	CGTCTTTTGGGGGCAACCTTGCGGCGAGCAGTCTTCCAGGCCCAAGAGAGGGTCTCTCAAC	2402
Oy	2590	CTTTTGGTCTGGTGAAGGAAGGTCTTAAGACGCTCTCGAAAAAGAAACGTCCGGTAAAGC	2649
Db	2403	CTCTGGGTCTGGTGAAGGAAGGCGCTTAAGAGGCTCTCGAAAAAGAAACGTCCGGTAAAGC	2462
Oy	2650	AGTCGCCACAAGAGCCAGACTCCCTCTCGGGCATTTGGCAAGACAGGCCAGACGCCGCTTA	2709
Db	2463	AGTCGCCACAAGAGCCAGACTCCCTCTCGGGCATCGGCAAGACAGGCCAGACGCCGCTTA	2522
Oy	2710	AAAAGAGACTCAATTTTGGTGCACATGCGGCACTACAGTCAAGTCCCGGACCCCAACACTC	2769
Db	2523	AAAAGAGACTCAATTTTGGTGCACATGCGGCACTACAGTCAAGTCCCGGATCCCAACACTC	2582
Oy	2770	TCCGAGAAACCTCCAGCAACCCCGCTCTGTGGGACCTTACATCAATGGCTTACAGCGGTG	2829
Db	2583	TCCGAGAAACCTCCAGCAACCCCGCTCTGTGGGACCTTACATCAATGGCTTACAGCGGTG	2642
Oy	2830	GCGCAACCAATGGCAGACATTAACGAGGCGCCGACGGAGTGGGTATATGCTCAGGAAATT	2889
Db	2643	GCGCAACCAATGGCAGACATTAACGAGGCGCCGACGGAGTGGGTATATGCTCAGGAAATT	2702
Oy	2890	GGCAATTGCGATTCCACATGGCTGGGGGACAGAGTCAATCAACACAGACACCGCAACATGGG	2949
Db	2703	GGCAATTGCGATTCCACATGGCTGGGGGACAGAGTCAATCAACACAGACACCGCAACCTGGG	2762
Oy	2950	CTTTGCCCACTTATTAACAACCACTCTTCAACAGCAAAATCTCAAGTCTTCAACGGGGCCA	3009
Db	2763	CTTTGCCCACTTATTAACAACCACTCTTCAACAGCAAAATCTCAAGTCTTCAACGGGGCCA	2822
Oy	3010	GCAACGACCAACTACTTCTGGGCTACAGCACCCCTGGGGGTATTTGATTTCAACAGAT	3069
Db	2823	GCAACGACCAACTACTTCTGGGCTACAGCACCCCTGGGGGTATTTGATTTCAACAGAT	2882
Oy	3070	TCCACTGCGATTTTCTCACACAGTACCTGGGACGACACTCATCAACAACAATTTGGGGATTCC	3129
Db	2883	TCCACTGCGATTTTCTCACACAGTACCTGGGACGACACTCATCAACAACAATTTGGGGATTCC	2942
Oy	3130	GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCAACATTCAGAGAGGTCAACGAGATG	3189
Db	2943	GGCCCAAGAGACTCAACTTCAACATCTTCAACATCAAGTCAAGAGAGGTCAACGAGATG	3002

QY	3150	ATGGGTCACGACCAATGCTTAATACTTACAGACAGGTTCAAGTCTTGGACCTGG	32459
Db	3003	ATGGGGTCACAACCAATCGCTAATACTTACAGACAGGTTCAAGTCTTGGACCTGG	30622
QY	3250	AGTACCAAGTCCCGTACGTCTCCGCTCTGGGCACCAAGGGTGCTCCCTCGTTCCGG	3309
Db	3063	AGTACCAAGTCCCGTACGTCTCCGCTCTGGGCACCAAGGGTGCTCCCTCGTTCCGG	31222
QY	3310	CGGAGCGTTCATGATTTCCGCAATTCGGCTACTTAAGCTCAACAATGGCAAGCGAG	33659
Db	3123	CGGAGCGTTCATGATTTCCGCAATTCGGCTACTTAAGCTCAACAATGGCAAGCGCG	31822
QY	3370	TGGGAGCGTCACTCTTACTACTGCGCGAATATTTCCATTCGAGATGCTGGAACGGGCA	34259
Db	3183	TGGGAGCGTCACTCTTACTACTGCGCGAATATTTCCATTCGAGATGCTGGAACGGGCA	32422
QY	3430	ATTAATTTACTCTTCAGCTACACTTTCGAGAGCGTGCTTTCACAGACGTACGCGACA	34899
Db	3243	ACAATTTTACTCTTCAGCTACACTTTCGAGAGCGTGCTTTCACAGACGTACGCGACA	33022
QY	3490	GCCAGAGCGCTGGACCGGCGTGAATGTAATCTCTCATTCGACACATTAACCTGTAACA	35459
Db	3303	GCCAGAGCGCTGGACCGGCGTGAATGTAATCTCTCATTCGACACATTAACCTGTAACA	33622
QY	3550	GAATCTCAAAATCAGTCCCGAAGTGCCCAAAACAAGACCTTGTTTAGCGGTGGTCTC	3609
Db	3363	GAATCTCAAAATCAGTCCCGAAGTGCCCAAAACAAGACCTTGTTTAGCGGTGGTCTC	34222
QY	3610	CAGCTGGCATGTCTGTTCAGCCCAAAAATGCGTACTTGACACCTGTTTACCGGACGACG	3669
Db	3423	CAGCTGGCATGTCTGTTCAGCCCAAAAATGCGTACTTGACACCTGTTTATGGGACGACG	3482
QY	3670	GCGTTTCTAAACCAAAAACAGACAACAACAAGCAATTTTAACTGACCTGGCTGGTCTTCAA	3729
Db	3483	GCGTTTCTAAACCAAAAACAGACAACAACAAGCAATTTTAACTGACCTGGCTGGTCTTCAA	3542
QY	3730	AATATTAACCTTAAATGGGCGTGAATCTTAAATCAACCCCTGGACCTGTAATGGGCTCACACA	3789
Db	3543	AATATTAACCTTAAATGGGCGTGAATCTTAAATCAACCCCTGGACCTGTAATGGGCTCACACA	3602
QY	3790	AAGACGACAAAGACAAGTTCTTTCCATGACGCGGTGCATGATTTTGGAAAGGAGAGCG	3849
Db	3603	AAGACGACAAAGACAAGTTCTTTCCATGACGCGGTGCATGATTTTGGAAAGGAGAGCG	3662
QY	3850	CCGAGGCTTCAAAACAATGCAATTTGACATGTCATGATCAACAAGAGAGAAATCAAG	3909
Db	3663	CCGAGGCTTCAAAACAATGCAATTTGACATGTCATGATTTCAACAAGAGAGAAATTAAG	3722
QY	3910	CCACTTAACCCCGTGGCCACCGAAGATTTGGGACTGTGGCACTCAATCTCCAGACGACA	3969
Db	3723	CCACTTAACCCCGTGGCCACCGAAGATTTGGGACTGTGGCACTCAATTTCCAGACGACA	3782
QY	3970	GCACAGACCTTCGCAACCGAGATGTGCATGTTATGGGAGCCTTACCTTGGAAATGGTGGGC	4029
Db	3783	GCACAGACCTTCGCAACCGAGATGTGCATGTTATGGGAGCCTTACCTTGGCAATGGTGGGC	3842
QY	4030	AAGACAGACGTAATCTGCAAGGGTCTTATTTGGGCCCAAAATTTCTTCAACGGAGTGAAC	4089
Db	3843	AAGATATGAGAGTGTACTGCAAGGGTCTTATTTGGGCCCAAAATTTCTTCAACAGATGAAC	3902
QY	4090	ACTTTACACCGGTCTCTCATATGGGCGGCTTTGACCTTAAGCAACCGGCTCTCAGATTC	4149
Db	3903	ACTTTACACCGGTCTCTCTTAATGGGCGGCTTTGACCTTCAAAACCGGCTCTCAGATTC	3962
QY	4150	TCATCAAAAACAGCGCTTGTCTGCGAATCTCCGCGAGAGTATTTGGCTTCAAAAGTTTG	4209
Db	3963	TCATCAAAAACAGCGCTTGTCTGCGAATCTCCGCGAGAGTATTTGAGCTTCAAAAGTTTG	4022
QY	4210	CTTCAATTCATCAACCAAGTATTCACAAGACAAAGTGAAGTGGAGATTTGGAGCTTCG	4269
Db	4023	CTTCAATTCATCAACCAAGTATTCACAAGACAAAGTGAAGTGGAGATTTGGAGCTTCG	4082

[illegible]

## RESULT 11

ID ADZ46594 standard; DNA; 4347 BP

AC ADZ46594;

DT 30-JUN-2005 (first entry)

DE HSV-AAV sequence rep2cap1 for AAV/HSV vectors

**KW** Genetic engineering; gene therapy; vector; cancer; neoplasm; cytostatic;

KW neuroprotective; ds.

05 Adeno-associated virus

XX

XX

XX

XX

XX



XX

XX

PT associated virus vec

PT respiratory diseases

PS Claim 1; SEQ ID NO 1; 79pp; Chinese.

CC The invention relates to a recombinant herpes simplex virus (HSV)

CC from nucleotide sequences of ADZ46594-ADZ46598 or their homologous

CC the construction of DNA fragments that contains sequences AD246594-

HSV by applying genetic engineering to give the recombinant HSV, large-

CC 1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-

CC corresponding vector cell-line with the 5 recombinant HSV, producing

the vector cell-line, separating and purifying the 5 serotype recombinant



crude lysate and further purification of rAAV by density-gradient centrifugation or affinity chromatography) and a recombinant vector plasmid pSNAP-NX (containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV-5 or AAV-6 genome, with immediate-early enhancer and promoter of cytomegalovirus, and a polyclonal site and a polyA signal, respectively, between the ITR (inverted terminal repeat), and neomycin-resistance gene-expressing cassette at outer edge of ITR). The DNA sequence is inserted into XbaI site in U2 or U44 gene in HSV genome. The DNA sequence of sequence AD246594-AD246598 can also be inserted into other non-essential gene regions in HSV genome. The recombinant HSV is optionally inserted with other DNA sequences homologous with the already-specified fragments. The vectors are for use in gene therapy of e.g. cancer, respiratory diseases and neural diseases. The virus vectors are safe, with long expression time and wide-spectrum of cell infection, even non-cleaved cells and reverse axonal conduction through the incorporated HSV vectors, and high transfer efficiently. The present sequence is the HSV-AAV sequence repCap1 for the AAV/HSV vectors of the invention.

Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

Query Match 81.2%; Score 3802; DB 14; Length 4347;

Best Local Similarity 92.6%; Pred. No. 0; Mismatches 315; Indels 5; Gaps 3;

Matches 4026; Conservative 0; Mismatches 315; Indels 5; Gaps 3;

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Qy 191 GTCCGTATTAGAGGTCACTGAGTGTGTCGACATTTTCGACACCATGTGTCTACGC 250
Db 6 GTCCGTATTAGAGGTCACTGAGTGTGTCGACATTTTCGACACCATGTGTCTACGC 65
Qy 251 TGGGTATTAAAGCCCGAGTGCACGACGAGGCTCTCCATTTTGAAGCGGAGTTGAACG 310
Db 66 TGGGTATTAAAGCCCGAGTGCACGACGAGGCTCTCCATTTTGAAGCGGAGTTGAACG 125
Qy 311 CGCAG-CGCCATGCGGGGGTTTACGAGATTGTGATTAAGTCCCGACGACTTTGACGA 369
Db 126 CGCAGCGCCATGCGGGGGTTTACGAGATTGTGATTAAGTCCCGACGACTTTGACG 185
Qy 370 GCATCTGCGCGGCAATTTCTGACAGCTTTGTGAACGTGGGTGCGGAGAGAGTGAATT 429
Db 186 GCATCTGCGCGGCAATTTCTGACAGCTTTGTGAACGTGGGTGCGGAGAGTGAATT 245
Qy 430 GCCGCCAGATTCTGACATGATCTGAATCTGATTGACAGGACCCCTGACCGTGGCGGA 489
Db 246 GCCGCCAGATTCTGACATGATCTGAATCTGATTGACAGGACCCCTGACCGTGGCGGA 305
Qy 490 GAAGCTGACGCGGCACTTCTGATCCATCTGAGCGCGCTGATGAAGGCCCGGAGGCCCT 549
Db 306 GAAGCTGACGCGGCACTTCTGATCCATCTGAGCGCGCTGATGAAGGCCCGGAGGCCCT 365
Qy 550 CTCTTTTGTTCGATTCGAGAGGAGGAGTCTTCACTTCCACTCATATTCTGTGAGAC 609
Db 366 TTTCTTTGTTCGATTCGAGAGGAGGAGTCTTCACTTCCACTCATATTCTGTGAGAC 425
Qy 610 CACGGGGTCAAAATTCATGTGTGTGGCGGCTTCTGTAGTCAGATTAACGACAGTGTGT 669
Db 426 CACGGGGTCAAAATTCATGTGTGTGGCGGCTTCTGTAGTCAGATTAACGACAGTGTGT 485
Qy 670 GCAGACCATCTACCGCGGGATTCAGCGCAGACCTCGCCCACTGTTCGCGGTGACCAAGC 729
Db 486 TCAGAGAAATTTACCGCGGGATTCAGCGCAGACCTTCGCAAACTGTTCGCGGTGACCAAGC 545
Qy 730 GCGTAAATGCGCGGAGGGGGGAAACAGAGTGTGACGAGTCTACATCCCACTACCT 789
Db 546 CAGAAATGCGCGGAGGGGGGAAACAGAGTGTGACGAGTCTACATCCCACTACCT 605
Qy 790 CTTGCCCAAGTACAGCCCGAGTGTGACGCGGTGACGCTAACTAGAGAGTATATAG 849
Db 606 GCTCCCAAAACCAAGCTGAGCTTCAGTGGCGGTGACGCTAAATGAGAACGATTTTAAAG 665
Qy 850 CGCGTGTTTAAACCTGCGCGGACCAACGCGCTCGTGGCGACGACGACCCAGCTGAG 909
Db 666 CGCGTGTTTAAACCTGCGCGGACCAACGCGCTCGTGGCGACGACGACCCAGCTGAG 725
Qy 910 CCAAGCCAGGAGCAAAAGAGATCTGAACCCCAATTCTGACGCGCTGTCTATCCG 969
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Db 726 GCAGACCGAGAGCAGAAACAAAGAGATCTGAATCCCAATTTCTGATCGCGGTGATCAG 785
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Qy 1030 CTCCGAGAGCAGAGTATCCAGAGAGACAGGCTCTGATATCTCTTCAACGCGGCTTC 1089
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Qy 1150 CAAATCCGCGCGGACCTACCTGTGAGGCCCCGCTCCGCGCGGACATTAACCAACCG 1209
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Qy 1270 CGGCTGGGCGGAGAAAAGTTTGGAAAACCAACATCATCTGCTGTTTGGGCGGCGCAC 1329
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Qy 1390 CAACTGAGCAATGAGATCTTCTCTTCAACGATTCGCTGACAGATGATGATCTGCTG 1449
Db 1206 AAATGAGCAATGAGATCTTCTCTTCAACGATTCGCTGACAGATGATGATCTGCTG 1265
Qy 1450 GAGAGAGGCAAGATGACGCGCAAGTCTGTGAGTCCGCGCAAGGCAATTTCTCGCGGAC 1509
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Db 1626 CAGTGAAGCAGATTAAGGCGAGCCCAAGCGGCGCTGCGGATGAGTGGAGCGCATGAC 1685
Qy 1870 GTCAGACGCGGAGAGGAGCTCGGAGGACTTTCGCGGACAGGATCAAAACAAATGTTCTCG 1929
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Qy 1930 TCAAGCGGCGATGCTTCAATGCTGTTTCCCTGCAAAACATGCGAGAAATGAATCAAGAA 1989
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Qy 1990 TTTCAATTTGCTTCAAGCAGGAGACAGAGACTGTTTCAGATGTTTCCCGCGGCTGTC 2049
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Db 1803 TTTCAACATTTGCTTACGCGACGGGACGAGACTGTTCAAGATGCTTTCCCGCGGTGTC 1862  
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Db 1863 AGAATCTCAACCGGTCGTGAGAAAGAGACGTAATGAAACCTGTGCAATTCATCATCT 1922  
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Db 1923 GCTGGGGGGGCTCCCGAGATTTGCTGTGCGCTGCGATCTGATCAACGATGATCTGGA 1982  
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Db 1983 TGACTGTGTTTCTGACCAATTAATGACTTAAACAGATATGCTGCGATGTTATCTTC 2042  
Qy 2230 CAGATTTGCTGAGGACAACTCTCTGAGGGCATTCGSCAGTGTGGAATTTGAACCTG 2289  
Db 2043 CAGATTTGCTGAGGACAACTCTCTGAGGGCATTCGSCAGTGTGGAATTTGAACCTG 2102  
Qy 2290 GAGCCCCGAAACCCAAACCAACAGCAAAAGCAGAGACGAGCGCGGGGTCTGTCCTTC 2349  
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Db 2343 CGTCTTTTGGGGGCAACTCGGGCGAGGACTTCTTCAGGCGCAAGAGAGGTTCTCGAC 2402  
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Db 2463 AGTGCACACAAGACCCAGACTCTCTCGGGCATTTGGCAAGACAGGACGCGGCTA 2522  
Qy 2710 AAAAGAGACTCAATTTTGTGACACTGCGACTGAGTCAAGTCCCGATCACAACCTC 2769  
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Qy 2770 TCGGAGAACTCTCAAGCAACCCCGCTGTGTGGGACCTAATCAATGCTTCAGGCGGTG 2829  
Db 2583 TCGGAGAACTCTCAAGCAACCCCGCTGTGTGGGACCTAATCAATGCTTCAGGCGGTG 2642  
Qy 2830 GCGACCAATTTGGCAGCAATTAACGAAGGCGCGACGAGGTGATGCTCAGAGAAAT 2889  
Db 2643 GCGACCAATTTGGCAGCAATTAACGAAGGCGCGACGAGGTGATGCTCAGAGAAAT 2702  
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Qy 3610 CAGCTGCAATGCTGTTCAAGCCCAAAACTGCTACCTGGAACCTGTTTACCGGACGAC 3669  
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Db 3963 TCAATCAAAAACAGGCTGTTCTGCGAATCTTCCGCGCGAGTTTTCAGCTTACAAAGTTTG 4022

QY 4210 CTTGATTCATCACCAGTATTCCACAGGACAAGTGAAGCGTGAATGAGATTCGAGCGTGC 4269  
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DB 4083 AGAAGAAAACAGCAAAACGCTGGAAATCCGGAAGTGCAGTATACATCTAATCTATGCAAAAT 4142  
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DB 4143 CTGCAACGTTGATTTTCACTGTGACCAACATGAGCTTTATACGAGCTGCGCCCAATG 4202  
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DB 4203 GCACCCGTTACCTGACCCGCTCCCTGTAATGTTGTTAATCAATAAACCGGTTAATTCG 4262  
QY 4450 TGTGAGTTGAACTTTGGTCTCATGTCTTATTTATCTATCTGTGACCATATGCAACCGGT 4509  
DB 4263 TTTGAGTTGAACTTTGGTCTCTGCTCTTATCTTATCTTATC-GGTTACCATGTTATAGCT 4321  
QY 4510 TACACATTAAGCTGCTGTTGTCGCTT 4535  
DB 4322 TACACATTAAGCTGCTGTTGTCGCTT 4347

## RESULT 12

AEF81093  
ID AEF81093 standard; DNA; 4347 BP.

AC AEF81093;

DT 06-APR-2006 (first entry)

DE Adeno-associated virus related rep2cap1 DNA SEQ ID NO 1.

KW growth; food; meat; rep2cap1; ds.

OS Adeno-associated virus.

PN CN162652-A.

PD 15-JUN-2005.

PF 08-DEC-2003; 2003CN-01117208.

PR 08-DEC-2003; 2003CN-01117208.

PA (ZHEN-) ZHENGYANG GENE TECH CO LTD BENYUAN.

PI Dong X;

DR WPI; 2005-749951/77.

PT Method for accelerating quick growth of animals and method for improving  
PT quality of meat.

PS Disclosure; SEQ ID NO 1; 28bp; Chinese.

CC The invention relates to a method for promoting fast growth of animal and  
CC improving its meat quality features that the adenovirus associated virus  
CC carrier, especially the type-A one, is introduced to the growth hormone  
CC gene or relative gene. The present sequence represents an adeno-  
CC associated virus related rep2cap1 DNA.

XX Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

Query Match 81.2%; Score 3802; DB 14; Length 4347;

Best Local Similarity 92.6%; Pred. No. 0;

Matches 4026; Conservative 0; Mismatches 315; Indels 5; Gaps 3;

QY 191 GTCTGTTATTTAGAGTCACTGAGTGTGTTTGGCAGATTTTGGCAGACCATATGTGTCAAGC 250  
DB 6 GTCTGTTATTTAGAGTCACTGAGTGTGTTTGGCAGATTTTGGCAGACCATATGTGTCAAGC 65

QY 251 TGGGATTTTAAGCCCGAGTGAGCAGCGAGGGTCTCCATTTTGAAGCGGAGGTTTGAACG 310  
DB 66 TGGGATTTTAAGCCCGAGTGAGCAGCGAGGGTCTCCATTTTGAAGCGGAGGTTTGAACG 125  
QY 311 CGCAG-GCCATGCGGGGGTTTTCAGAGATTGATTAAAGTCCCGACGACCTTGACGA 369  
DB 126 CGCAGCGCCGATCGGGGGTTTTCAGAGATTGATTAAAGTCCCGACGACCTTGACG 185  
QY 370 GCATCTGCCCGGATTTCTGACAGCTTTTGAACTGGGTGGCGGAGAGGAATGGAGTT 429  
DB 186 GCATCTGCCCGGATTTCTGACAGCTTTTGAACTGGGTGGCGGAGAGGAATGGAGTT 245  
QY 430 GCCGCAGATTCTGACATGTGATCTGATTGATGACAGCACCCTGACCGTGGCGGA 489  
DB 246 GCCGCAGATTCTGACATGTGATCTGATTGATGACAGCACCCTGACCGTGGCGGA 305  
QY 490 GAACTGCGACCGGACTTCTGTGCACTGGCGCGCGTGAATGAGGCCCGGAGGCTT 549  
DB 306 GAACTGCGACCGGACTTCTGTGCACTGGCGCGCGTGAATGAGGCCCGGAGGCTT 365  
QY 550 CTTCCTTTGTTCACTTGAGAGAGGGCGAGTCTTCCACCTGCATATTCGTGGAGAC 609  
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Db 1686 GTCAAGCAGCGA - - - AGCTTGATCACTACGCAACAGGTACCAAAACAATGTTCTCG 1742  
QY 1930 TCACCGCGGACGTCTTCAAGATGCTGTCTTCCCTGCAAGACATGCGAGAGATGAATCAGAA 1989  
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QY 2050 AGAATCTCAACCGGTCTGTCAGAAAGAGACGATCGGAAACTGTGCGCATTCATCATCT 2109  
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QY 2770 TCGAGAACTTCAGCAACCCCGCTGCTGTGGACTTACTTACATGCTTCAAGCGGTG 2829  
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Db 2703 GGCATTGAGATTCAATGAGTGGGGCGACAGATCATACACACGACCCGACCTGG 2762  
QY 2950 CTTGCGCACCTTATTAACCAACCACTCTTACAGCAAAATCTCCAGTCTTCAACGGGGGCA 3009  
Db 2763 CTTGCGCACCTTATTAACCAACCACTCTTACAGCAAAATCTCCAGTCTTCAACGGGGGCA 2822  
QY 3010 GCAACGACCACTACTCTGCGCTTACAGACCCCTGGGGGTATTTGATTTCAACAGAT 3069  
Db 2823 GCAACGACCACTACTCTGCGCTTACAGACCCCTGGGGGTATTTGATTTCAACAGAT 2882  
QY 3070 TCCACTGCACTTCTCACACGATGACGAGCGGACCTCAACAAATTGGGGATTC 3129  
Db 2883 TCCACTGCACTTCTCACACGATGACGAGCGGACCTCAACAAATTGGGGATTC 2942  
QY 3130 GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATTCGAAGTCAAGAGGTCAAGCAATG 3189  
Db 2943 GGCCCAAGAGACTCAACTTCAACATTCGAAGTCAAGAGGTCAAGCAATG 3002  
QY 3190 ATGAGCTACGACCATGCTATTAATTAACCTTACAGACAGGTTCAAGTCTTGTGGACTCG 3249  
Db 3003 ATGAGCTACGACCATGCTATTAATTAACCTTACAGACAGGTTCAAGTCTTGTGGACTCG 3062  
QY 3250 AGTACCACTTCCCGTAAAGTCTGCGCTGTGGGACAGAGGTGCTCCCTCCGTTCCCG 3309  
Db 3063 AGTACCACTTCCCGTAAAGTCTGCGCTGTGGGACAGAGGTGCTCCCTCCGTTCCCG 3122  
QY 3310 CGGACGTGTCAATATTCGAGATGAGGCTTACCTTCAAGGCTCAACATGAGGAGCCAG 3369  
Db 3123 CGGACGTGTCAATATTCGAGATGAGGCTTACCTTCAAGGCTCAACATGAGGAGCCAG 3182  
QY 3370 TGGAGCTCATCTTTTACTGCTGGAATATTTCCATGCGAGATGCTGGAACGGGCA 3429  
Db 3183 TGGAGCTCATCTTTTACTGCTGGAATATTTCCATGCTGGAACGGGCA 3242  
QY 3430 ATTACTTACTTCAAGTCAACCTTGAAGACGTCCTTTCACAGAGACTACGGGCA 3489  
Db 3243 ACAACTTACTTCAAGTCAACCTTGAAGAGGCTTTTTCACAGAGACTACGGGCA 3302  
QY 3490 GCCAGAGCTGAGCCGCTGATGAATCTCTCATCGACAGTACTGTATTAACCTGAACA 3549

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Dh 3303 GCCAGAGCCTGGACCGGCTGATGAATCCTCATCGAACCAATATCTGATTACTGAACA 3362
Qy 3550 GAATCACAATCACTGCGGGAAGTGGCCAAAACAAGAACTTGTCTGTGTTAGCCGTGGTCTC 3609
Db 3363 GAATCAAAATCAGTCCGGAAGTGCCTAAAACAAGAACTTGTCTGTGTTAGCCGTGGTCTC 3422
Qy 3610 CAGCTGCATGCTGTTGAGCCCAAAAACCTGCTACTGAGCCCGTTACGGGAGCAGC 3669
Db 3423 CAGCTGCATGCTGTTGAGCCCAAAAACCTGCTACTGAGCCCGTTATGCGAGCAGC 3482
Qy 3670 GCGTTTCTAAAACAAAAACAACAACAACAAGCACTTTACTGGACTGTGCTTCAA 3729
Db 3483 GCGTTTCTAAAACAAAAACAACAACAACAAGCACTTTACTGGACTGTGCTTCAA 3542
Qy 3730 AATATTAACCTTAAGGGGCGTAATCTATATCAACCCGSGACGCTATGCGCTCACCA 3789
Db 3543 AATATTAACCTTAAGGGGCGTAATCTATATCAACCCGSGACGCTATGCGCTCACCA 3602
Qy 3790 AAGACGACAAAGACAAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGCG 3849
Db 3603 AAGACGACAAAGACAAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGCG 3662
Qy 3850 CCGAGACTTCAAACCTGCAATGGAACAATGTCATGATCAACAGACGAGAGAAATCAAAG 3909
Db 3663 CCGAGACTTCAAACCTGCAATGGAACAATGTCATGATCAACAGACGAGAGAAATCAAAG 3722
Qy 3910 CCACATAACCCGCTGGCCACCGAAAGATTGGGACGTGTGGCAATCTCCAGAGCGCA 3969
Db 3723 CCACATAACCCGCTGGCCACCGAAAGATTGGGACGTGTGGCAATCTCCAGAGCGCA 3782
Qy 3970 GCACAGACCTTGCGACCGGAGATGTCATGTTATGGAGCCTTACTGGAATGGTGTGGC 4029
Db 3783 GCACAGACCTTGCGACCGGAGATGTCATGTTATGGAGCATTTACTGCGATGGTGTGGC 3842
Qy 4030 AAGACAGAGAGTATCTGCAAGGCTCTATTTGGGCAAAATCTCTACACGATGAGAC 4089
Db 3843 AAGATAGAGAGTATCTGCAAGGCTCTATTTGGGCAAAATCTCTACACGATGAGAC 3902
Qy 4090 ACTTACACCGCTCTCTCANAGGGCGCTTGGACCTTAAGCAACCCGCTCTCAGATCC 4149
Db 3903 ACTTACACCGCTCTCTCTATAGGGCGCTTGGACCTTAAGCAACCCGCTCTCAGATCC 3962
Qy 4150 TCATCAAAAACACGCGTGTCTCTGCGAATCTCCGCGACAGTTTTCGGCTACAAAGTTTG 4209
Db 3963 TCATCAAAAACACGCGTGTCTCTGCGAATCTCCGCGCGAAGTTTTCAGCTACAAAGTTTG 4022
Qy 4210 CTTCAATTATCAACCAAGTATTCACAGACAAAGTACGCTGGAATTAATGGAGCTGC 4269
Db 4023 CTTCAATTATCAACCAAGTATTCACAGACAAAGTACGCTGGAATTAATGGAGCTGC 4082
Qy 4270 AGAAGAAAAACAGCAAAAGCTGGAATCCGGAAGTACATATCACTTAATGCAAAAT 4329
Db 4083 AGAAGAAAAACAGCAAGGCTGGAATCCGGAAGTACATATCACTTAATGCAAAAT 4142
Qy 4330 CTGCAACGTTGATTTCACTGTGACAAACAATGACCTTATATCTGAGCCCTGCCCATTTG 4389
Db 4143 CTGCAACGTTGATTTCACTGTGACAAACAATGACCTTATATCTGAGCCCTGCCCATTTG 4282
Qy 4390 GCACCCGTTACTCTACCCGCTGCTGATATGTTGTTAATCAATAAACCGGTTAATTCG 4449
Db 4203 GCACCCGTTACTCTACCCGCTGCTGATATGTTAATCAATAAACCGGTTAATTCG 4262
Qy 4450 TGTGAGTTGAACCTTGTGCTCATGCTTATATCTTATGTCACCATATGCAACCGGT 4509
Db 4263 TTTGAGTTGAACCTTGTGCTCATGCTTATATCTTATATTC-GGTTACCATGTTATAGCT 4321
Qy 4510 TACAATTAATCTGTTAGTGGCTT 4535
Db 4322 TACAATTAATCTGTTAGTGGCTT 4347
```

RESULT 13  
ADE76502

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ID ADE76502 standard; DNA; 4721 BP.
XX
AC ADE76502;
XX
DT 29-JAN-2004 (first entry)
XX
DE Adeno-associated virus (AAV) related DNA, SEQ ID NO 1.
XX
KW adeno-associated virus; AAV; cytosolic; antiposrotic; antirheumatic;
KW antirheumatic; antiprotective; antidiabetic; antithyroid;
KW dermatological; antineoplastic; gene therapy; vaccine;
KW hyperproliferative; cancer; psoriasis; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; diabetes;
KW autoimmune thyroiditis; scleroderma; Crohn's disease; gene; de.
XX
OS Adeno-associated virus 7.
XX
PN EPI310571-A2.
XX
PD 14-MAY-2003.
XX
PE 12-NOV-2002; 2002EP-00257826.
XX
PR 13-NOV-2001; 2001US-0350607P.
PR 17-DEC-2001; 2001US-0341117P.
PR 01-MAY-2002; 2002US-037066P.
PR 05-JUN-2002; 2002US-0386675P.
XX
PA (UNP-) UNIV PENNSYLVANIA.
PI Gao G, Wilson JM, Alvira M;
P1 WPI: 2003-450984/43.
DR P-PSDB: ADE76503.
XX
XX
XX Detecting adeno-associated virus sequences in a sample, useful for e.g.
PT preventing or treating hyperproliferative or autoimmune diseases,
PT comprising subjecting a sample having a DNA to amplification via
PT polymerase chain reaction.
XX
XX
XX Claim 17; SEQ ID NO 1; 419bp; English.
XX
XX The invention relates to a novel method for detecting adeno-associated
XX virus (AAV) sequences in a sample, which comprises subjecting a sample
XX containing a DNA to amplification via a polymerase chain reaction (PCR).
XX The AAV sequence have the following activities: cytosolic,
XX antiposrotic, antirheumatic, antirheumatic, antineoplastic,
XX antidiabetic, antithyroid, dermatological, and antineoplastic. The AAV
XX sequence can be used in gene therapy or as part of a vaccine to treat
XX disorders. The method is useful in detecting and/or identifying AAV
XX sequences and isolating novel sequences that are identified. The
XX sequences may be used e.g. for preventing or treating hyperproliferative
XX conditions such as cancers and psoriasis, and other autoimmune diseases
XX like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
XX thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence
XX represents an AAV related DNA sequence of the invention.
XX
XX Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;
XX
XX Query Match 78.5%; Score 3678.4; DB 10; Length 4721;
XX Best Local Similarity 87.5%; Pred. No. 0;
XX Matches 4135; Conservative 0; Mismatches 541; Indels 52; Gaps 8;
Qy 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTGCTCACTGAGCCCGGCGACCAAGTCCG 60
Db 1 TTGGCCACTCCCTCTCTGCGCGCTCGCTGCTGCTGCGCGCTCGCGACCAAGTCCG 60
Qy 61 CGAGCCCGGCTTTGGCCCGGCGGCTCTGAGTACGAGCGAGCGCGACGAGGAGTG 120
Db 61 AGAGCGGAGAGCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTG 120
Qy 121 GCCAACTCACTAGGAGGCTTCTGAGG-----GCTGAGTCTGAC 164
```

Dh 121 GCCAACTCCATCACTAGGGGTACGGCGAAGCGCTCCACGCTGCGGCTGACGCTAC 180  
Qy 165 GTGAATTACGTCATAGGGTTAGGAGGCTCTGTATTAGAGTCACTGATG-TTTTGCG 223  
Db 181 GTAATCACTGTCATAGGG---GAGTGTCTGTATTACCTGTCACTGATGCTTTTCG 237  
Qy 224 ACATTTTGCAGACCATGTGTGTCAGCTGTGATTATTAAGCCGAGTGAACAAGGAGTC 283  
Db 238 ACATTTTGCAGACCATGTGTGTCAGCTGTGATTATTAAGCCGAGTGAACAAGGATC 297  
Qy 284 TCATTTTGAACCGGAGGTTTGAACGCGACAGCCCATGCGGGTTTATGAGATTG 343  
Db 298 TCATTTTGAACCGGAGGTTTGAACGAGACAGCATGCGGGTTTATGAGATTG 357  
Qy 344 ATTAAAGTCCCGAGGACCTTGAAGAGATCTGCCGCAATTTCTGACAGCTTGTGAC 403  
Db 358 ATCAAGGTCGAGAGCATGTGACAGACCTGCGGCATTTCTGACTCGTTGTGTAAC 417  
Qy 404 TGGGTGGCGGAGGAAATGGGAGTTGCGCGCAATTTGACATGAGATCTGATCTGATT 463  
Db 418 TGGGTGGCGGAGGAAATGGGAGTTGCGCGCAATTTGACATGAGATCTGATCTGATT 477  
Qy 464 GAGCAGGACCCCTGACCGTGGCGGAGAGCTGACGCGCATTTCTGTGTCACCTGCGC 523  
Db 478 GAGCAGGACCCCTGACCGTGGCGGAGAGCTGACGCGCATTTCTGTGTCATGCGC 537  
Qy 524 CGCTGAGTAAAGCCCGGAGGCTCTTTCTTTGTTCACTTGTGAGAGGGCGAGTCTAC 583  
Db 538 CGCTGAGTAAAGCCCGGAGGCTCTTTCTTTGTTCACTTGTGAGAGGGCGAGTCTAC 597  
Qy 584 TTCCACCTCCATTTCTGTGAGAGCAGCGGGGGTCAATCCATGAGTCTGGGCGCTTC 643  
Db 598 TTCCACCTCCATTTCTGTGAGAGCAGCGGGGGTCAATCCATGAGTCTGGGCGCTTC 657  
Qy 644 CTGAGTCAGATTAGCAGCAAGCTGGTGGAGCACTCTACCGCGGGATGAGCCGACCTG 703  
Db 658 CTGAGTCAGATTAGCAGCAAGCTGGTGGAGCACTCTACCGCGGGATGAGCCGACCTG 717  
Qy 704 CCCAACTGTTCGCGGTGACCAAGACGCTGATGAGCGCGGAGGGGGAACAAGTGTG 763  
Db 718 CCCAACTGTTCGCGGTGACCAAGACGCTGATGAGCGCGGAGGGGGAACAAGTGTG 777  
Qy 764 GAGAGTCTACATCCCACTACCTCTGCGCAAGACTGACGCGGACGTCAGTGGGCG 823  
Db 778 GAGAGTCTACATCCCACTACCTCTGCGCAAGACTGACGCGGACGTCAGTGGGCG 837  
Qy 824 TGAATCAATGAGAGTATATAAGCGCTGTTTAACTGCGCGAGCGCAACGCGTC 883  
Db 838 TGAATCAATGAGAGTATATAAGCGCGCTGTTTAACTGCGCGAGCGCAACGCGTC 897  
Qy 884 GTGGCGCAGACTGACCTGACCTGACCGCAAGCCAGAGAGCAACAAGAGATCTGAC 943  
Db 898 GTGGCGCAGACTGACCTGACCTGACCGCAAGCCAGAGAGCAACAAGAGATCTGAC 957  
Qy 944 CCCAACTGTGCGGCGCTGATCCGCTCAAAAACCTCCGCAAGCTCTCATGAGACTGTC 1003  
Db 958 CCCAACTGTGCGGCGCTGATCCGCTCAAAAACCTCCGCTCAATGAGACTGTC 1017  
Qy 1004 GGGTGTGTGTGACCGGGGATCACTCGAGAGAGAGTGAATCCAGAGAGCAAGGCG 1063  
Db 1018 GGGTGTGTGTGACCGGGGATCACTCGAGAGAGAGTGAATCCAGAGAGCAAGGCG 1077  
Qy 1064 TCGTATCTTCTTCAACCGCGCTTCAACTGCGGTCCAGATCAAGGCGCTGTGAC 1123  
Db 1078 TCGTATCTTCTTCAACCGCGCTTCAACTGCGGTCCAGATCAAGGCGCTGTGAC 1137  
Qy 1124 AATGCGGAGAGATGAGGCTGACCAATCGGCGCGCACTGCTGAGGCGCGCT 1183  
Db 1138 AATGCGGAGAGATGAGGCTGACCAATCGGCGCGCACTGCTGAGGCGCGCT 1197  
Qy 1184 CGCGCGGAGATTAACCAACCGGATTTACCGCATCTGAGCTGAACGAGTACGAC 1243  
Db 1198 CTGCGCGGAGATTAACCAACCGGATTTACCGCATCTGAGCTGAACGAGTACGAT 1257

Qy 1244 CTGCTTACGCGGCTCGCTCTTTCTGCGCTGGGCGGACCAAGAAAGTTGAGAAACGACAC 1303  
Db 1258 CTGCTTACGCGGCTCGCTCTTTCTGCGCTGGGCGGACCAAGAAAGTTGAGAAACGACAC 1317  
Qy 1304 ACCATCTGAGTGTGAGGCGGACCAAGGAGCAACCATGCGGAGAGCCATGCGC 1363  
Db 1318 ACCATCTGAGTGTGAGGCGGACCAAGGAGCAACCATGCGGAGAGCCATGCGC 1377  
Qy 1364 CAGCGCTGCTTTCTACGCGTGCATGACCAATGAGAACTTTCCTTCAAGAT 1423  
Db 1378 CAGCGCTGCTTTCTACGCGTGCATGACCAATGAGAACTTTCCTTCAAGAT 1437  
Qy 1424 TGCCTGCAAGATGATGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1483  
Db 1438 TGCCTGCAAGATGATGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1497  
Qy 1484 TCGGCAAGGCAATTCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1543  
Db 1498 TCGGCAAGGCAATTCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1557  
Qy 1544 GCCAGATGATCCACCCCGTGTATGTCATCTTCAACACCAATGTGCGCGTGAAT 1603  
Db 1558 GCCAGATGATCCACCCCGTGTATGTCATCTTCAACACCAATGTGCGCGTGAAT 1617  
Qy 1604 GAGGGAACAGCACACCTTGTAGACACGAGCGCTTGTGAGGAGCGGATTTCAATTT 1663  
Db 1618 GAGGGAACAGCACACCTTGTAGACACGAGCGCTTGTGAGGAGCGGATTTCAATTT 1677  
Qy 1664 GAATCAACCGCGCTGAGAGATGATTTGGCAAGGAGCAAGAGCAAGAGGATCAAGAG 1723  
Db 1678 GAATCAACCGCGCTGAGAGATGATTTGGCAAGGAGCAAGAGGATCAAGAGGATCAAGAG 1737  
Qy 1724 TTCTTCGCTGGGCGGAGATCAAGTACCGAGTGGCGGATGATTTCTACGTCAAGAA 1783  
Db 1738 TTCTTCGCTGGGCGGAGATCAAGTACCGAGTGGCGGATGATTTCTACGTCAAGAA 1797  
Qy 1784 GGTGAGACCAACAACAACCGCGCGGATGAGCGGAGTAAAGCGAGCCCAAGCGGCGC 1843  
Db 1798 GGTGAGACCAACAACAACCGCGCGGATGAGCGGAGTAAAGCGAGCCCAAGCGGCGC 1857  
Qy 1844 TGCCCTCAGTGGGAGATTCATGAGTCAAGCGCGGAGGAGGAGTCCGGTGGACTTTGCC 1903  
Db 1858 TGCCCTCAGTGGGAGATTCATGAGTCAAGCGCGGAGGAGGAGTCCGGTGGACTTTGCC 1917  
Qy 1904 GACAGTACCAAAACAATGTTCTGTCAGCGCGGATGCTTCAAGTGTCTTCCCTGC 1963  
Db 1918 GACAGTACCAAAACAATGTTCTGTCAGCGCGGATGCTTCAAGTGTCTTCCCTGC 1977  
Qy 1964 AAAACATGCGAGAGATGAATCAAGATTTCAACTTTGCTTACGACCGGAGCAAGAGAC 2023  
Db 1978 AAAACATGCGAGAGATGAATCAAGATTTCAACTTTGCTTACGACCGGAGTCAAGAGAC 2037  
Qy 2024 TGTTCAGATGTTTCCCGGCGGTGAGATTCGAATCCAGTCCGCAAGAGAGGACGAT 2083  
Db 2038 TGTTCAGATGTTTCCCGGCGGTGAGATTCGAATTCGAATCCAGTCCGCAAGAGAGGACGAT 2097  
Qy 2084 CGGAACTGTGTGCAATTCATCTGCTGGGCGGCTCCGAGATGTGCTGCGGC 2143  
Db 2098 CGGAACTGTGTGCAATTCATCTGCTGGGCGGCTCCGAGATGTGCTGCGGC 2157  
Qy 2144 TGGCATTTGTGCAAGTGAATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAAC 2203  
Db 2158 TGGCATTTGTGCAAGTGAATCTGATGACTGTGTTTCTGAGCAATTAATGACTTAAAC 2217  
Qy 2204 AGGATGCTGCGGATGATTTCTTCCAGATTGGCTGAGAGCAACTCTCTGAGGGCAT 2263  
Db 2218 AGGATGCTGCGGATGATTTCTTCCAGATTGGCTGAGAGCAACTCTCTGAGGGCAT 2277  
Qy 2264 TCGCAGTGTGTGAGCTTGAACCTGAGGCTCGGAAACCCAAAGCCAAACGAGCAAAAGCA 2323  
Db 2278 TCGCAGTGTGTGAGCTTGAACCTGAGGCTCGGAAACCCAAAGCCAAACGAGCAAAAGCA 2337

QY 2324 GGAAGAGCGCGGGGCTGTGCTTCTCGGCTACAAAGTACCTCGGACCCCTTCAACGAGCT 2383  
| | | | |  
Db 2338 GGAACAACGGCCGGGGTCTGGTCTTCTCGGCTACAAAGTACCTCGGACCCCTTCAACGAGCT 2397  
| | | | |  
QY 2384 CGACAAAGGGGAGCCCGTCAACGGCGGATGACGGGCCCTCGACACGACAAAGGCTTA 2443  
| | | | |  
Db 2398 CGACAAAGGGGAGCCCGTCAACGGCGGATGACGGGCCCTCGACACGACAAAGGCTTA 2457  
| | | | |  
QY 2444 CGACGAGAGCTCAAAAGCGGGGATCAATCCGTACCTCGGATTAACCAACGGCGACGGCGGA 2503  
| | | | |  
Db 2458 CGACGAGAGCTCAAAAGCGGGGATCAATCCGTACCTCGGATTAACCAACGGCGACGGCGGA 2517  
| | | | |  
QY 2504 GTTTCAGAGGCGTTCGACAAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGACGTCTT 2563  
| | | | |  
Db 2518 GTTTCAGAGGCGTTCGACAAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGACGTCTT 2577  
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QY 2564 CCAGGCCAAGAAAGAGGTTCTCGAACTTTTGGTTCGTTTGAAGAAAGGTGCTAAGACGGC 2623  
| | | | |  
Db 2578 CCAGGCCAAGAAAGAGGTTCTCGAACTTTTGGTTCGTTTGAAGAAAGGTGCTAAGACGGC 2637  
| | | | |  
QY 2624 TCCTGAAAAGAAACGTCCGATAGAGCAGTTCGACACA---AGAGCCAGACTCTCTCGGG 2680  
| | | | |  
Db 2638 TCCTGCAAGAAAGAACCGGATAGACCCGTCACTCAGGCTTCCCGACCTCTTCAACGGG 2697  
| | | | |  
QY 2681 CATTGGCAAGACAGGCCAGACCCGCTAAAAAGACTCAATTTTGGTCAACTGGCGA 2740  
| | | | |  
Db 2698 CATCGGCAAGAAAGGCCAGACCCGCGCAAAAGAGACTCAATTTTGGTCAACTGGCGA 2757  
| | | | |  
QY 2741 CTCAGAGTCACTCCCGGACCCCAAACTCTTGGAGAACTCTCAAGAACCCCGCTGCTGT 2800  
| | | | |  
Db 2758 CTCAGAGTCACTCCCGGACCCCAAACTCTTGGAGAACTCTCAAGAGGCGCTTCAAGT 2817  
| | | | |  
QY 2801 GGGAGCTTACTCAATTGGCTTCAGGGCGTGGCGACCAATGGCAGACAATAAGAAAGGCG 2860  
| | | | |  
Db 2818 GGGAGCTTGGTACAGTGGCTGAGGGGGTGGCGCACCAATGGCAGACAATAAGAAAGGCG 2877  
| | | | |  
QY 2861 CGACGAGTGGGTATGCTCAGAAATTTGGCATTTGCATTTCCACATGGCTGGCGACAG 2920  
| | | | |  
Db 2878 CGACGAGTGGGTATGCTCAGAAATTTGGCATTTGCATTTCCACATGGCTGGCGACAG 2937  
| | | | |  
QY 2921 AGTCATCACCAACGACACCCGAAACATGGGCTTGGCCCACTTAAACACACCTCTACAA 2980  
| | | | |  
Db 2938 AGTCATTAACCAACGACACCCGAAACCTGGGCCCTGCCCACTTAAACACACCTCTACAA 2997  
| | | | |  
QY 2981 GCAATCTCCAGTCTTCAACGGGGGCCAGGACCAACCAACTACTTCCGCTACAGAC 3040  
| | | | |  
Db 2998 GCAATCTCCAGTCTTCAACGGGGGCCAGGACCAACCAACTACTTCCGCTACAGAC 3057  
| | | | |  
QY 3041 CCCCTGGGGGTATTTGATTTCAACAGATTCACCTGCATTTCTCACACGCTGAC 3100  
| | | | |  
Db 3058 CCCCTGGGGGTATTTGATTTCAACAGATTCACCTGCATTTCTCACACGCTGAC 3117  
| | | | |  
QY 3101 GCGACTCATCAACCAATTTGGGGATTTCCGGCCCAAGAGACTCAACTTCAGCTCTTCAA 3160  
| | | | |  
Db 3118 GCGACTCATCAACCAACTGGGGATTTCCGGCCCAAGAGACTTCAGCTCTTCAA 3177  
| | | | |  
QY 3161 CATCCAGTCAAGAGGTCACGACGAATGATGCGTCAACGACCACTCGTAAATTAACCTTAC 3220  
| | | | |  
Db 3178 CATCCAGTCAAGAGGTCACGACGAATGATGCGCTTTCAGACACTCGTAAATTAACCTTAC 3237  
| | | | |  
QY 3221 CAGCAGGTTCAAGTCTTTGCGACTCGGAGTCCAGTTCCCGTACGCTCGGCTGCG 3280  
| | | | |  
Db 3238 CAGCAGGTTCAAGTCTTTGCGACTCGGAGTCCAGTTCCCGTACGCTCGGCTGCG 3297  
| | | | |  
QY 3281 GCACACAGGCTGCTCCCTCGCTTCCGGCGGACGTGTTCAATGATTCGGCAGTACGGGTA 3340  
| | | | |  
Db 3298 GCACACAGGCTGCTCCCTCGCTTCCGGCGGACGTGTTCAATGATTCCTCGATACGGGTA 3357  
| | | | |  
QY 3341 CCTAAGCTCAACCAATGGCAGGCGAGTGGGACGTCACTCTTTTACCTCGTGAATA 3400  
| | | | |  
Db 3358 CCTAAGCTCAACCAATGGCAGTGGGACGTCTGCGAGGTTCTCTTCTACCTGCTGAGATA 3417  
| | | | |  
QY 3401 TTTCCTCATGAGATGCTGAGAAACGGGCAATTAATTTCCTTCAAGCTTACACCTTCGAGGA 3460  
| | | | |

Db 3418 CTTCCCTCTCAAGTGTGAGAAACGGGCAACAATTGAGTTCAGTACAGTTCGAGGA 3477  
| | | | |  
QY 3461 CGTGGCTTTTCAACAGACGCTAACCGGCAACGCCAGAGCTGGACCGGTATGTAATCCTCT 3520  
| | | | |  
Db 3478 CGTGGCTTTTCAACAGACGCTAACCGGCAACGCCAGAGCTGGACCGGTATGTAATCCTCT 3537  
| | | | |  
QY 3521 CATGACCACTTACCTGATTAACCTGAAACAGAACTCAATCACTGTCGGA---AGTGCCA 3577  
| | | | |  
Db 3538 CATGACCACTTACCTGATTAACCTGCGCAACAGAGTAAACCGAGGACGACAGTGG 3597  
| | | | |  
QY 3578 AAACAGGACTTGTGTTTACCGTGGGTCTCCAGCTGGCATGTCTGTTAGGCCAAAAA 3637  
| | | | |  
Db 3598 CAATCGGAACTGAGTTTACAGAGGCGGCGCTTCAACTATGCGCAACACCAAGAA 3657  
| | | | |  
QY 3638 CTGGCTACCTGGACCCGTTAACGGGACGAGCGGTTCTTAAACAAAAACAGACAA 3697  
| | | | |  
Db 3658 TTGGTTACCTGAGCTTGTCTTCCGGCAACAAAGTCTCCAAACCGTGGATCAAAACAA 3717  
| | | | |  
QY 3698 CAACAGCACTTTTACCTGACTGGTGTCTTCAAAATATTAACCTTAATGGCGTGAATCTAT 3757  
| | | | |  
Db 3718 CAACAGCACTTTTGTGACTGGTGTGCACTGGTGCACCAATATCACTGAAGCGGAGAACTGTT 3777  
| | | | |  
QY 3758 AATCAACCTTGGCACTGCTATGCGCTTCAACAAAGACGACAAAGACAAAGTCTTTCCAT 3817  
| | | | |  
Db 3778 GATTAAATCCCGCGCTCCGATGGCACTCAAGAGACGACGAGGACCGCTTTTCCATC 3837  
| | | | |  
QY 3818 GAGCGGTGATGATTTTGGAAAGGAGAGCGCGGACTTCAAAACCTGCATTTGACAA 3877  
| | | | |  
Db 3838 CAGCGAGTCTCTGATTTTGGAA---AACTGGAGCACTTAACAAACTCATTTGGAAAA 3894  
| | | | |  
QY 3878 TGTCTATGATCAACAGACGAAGAGAAATCAAGCACTAACCCCGTGGCCACCGAAAGATT 3937  
| | | | |  
Db 3895 TGTGTTAATGCAAAATGAAGAAATTCGCTCACTATCTGTAGCCACGGAAGATA 3954  
| | | | |  
QY 3938 TGGGACTGTGGCACTCAATCTCCAGACAGACAGACCACTTGGCCAGCGGAATGTGCA 3997  
| | | | |  
Db 3955 CGGGATGTGACAGCAACTTAACAGCGGCTAATACGCGCCAGACCAAAATTTGCA 4014  
| | | | |  
QY 3998 TGTATGGGACCTTACCTGGAATGCTGTGGCAAGACGAGATTAATCTGACGGGTTC 4057  
| | | | |  
Db 4015 CAACAGGAGCCTTACTGTCATGCTGTGGCAAGACGGGAGCTGTACTCGACGGGTTC 4074  
| | | | |  
QY 4058 TATTTGGGCAAAATTCCTCACACGATGACACTTTCACCCGCTCTCTCAATGGGCGG 4117  
| | | | |  
Db 4075 CATCTGGGCAAGATTCCTCACACGATGACACTTTCACCCGCTCTTGTGATGGGCGG 4134  
| | | | |  
QY 4118 CTTTGAATTAAGCACCCGCTCTCTCAGATCTCATTAATAAACACGCTGTTCTCTGGA 4177  
| | | | |  
Db 4135 CTTTGAATTAACATCCGCTCTCTCAGATCTCATTAATAAACACCTCCGTTCCCGTTAA 4194  
| | | | |  
QY 4178 TCCCTCGGAGAGTTTCCGCTCAAAAGTTTGTCTTCAATCATCAACCAATTCACAGG 4237  
| | | | |  
Db 4195 TCCCTCGGAGAGTTTCTCTCGCAAGTTTGTCTTCAATCATCAACCAATTCACAGG 4254  
| | | | |  
QY 4238 ACAAGTAGCGTGAAGATTAATGAGAGCTGACAAAGAAAGAAACGACAAACGCTGAATCC 4297  
| | | | |  
Db 4255 ACAAGTAGCGTGAATTAATGAGAGCTGACAAAGAAAGAAACGACAAACGCTGAATCC 4314  
| | | | |  
QY 4298 CGAAGTCAATTAATCACTTAATGCAAAATCTGCCAAGTTGATTTCACTGTGACAA 4357  
| | | | |  
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| | | | |  
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| | | | |  
Db 4435 ATTGATGTTAATCAATTAACCGGTTAATTCGTTTCAATGAACTTTGATCTCTGCTGCT 4494  
| | | | |  
QY 4478 TATTATCTTAATCTGCTACCAATAGCAACCGGTTACATTAATCTGCTTAATGCTGCTTCG 4537  
| | | | |







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Qy 944 CCCAATTCTGACGGCGCTGTCATCCGGTCAAAAACCTCCGACGCTCATGAGACTGTC 1003  
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Qy 1004 GGGTGGCTGTGAGACCGGGGATCACTCCGAGAAAGAGTGGATCCAGAGAGACCAAGCC 1063  
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AC 10-MAR-2005 (first entry)
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DE Nucleotide sequence of AAV serotype 7.
XX
XX antiarteriosclerotic; antilipemic; gene therapy; cholesterol;
KW apolipoprotein B; apob; apolipoprotein A; apoa; atherosclerosis;
KW lipoprotein defect; ss.
XX
XX Adeno-associated virus.
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XX
XX 16-DEC-2004.
XX

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	4253.2	90.8	4718	2	BD242766 Adeno-ass
5	4253.2	90.8	4718	2	ARS62498 Sequence
6	4253.2	90.8	4718	2	AX753251 Sequence
7	4253.2	90.8	4718	10	AF063497 Adeno-ass
8	3678.4	78.5	4721	2	CQ972062 Sequence
9	3678.4	78.5	4721	2	CS073592 Sequence
10	3678.4	78.5	4721	2	AX753246 Sequence
11	3678.4	78.5	4721	10	AF513851 Adeno-ass
12	3404.6	72.0	4385	2	AX753250 Sequence
13	3370.4	72.0	4393	2	CQ972063 Sequence
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15	3370.4	72.0	4393	2	AX753249 Sequence
16	3370.4	70.4	4393	10	AF513852 Adeno-ass
17	3296.2	70.4	4679	2	AR762859 Sequence
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19	3296.2	70.4	4679	10	AF043303 Adeno-ass
20	3296.2	70.4	8698	2	AR222044 Sequence
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22	3270.8	69.8	4680	2	AR028767 Sequence
23	3270.8	69.8	4680	2	I62303 Sequence 1
24	3267.8	69.8	4681	2	BD242774 Adeno-ass
25	3267.8	69.8	4681	2	ARS62506 Sequence
26	3255.4	69.8	4102	10	AF631965 Adeno-ass
27	3244.2	69.3	4675	2	BD094552 Method of
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30	3244.2	69.3	4675	2	AX135805 Sequence
31	3244.2	69.3	4675	2	AX286292 Sequence
32	3244.2	69.3	4675	2	AX753252 Sequence
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34	3182.8	68.0	4722	10	AF028705 Adeno-ass
35	3149	67.2	4726	2	AX753253 Sequence
36	3149	67.2	4726	10	U48704 Adeno-assoc
37	3114.4	66.5	7557	2	AR222045 Sequence
38	3114.4	66.5	7557	2	AX205073 Sequence
39	3106.6	66.3	4430	10	AY695374 Adeno-ass
40	3106.4	66.3	4429	10	AY695375 Adeno-ass
41	3101.6	66.2	4429	10	AY695372 Adeno-ass
42	3100	66.2	4429	10	AY695371 Adeno-ass
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#### ALIGNMENTS

RESULT 1					
LOCUS	BD242775	4683 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same.				
ACCESSION	BD242775				
VERSION	BD242775.1	GI:33052545			
KEYWORDS	JP 2002529098-A/10.				
SOURCE	unidentified				
ORGANISM	unclassified sequences.				
REFERENCE	1 (bases 1 to 4683)				
AUTHORS	Wilson,J.M. and Xiao,W.				
TITLE	Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same				
JOURNAL	Patent: JP 2002529098-A 10 10-SEP-2002; THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA				
COMMENT	OS aav-6				
	PN JP 2002529098-A/10				
	PD 10-SEP-2002				
	PF 02-NOV-1999 JP 2000581227				
	PR 05-NOV-1998 US 60/107114				
	PI JAMES M WILSON,WEIDONG XIAO				
	PC C12N1/09,A61K31/711,A61K48/00,A61P43/00,C12N1/15,C12N1/19, PC				
	C12N1/11				
	PC C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00 CC				
	Adeno-associated virus serum type 1 nucleic acid sequence, CC vector and host				
	CC cell containing the same				
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	FT source	1..4683			
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		Location/Qualifiers			
		1..4683			
FEATURES	source				
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ORIGIN					
Query Match	100.0%;	Score 4683;	DB 2;	Length 4683;	
Best Local Similarity	100.0%;	Pred. No. 0;			

Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCAGAGCGGCGCAGAGAGGAGTG 120  
Db 61 CGAGCGCCGGGCTTGGCCGGGCGGCTCAGTGAAGCAGAGCGGCGCAGAGAGGAGTG 120

QY 121 GCCAATCTCATCTAGAGGTTCTCGAGAGGGTGAAGTCTGACGTGAATTACGTATAG 180  
Db 121 GCCAATCTCATCTAGAGGTTCTCGAGAGGGTGAAGTCTGACGTGAATTACGTATAG 180

QY 181 GGTTAAGGAGTCTCTGATTAAGAGTCAAGTGAATGTTTGGCATTTTGGCAGCAT 240  
Db 181 GGTTAAGGAGTCTCTGATTAAGAGTCAAGTGAATGTTTGGCATTTTGGCAGCAT 240

QY 181 GGTTAAGGAGTCTCTGATTAAGAGTCAAGTGAATGTTTGGCATTTTGGCAGCAT 240  
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QY 241 GTGGTCAAGCTGGGTATTTAAAGCCGAGTGAAGCAGAGGCTTCCATTTTGAAGCGGA 300  
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Db 301 GGTTTGAACGCGCAGCGCCCATGCGGGGTTTACGAGATTGTGATTAAAGTCCGACGA 360

QY 361 CTTTGAAGAGATGTCGCCGSCATTTCTGACAGCTTTGTGAAGTGGGTGGCGGAAGGA 420  
Db 361 CTTTGAAGAGATGTCGCCGSCATTTCTGACAGCTTTGTGAAGTGGGTGGCGGAAGGA 420

QY 421 ATGGAGATTGCCGCAATCTGACATGATCTGAATCTGAATTGAGAGGACCCCTGAC 480  
Db 421 ATGGAGATTGCCGCAATCTGACATGATCTGAATCTGAATTGAGAGGACCCCTGAC 480

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QY 541 GGAAGCCCTCTTCTTTGTTGAGTTCGAGAGGGGAGTCCACTCAACCTCCCATATTCT 600  
Db 541 GGAAGCCCTCTTCTTTGTTGAGTTCGAGAGGGGAGTCCACTCAACCTCCCATATTCT 600

QY 601 GGTGAGAGCAGAGGGGGTCAAAATCCATGTGCTGGGCGCTTCTGAGTCAGATTAGCGA 660  
Db 601 GGTGAGAGCAGAGGGGGTCAAAATCCATGTGCTGGGCGCTTCTGAGTCAGATTAGCGA 660

QY 661 CAAGCTGTGACACATCTACCGCGGGATGAGCCGACCTGCCCAATCTGTTCGGGT 720  
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QY 721 GACCAAGCGGTAATGGCGCGGAGGGGGAGCAAGGTGTGAGCAGATCTCATTC 780  
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QY 781 CAATCACTCTGCGCAAGACTCAGCCGAGCTCAGTGGCGTGAATTAATGAGGA 840  
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QY 841 GTATATTAAGCGCGTGTAAACCTGCGGAGCGCAAAAGCTGTGGCGACGACTGAC 900  
Db 841 GTATATTAAGCGCGTGTAAACCTGCGGAGCGCAAAAGCTGTGGCGACGACTGAC 900

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QY 961 TGTTCATCCGATCAAAAACCTCCGACGCTACATGAGTGTGCGGTGCTGTGACCG 1020  
Db 961 TGTTCATCCGATCAAAAACCTCCGACGCTACATGAGTGTGCGGTGCTGTGACCG 1020

QY 1021 GGGGATCACTCCGAGAAAGAGTGAATCAGAGAGACCAAGGCTCTGTACATCTCTTCAA 1080  
Db 1021 GGGGATCACTCCGAGAAAGAGTGAATCAGAGAGACCAAGGCTCTGTACATCTCTTCAA 1080

QY 1081 CGCGGCTCCAACTCGGCGTCCAGATCAAGGCGCTTGAACAATGCGGCAAGATCAT 1140  
Db 1081 CGCGGCTCCAACTCGGCGTCCAGATCAAGGCGCTTGAACAATGCGGCAAGATCAT 1140

QY 1141 GGGCTGACCAAAATCCGCGCCGACTACCTGTAGGACCCCGCTCCGCGCGCAATTAA 1200  
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QY 1201 AACCAACCGATTTACCGCATCTGTGAGCTGAAGCGCTACGACCTGGCTACGCGGGCTC 1260  
Db 1201 AACCAACCGATTTACCGCATCTGTGAGCTGAAGCGCTACGACCTGGCTACGCGGGCTC 1260

QY 1261 GGTCTTTCTCGGCTGGGCGCAGAAAAGTTTCGAAAAACGCAACCATCTGCTGTTGG 1320  
Db 1261 GGTCTTTCTCGGCTGGGCGCAGAAAAGTTTCGAAAAACGCAACCATCTGCTGTTGG 1320

QY 1321 GCCGGCCACAGGAGCAAGCAATCGCGAAGCCATGCGCCAGCGGCTCTTCTA 1380  
Db 1321 GCCGGCCACAGGAGCAAGCAATCGCGAAGCCATGCGCCAGCGGCTCTTCTA 1380

QY 1381 CGGCTGCTCAACTGGAACCAATGAAGACTTCCCTTCAAGATTTGGTGAAGAGTGT 1440  
Db 1381 CGGCTGCTCAACTGGAACCAATGAAGACTTCCCTTCAAGATTTGGTGAAGAGTGT 1440

QY 1441 GATCTGGGAGAGGAGCAAGATGACGCGCAAGTCTGTGAGTCCGCCAAGGCCATTCT 1500  
Db 1441 GATCTGGGAGAGGAGCAAGATGACGCGCAAGTCTGTGAGTCCGCCAAGGCCATTCT 1500

QY 1501 CGGCGGAGCAAGAGTGGCGGTGAGCAAAAATGCAAGTGTCCGCCAGATCATCCAC 1560  
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QY 1561 CCGCGTGAATGTAACCTTCAACCAACCAATGTCGCGTATGAGCGGAAACGACAC 1620  
Db 1561 CCGCGTGAATGTAACCTTCAACCAACCAATGTCGCGTATGAGCGGAAACGACAC 1620

QY 1621 CTTGAGACACACAGCGGTTGACAGACCGAGATTCAAAATTTGAATCCACCCGCGTCT 1680  
Db 1621 CTTGAGACACACAGCGGTTGACAGACCGAGATTCAAAATTTGAATCCACCCGCGTCT 1680

QY 1681 GAGCATGACTTTGGCAAGGTGAACAAAGCAAGAAATCTTCCGCTGGCGCA 1740  
Db 1681 GAGCATGACTTTGGCAAGGTGAACAAAGCAAGAAATCTTCCGCTGGCGCA 1740

QY 1741 GATTCACGTGACCGAGGTGCGATGATGTTCTACGTCAAGAAAGGTGAGCCAAACAG 1800  
Db 1741 GATTCACGTGACCGAGGTGCGATGATGTTCTACGTCAAGAAAGGTGAGCCAAACAG 1800

QY 1801 ACCCGCCCGATGACGCGGATTAAGCGAGCCCAAGCGGCGCTGCGCTCAGTGGCGA 1860  
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QY 1861 TCCATGAGCTGACAGCGCGGAAGAGTCCGCTGAGACTTTGCCGACAGTACCAAAACAA 1920  
Db 1861 TCCATGAGCTGACAGCGCGGAAGAGTCCGCTGAGACTTTGCCGACAGTACCAAAACAA 1920

QY 1921 ATGTTCTCGTCAAGCGGCGCATGCTCAGATGCTGTTTCCCTGAAAAACATGCGAGAAAT 1980  
Db 1921 ATGTTCTCGTCAAGCGGCGCATGCTCAGATGCTGTTTCCCTGAAAAACATGCGAGAAAT 1980

QY 1981 GAATCAGAAATTTCAACATTTTCTTCAACGACGCGGACAGAGACTGTTTCAAGATGTTTCCC 2040  
Db 1981 GAATCAGAAATTTCAACATTTTCTTCAACGACGCGGACAGAGACTGTTTCAAGATGTTTCCC 2040

QY 2041 CGGCTGTCAAGATTTCAACCGGTCTGAGAAAGAGACCTATTCGAAATCTGTGCGCAT 2100  
Db 2041 CGGCTGTCAAGATTTCAACCGGTCTGAGAAAGAGACCTATTCGAAATCTGTGCGCAT 2100

QY 2101 TCAATCATCTGCTGGGCGGCTCCGAGATTGCTGCTGGCGCTCGCATCTGATCAAAGT 2160  
Db 2101 TCAATCATCTGCTGGGCGGCTCCGAGATTGCTGCTGGCGCTCGCATCTGATCAAAGT 2160



QY	2161	GGATCTGGATGATGACTGTGTTTCTTGAGCAATAAATGACTTAAACAGAGTATGCTGCCGATG	2222
Db	2161	GGATCTGGATGATGACTGTGTTTCTTGAGCAATAAATGACTTAAACAGAGTATGCTGCCGATG	2222
QY	2221	GTTATCTTCCAAATTTGGGCTCGAGGACAACCTCTCGAGGGGCAATTGGGCAAGTGTGTGGACT	2288
Db	2221	GTTATCTTCCAAATTTGGGCTCGAGGACAACCTCTCGAGGGCAATTGGGCAAGTGTGTGGACT	2288
QY	2281	TGAAACCTGAGACCCCGAAACCCAAAGCCCAACAGCAAAAGCAGAGACGACGGCCGGGGTTC	2340
Db	2281	TGAAACCTGAGACCCCGAAACCCAAAGCCCAACAGCAAAAGCAGAGACGACGGCCGGGGTTC	2340
QY	2341	TGTCGCTTCTTGCTTACAAATCTCTCGACCTTTCAACGGACTCGACAAGGGGGAGCCCG	2400
Db	2341	TGTCGCTTCTTGCTTACAAATCTCTCGACCTTTCAACGGACTCGACAAGGGGGAGCCCG	2400
QY	2401	TCAAAGCCGGCCGATACAGCGGGCCCTCGAGCAAGCAAGGCCCTTACAGCAAGGACTCAAG	2460
Db	2401	TCAAAGCCGGCCGATACAGCGGGCCCTCGAGCAAGCAAGGCCCTTACAGCAAGGACTCAAG	2460
QY	2461	CGGGTGACAAATCCGTAACCTCGGCTTAAACAAGCCGACGCGCAGTTTTCAGAGACTCTGAC	2520
Db	2461	CGGGTGACAAATCCGTAACCTCGGCTTAAACAAGCCGACGCGCAGTTTTCAGAGACTCTGAC	2520
QY	2521	AAGAAAGATAGCTCTTTTGGGGGCAACTTCGGCGAGCAGCTCTTTCAGGCAAGAAAGAGGG	2580
Db	2521	AAGAAAGATAGCTCTTTTGGGGGCAACTTCGGCGAGCAGCTCTTTCAGGCAAGAAAGAGGG	2580
QY	2581	TTCTTGAAACCTTTTGTGTGTGTGAGGAAGTGTCTTAAACGGCTCTTGAAAGAAACGTTC	2640
Db	2581	TTCTTGAAACCTTTTGTGTGTGTGAGGAAGTGTCTTAAACGGCTCTTGAAAGAAACGTTC	2640
QY	2641	CGGTGAGCAGTCGCGCAACAAGGCCAGACTCCTCCTCGGGCAATTGGCAAGACAGGCCACGC	2700
Db	2641	CGGTGAGCAGTCGCGCAACAAGGCCAGACTCCTCCTCGGGCAATTGGCAAGACAGGCCACGC	2700
QY	2701	AGCCCGCTAAAAAAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCGACCC	2760
Db	2701	AGCCCGCTAAAAAAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCGACCC	2760
QY	2761	CACAACTCTCGGAAACCTTCAGAACCCCGCTGTGTGGAACTTCAACAAAGGCTT	2820
Db	2761	CACAACTCTCGGAAACCTTCAGAACCCCGCTGTGTGGAACTTCAACAAAGGCTT	2820
QY	2821	CAGGCGGTGGCGCAACCAATGGCAGCAATTAACGAAGCGCCGACGGAATGGGTAATGCTT	2880
Db	2821	CAGGCGGTGGCGCAACCAATGGCAGCAATTAACGAAGCGCCGACGGAATGGGTAATGCTT	2880
QY	2881	CAGGAAATTTGGCATTTGCATTTGCATGAGCTGGGGGACAGAGTATCAACACAGCACCC	2940
Db	2881	CAGGAAATTTGGCATTTGCATTTGCATGAGCTGGGGGACAGAGTATCAACACAGCACCC	2940
QY	2941	GAACTATGGGCTTTGGCCCACTTAACAACCACTTCAACAGCAAAATTTCAAGTGGCTTCAA	3000
Db	2941	GAACTATGGGCTTTGGCCCACTTAACAACCACTTCAACAGCAAAATTTCAAGTGGCTTCAA	3000
QY	3001	CGGGGGCCAGCAAGCAACAACATCTTCGCTTACAGCAACCCCTGGGGGTAATTTGATTT	3060
Db	3001	CGGGGGCCAGCAAGCAACAACATCTTCGCTTACAGCAACCCCTGGGGGTAATTTGATTT	3060
QY	3061	TCACAGATTTCCACTGCGCATTTCTACGACAGCTGACGTGACGAGCTCAACACAACATTT	3120
Db	3061	TCACAGATTTCCACTGCGCATTTCTACGACAGCTGACGTGACGAGCTCAACACAACATTT	3120
QY	3121	GGGGAATTCGGGCTCAAAGACTCAACCTTCAGCTTTCAACATCCAGTCAAGAGGTCTCA	3180
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QY	3181	CGACCAATGATGGGCTCAAGCAACATCGGCTTAATTAACGACGAGTTCAGAGTCAAGTCTGT	3240
Db	3181	CGACCAATGATGGGCTCAAGCAACATCGGCTTAATTAACGACGAGTTCAGAGTCAAGTCTGT	3240
QY	3241	CGGACTCGGAGTACAGTTCCTGTAAGTCTTCTGAGCTTGGCGCACCAAGGACTGCTCCCTC	3300

Db	3241	CGAGCTCGGATACCAAGTTCCTGTAAGCTTCGCTGCGCACAGGCGCTCCCTC	3300
Qy	3301	CGTTCGCCGCGGACGCTGTTCAATGCAATTCGCGAGTACGCGCTACCTTAACGCTCAACAATGGCA	3360
Db	3301	CGTTCGCCGCGGACGCTGTTCAATGCAATTCGCGAGTACGCGCTACCTTAACGCTCAACAATGGCA	3360
Qy	3361	GCCAGGACGTGGGACGCTCATCTCTTTTACGTGCTGGAAATATTTCCATCGAGATGCTGA	3420
Db	3361	GCCAGGACGTGGGACGCTCATCTCTTTTACGTGCTGGAAATATTTCCATCGAGATGCTGA	3420
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Db	3421	GAACGGGCAATTAACCTTTACCTTCACGCTACACCTTCGAGAGTGCCTTTCCAGACGACCT	3480
Qy	3481	ACGCGCACGCGACGAGCCTGGACCGGCGTGATGAATCCCTCATGACCAAGTACCTGTAAT	3540
Db	3481	ACGCGCACGCGCACGAGCCTGGACCGGCGTGATGAATCCCTCATGACCAAGTACCTGTAAT	3540
Qy	3541	ACCTGAACAGAACTCAACAATGATCGGAGTGCCTCAAAACAGAGACTTGTGTTTATCC	3600
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Qy	3601	GTCGGTCTCCAGCTGGGCAATGCTGTTACGCCCAAAAATGCGCTACCTGGACCTGTATAC	3660
Db	3601	GTCGGTCTCCAGCTGGGCAATGCTGTTACGCCCAAAAATGCGCTACCTGGACCTGTATAC	3660
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Qy	4081	CGGATGACACTTTCAACCCGCTCTCTCTCATGGGCGGCTTTGACATTAAAGACCCGCTC	4140
Db	4081	CGGATGACACTTTCAACCCGCTCTCTCTCATGGGCGGCTTTGACATTAAAGACCCGCTC	4140
Qy	4141	CTCAGATCTCATCAAAAACAAGCGCTGTCTCTGCGAAATCTTCGCGCAGAATTTTCGCTA	4200
Db	4141	CTCAGATCTCATCAAAAACAAGCGCTGTCTCTGCGAAATCTTCGCGCAGAATTTTCGCTA	4200
Qy	4201	CAAAGTTTGCCTTCACTTATCAACCAAGTAATTCAGAGACAAGTAAGGTGGAGATTGAAT	4260
Db	4201	CAAAGTTTGCCTTCACTTATCAACCAAGTAATTCAGAGACAAGTAAGGTGGAGATTGAAT	4260
Qy	4261	GGGAGCTGCAAAAAGAAAACAGCAAAACGCTGGAAATCCGGAAGTCAAGTATACATTAAT	4320
Db	4261	GGGAGCTGCAAAAAGAAAACAGCAAAACGCTGGAAATCCGGAAGTCAAGTATACATTAAT	4320
Qy	4321	ATGCAAAATCTGCAACGTTGATTTCACTGTGACAAATGACCTTTATCTAGCCTC	4380

Db 4321 ATGCAAAATCTGCCAACGTTGATTTCACGTGTGACAAACATGAGACTTTATAGAGCTC 4380  
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Qy 4621 TCTGCGGACCTTTGTTGTCGCGAGCGCCCAACGAGCGAGCGAGCGCATAGAGAGTGGC 4680  
Db 4621 TCTGCGGACCTTTGTTGTCGCGAGCGCCCAACGAGCGAGCGAGCGCATAGAGAGTGGC 4680  
Qy 4681 CAA 4683  
Db 4681 CAA 4683

## RESULT 2

AR562507

LOCUS AR562507 4683 bp DNA linear PAT 08-OCT-2004

DEFINITION Sequence 19 from patent US 6759237.

ACCESSION AR562507

VERSION AR562507.1 GI:53976573

KEYWORDS

SOURCE Unknown.

ORGANISM

Unknown:  
Unclassified.

REFERENCE 1 (bases 1 to 4683)

AUTHORS Wilson,J.M. and Xiao,W.

TITLE Adeno-associated virus serotype 1 nucleic acid sequences, vectors  
and host cells containing same

JOURNAL Patent: US 6759237-A 19 06-JUL-2004;

The Trustees of the University of Pennsylvania; Philadelphia, PA

FEATURES

Location/Qualifiers

1..4683

/organism="Unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 4683; DB 2; Length 4683;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAACAAAGGTGGC 60  
Db 1 TTGGCCACTCCCTCTCTGCGCGCTGCTGCTCACTGAGCGCGGCGCAACAAAGGTGGC 60  
Qy 61 CGAGCGCGCGGCTTTGCGCGCGGCGCTCAGTGAAGCGAGCGGCGGAGAGAGAGTGG 120  
Db 61 CGAGCGCGCGGCTTTGCGCGCGGCGCTCAGTGAAGCGAGCGGCGGAGAGAGAGTGG 120  
Qy 121 GCCAACTTCATCACTAGGGGTTCTGTGAAGGGTGGAGTCTGTAGCGTGAATTCGTATAG 180  
Db 121 GCCAACTTCATCACTAGGGGTTCTGTGAAGGGTGGAGTCTGTAGCGTGAATTCGTATAG 180  
Qy 181 GGTTAGGAGAGTCTGTATTTAGAGTCACTGAGTGTGTTTCCGACATTTTCCGACCAT 240  
Db 181 GGTTAGGAGAGTCTGTATTTAGAGTCACTGAGTGTGTTTCCGACATTTTCCGACCAT 240  
Qy 241 GTGTGTCACGTGGGATTTAAGCCGAGTGAACAACGAGGCTTCATTTTGAAGCGGGA 300  
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Query Match

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Db 1621 CTTGAGACCAAGACCGCTTTCAGACCGGATGTTCAATTTGAATCAACCCGCTCT 1680
Qy 1681 GGAACATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAGAGTCTTCCGCTGGGCGCA 1740
Db 1681 GGAACATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAGAGTCTTCCGCTGGGCGCA 1740
Qy 1741 GGATCAGTGAACGAGGTGGCGATGATTCTACGTGAGAAAGGTGAGGCCAACAG 1800
Db 1741 GGATCAGTGAACGAGGTGGCGATGATTCTACGTGAGAAAGGTGAGGCCAACAG 1800
Qy 1801 ACCCGCCCCGATGACCGCGATTAAGCGAGCCCAAGCGGGCTGCCCCCTCAGTGGGGA 1860
Db 1801 ACCCGCCCCGATGACCGCGATTAAGCGAGCCCAAGCGGGCTGCCCCCTCAGTGGGGA 1860
Qy 1861 TCCATGACGTCAGACCGCGAGGAGCTCCGCTGAGCTTTGGCGACAGATACCAAAACAA 1920
Db 1861 TCCATGACGTCAGACCGCGAGGAGCTCCGCTGAGCTTTGGCGACAGATACCAAAACAA 1920
Qy 1921 ATGTTCTGTCACCGCGGCAATGCTTCAGATGCTGTTCCCTGCAAAACATGCGAGAT 1980
Db 1921 ATGTTCTGTCACCGCGGCAATGCTTCAGATGCTGTTCCCTGCAAAACATGCGAGAT 1980
Qy 1981 GAATCAGATTTTCAACTTTGCTTACGCAACGGGACCAAGACTGTTCAAGATGTTTCCC 2040
Db 1981 GAATCAGATTTTCAACTTTGCTTACGCAACGGGACCAAGACTGTTCAAGATGTTTCCC 2040
Qy 2041 CGGCTGTCAAGATCTCAACCGGTCGTCAGAAAGAGACGATTCGAAATCTGTGCAT 2100
Db 2041 CGGCTGTCAAGATCTCAACCGGTCGTCAGAAAGAGACGATTCGAAATCTGTGCAT 2100
Qy 2101 TCATCATCTGCTGGGGGCGGCTCCGAGATTTGCTTGGCGCTGCGATCTGGTCAAGCT 2160
Db 2101 TCATCATCTGCTGGGGGCGGCTCCGAGATTTGCTTGGCGCTGCGATCTGGTCAAGCT 2160

```

QY 2161 GGATCTGGATGACTGTGTTTCTGAGCAATAATGACTTAAACAGGTATGGCTGCCAGT 2220  
DB 2161 GGATCTGGATGACTGTGTTTCTGAGCAATAATGACTTAAACAGGTATGGCTGCCAGT 2220  
QY 2221 GTTATCTTCCAGATTGGCTCGAGGACAACTCTCTGAGGGGATTCCGAGTGTGGAGCT 2280  
DB 2221 GTTATCTTCCAGATTGGCTCGAGGACAACTCTCTGAGGGGATTCCGAGTGTGGAGCT 2280  
QY 2281 TGAACCTGGAGCCCGGAAACCCMAAGCCMACAGCAAAACAGAGACACCGCGGGTCT 2340  
DB 2281 TGAACCTGGAGCCCGGAAACCCMAAGCCMACAGCAAAACAGAGACACCGCGGGTCT 2340  
QY 2341 TGGTGCTTCTGGCTGACAAAGTACCTCGGAGCCCTTCAACGAGCTCGACAAAGGGGAGCCG 2400  
DB 2341 TGGTGCTTCTGGCTGACAAAGTACCTCGGAGCCCTTCAACGAGCTCGACAAAGGGGAGCCG 2400  
QY 2401 TCAACGCGGCGAGTGCAGACGCGCCCTCGAGCAAGCAAGGCTTACGACCGAGCTCAAG 2460  
DB 2401 TCAACGCGGCGAGTGCAGACGCGCCCTCGAGCAAGCAAGGCTTACGACCGAGCTCAAG 2460  
QY 2461 CCGGTGACAAATCCGTAACCTGCGGTATACCAAGCCGAGCCGAGTTCAGAGGCTCTGC 2520  
DB 2461 CCGGTGACAAATCCGTAACCTGCGGTATACCAAGCCGAGCCGAGTTCAGAGGCTCTGC 2520  
QY 2521 AAGAAATACGCTCTTTTGGGGCAACCTCGGCGAGCAGTCTTCCAGGSCAAAGAAAGAGG 2580  
DB 2521 AAGAAATACGCTCTTTTGGGGCAACCTCGGCGAGCAGTCTTCCAGGSCAAAGAAAGAGG 2580  
QY 2581 TTCTCGAACTTTTGTGTGTGTGAGAAAGTGTCTAAGACGCGCTCTGAAAAAAACGTC 2640  
DB 2581 TTCTCGAACTTTTGTGTGTGTGAGAAAGTGTCTAAGACGCGCTCTGAAAAAAACGTC 2640  
QY 2641 CGGTAGACAAATCCGTAACCTGCGGTATACCAAGCCGAGCTTCCAGGSCAAAGAAAGAGG 2700  
DB 2641 CGGTAGACAAATCCGTAACCTGCGGTATACCAAGCCGAGCTTCCAGGSCAAAGAAAGAGG 2700  
QY 2701 AGCCGCTAAAAAGAGCTCAATTTTGGTTCAGACTGCGGACTCAGAGTCAATCCCGAGC 2760  
DB 2701 AGCCGCTAAAAAGAGCTCAATTTTGGTTCAGACTGCGGACTCAGAGTCAATCCCGAGC 2760  
QY 2761 CACAACTCTCGAGAACTCTCAGCAACCCCGCTGTGTGGAGCTTCAATGAGCTT 2820  
DB 2761 CACAACTCTCGAGAACTCTCAGCAACCCCGCTGTGTGGAGCTTCAATGAGCTT 2820  
QY 2821 CAGCGGTGGGCGACCAATGGCAGACAAATGAGAGGGCGGACGAGTGGGTAAATGCT 2880  
DB 2821 CAGCGGTGGGCGACCAATGGCAGACAAATGAGAGGGCGGACGAGTGGGTAAATGCT 2880  
QY 2881 CAGGAATTTGGCATTTGCGATTCACATGCTGGGCGAGAGTCAACACAGCACCC 2940  
DB 2881 CAGGAATTTGGCATTTGCGATTCACATGCTGGGCGAGAGTCAACACAGCACCC 2940  
QY 2941 GAACATGGGCTTGGCCACTATTAACAACCTCTCAAGCAAAATCTCCAGTGTCTCA 3000  
DB 2941 GAACATGGGCTTGGCCACTATTAACAACCTCTCAAGCAAAATCTCCAGTGTCTCA 3000  
QY 3001 CCGGGGCGAGCAACCAACCACTTCTGGCTAAGACCCCTGGGGGTATTTTGAAT 3060  
DB 3001 CCGGGGCGAGCAACCAACCACTTCTGGCTAAGACCCCTGGGGGTATTTTGAAT 3060  
QY 3061 TCAACAGATTGCACTGCAATTTCTCACCAGCTGAGTGGAGGACTCATCAACAACTT 3120  
DB 3061 TCAACAGATTGCACTGCAATTTCTCACCAGCTGAGTGGAGGACTCATCAACAACTT 3120  
QY 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTTCAACATCAAGTCAAGGAGTCA 3180  
DB 3121 GGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTTCAACATCAAGTCAAGGAGTCA 3180  
QY 3181 CGAGCAATGATGGCTCAAGCAATGCTAATTAACCAAGCAAGCTTCAAGCTTCT 3240  
DB 3181 CGAGCAATGATGGCTCAAGCAATGCTAATTAACCAAGCAAGCTTCAAGCTTCT 3240

QY 3241 CGGACTGGAGTACCAATTCCTGACTCTCTCGCTTCGCGACACAGGCTGCTCCCTC 3300  
DB 3241 CGGACTGGAGTACCAATTCCTGACTCTCTCGCTTCGCGACACAGGCTGCTCCCTC 3300  
QY 3301 CGTTCCCGCGAGCTGTTATGATTCGCGAGTACGGCTTACTTACGCTCAACATGGCA 3360  
DB 3301 CGTTCCCGCGAGCTGTTATGATTCGCGAGTACGGCTTACTTACGCTCAACATGGCA 3360  
QY 3361 GCCAGGAGTGGAGCGCTCATCTCTTATCGCTGGAAATTTTCCATCCGAGATGCTGA 3420  
DB 3361 GCCAGGAGTGGAGCGCTCATCTCTTATCGCTGGAAATTTTCCATCCGAGATGCTGA 3420  
QY 3421 GAACGGCAATTAATTTACTTACCTTACGCTTACGCTTACGAGAGCTGCTTTCACAGAGCT 3480  
DB 3421 GAACGGCAATTAATTTACTTACCTTACGCTTACGCTTACGAGAGCTGCTTTCACAGAGCT 3480  
QY 3481 ACCGCGACAGCAGAGCTTGAACCGGCTGATGAACTCTCTCATTCGACCACTGATTT 3540  
DB 3481 ACCGCGACAGCAGAGCTTGAACCGGCTGATGAACTCTCTCATTCGACCACTGATTT 3540  
QY 3541 ACCGCGACAGCAGAGCTTGAACCGGCTGATGAACTCTCTCATTCGACCACTGATTT 3600  
DB 3541 ACCGCGACAGCAGAGCTTGAACCGGCTGATGAACTCTCTCATTCGACCACTGATTT 3600  
QY 3601 GTGGTCTCCAGCTGGCATGTCTGTTCAAGCCCAAAAATGGCTTACCTGACCTGTTACC 3660  
DB 3601 GTGGTCTCCAGCTGGCATGTCTGTTCAAGCCCAAAAATGGCTTACCTGACCTGTTACC 3660  
QY 3661 GGCAGAGCGCGCTTCTTAAAAAACAACAACAACAACAACAACAACAACAACAACAACA 3720  
DB 3661 GGCAGAGCGCGCTTCTTAAAAAACAACAACAACAACAACAACAACAACAACAACAACA 3720  
QY 3721 GTGCTTCAAAATATTAATTAATGGGCGTAACTTAACTTAACTTAACTTAACTTAACT 3780  
DB 3721 GTGCTTCAAAATATTAATTAATGGGCGTAACTTAACTTAACTTAACTTAACTTAACT 3780  
QY 3781 CCTCACAACAAAGCAGCAAAAGCAAGTCTTCTCCATGAGCGGTGTCATGATTTTGGAA 3840  
DB 3781 CCTCACAACAAAGCAGCAAAAGCAAGTCTTCTCCATGAGCGGTGTCATGATTTTGGAA 3840  
QY 3841 AGGAGAGCGCGGAGCTTCAAAACATGCTGATTTGACAAATGTCATGATGACAGAGAGG 3900  
DB 3841 AGGAGAGCGCGGAGCTTCAAAACATGCTGATTTGACAAATGTCATGATGACAGAGAGG 3900  
QY 3901 AAATCAAGCACTAACCCCGTGGCCACGAAAGATTTGGGACTGTGGCACTCTCC 3960  
DB 3901 AAATCAAGCACTAACCCCGTGGCCACGAAAGATTTGGGACTGTGGCACTCTCC 3960  
QY 3961 AGAGCAGCAGCAGACCTTGCAGCGGAGATGTGCATGTTATGGAGCTTAACTTGGAA 4020  
DB 3961 AGAGCAGCAGCAGACCTTGCAGCGGAGATGTGCATGTTATGGAGCTTAACTTGGAA 4020  
QY 4021 TGGTGTGGCAAGACAGAGATTAATCTGCAAGGTCTTATTTGGGCCAAATTCCTCACA 4080  
DB 4021 TGGTGTGGCAAGACAGAGATTAATCTGCAAGGTCTTATTTGGGCCAAATTCCTCACA 4080  
QY 4081 CCGATGACACTTTCACCCGCTCTCTCATGAGGCGCTTTGACCTTAAACACCCGCTC 4140  
DB 4081 CCGATGACACTTTCACCCGCTCTCTCATGAGGCGCTTTGACCTTAAACACCCGCTC 4140  
QY 4141 CTCAGATCTCATCAAAAACAAGCTGTTCTGCGAATCTCTCGGCGAGATTTTGGCTTA 4200  
DB 4141 CTCAGATCTCATCAAAAACAAGCTGTTCTGCGAATCTCTCGGCGAGATTTTGGCTTA 4200  
QY 4201 CAAAGTTTGTCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 4260  
DB 4201 CAAAGTTTGTCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 4260  
QY 4261 GGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGGAAGTGCAGTATACCTTAAT 4320  
DB 4261 GGGAGCTGCAAGAAAGAAACAGCAACGCTGGAATCCGGAAGTGCAGTATACCTTAAT 4320  
QY 4321 ATGCAAAATCTGCCAAGCTTGAATTTCACTGTGACAACTTAATTAATGAGCTTC 4380



Db	4331	ATGCAAAATCTGGCAACGCTGATTTTCACTGTGGAGAAACATGGACTTTATATCTAGCCTC	4380
Qy	4381	GCCCCATTGGCAACCCGTTACCTCAACCCGCCCTGTAAATTGNTTATCAATAAACG	4440
Db	4381	GCCCCATTGGCAACCCGTTACCTCAACCCGCCCTGTAAATTGNTTATCAATAAACG	4440
Qy	4441	GTTAATTCGTCTCACTGTAACCTTTGATGTCATAGTCTTATTATCTTATCTGTGCATA	4500
Db	4441	GTTAATTCGTCTCACTGTAACCTTTGATGTCATAGTCTTATTATCTTATCTGTGCATA	4500
Qy	4501	GCAACCGGTTACACATTAACCTGCTTAGTTGGCTTCGGAAATACCCCTAGTATGAGTT	4560
Db	4501	GCAACCGGTTACACATTAACCTGCTTAGTTGGCTTCGGAAATACCCCTAGTATGAGTT	4560
Qy	4561	GCCCCATCTCTCTATATGCGCGCTCGCTCGCTGTGGTGGGACCGGACAGAGACTTCGCG	4620
Db	4561	GCCCCATCTCTCTATATGCGCGCTCGCTCGCTGTGGTGGGACCGGACAGAGACTTCGCG	4620
Qy	4621	TCTGGGACCTTTTGGTCCGCAAGGCCCAACCGAGCGAGCGCGCATATAGAGGATGAGC	4680
Db	4621	TCTGGGACCTTTTGGTCCGCAAGGCCCAACCGAGCGAGCGCGCATATAGAGGATGAGC	4680
Qy	4681	CAA 4683	
Db	4681	CAA 4683	

RESULT 4	BD242766	LOCUS	BD242766	4718 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same.						

ACCESSION	BD242766
VERSION	BD242766.1
KEYWORDS	UP 2002529098-A/1.
SOURCE	unidentified
ORGANISM	unidentified

REFERENCE	unclassified sequences. 1 (bases 1 to 4718)
AUTHORS	Wilson, J. M. and Xiao, W.
TITLE	Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
JOURNAL	Patent: JP 200258098-A 1 10-SEP-2002;
COMMENT	THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
OS	AAV-1

PN	JP 2002529098-A/1	
PD	10-SEP-2002	
PF	02-NOV-1999	JP 2000581227
PI	05-NOV-1998	US 60/107114
PR	JAMES M WILSON, WEIDONG XIAO	
PC	C12N15/09,A61K31/711,A61K48/00,A61P43/00,C12N1/15,C12N1/19,C12N1/21,PC C12N15/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00 CC	
Adeno-associated virus serum type 1 nucleic acid sequence,	CC	
vector and host		
CC	cell containing the same	
FH	Key	Location/Qualifiers
FT	CDS	(335) .. (4206)
FT	CDS	(4223) .. (4430).
FEATURES	Location/Qualifiers	
source	1..4718	

**ORIGIN**

Query Match	90.8%	Score 4253.2;	DB 2;	Length 4718;
Best Local Similarity	94.7%	Pred. No. 0;		
Matches 4471; Conservative	0;	Mismatches 208;	Indels 43;	Gaps 5;

1 TTGGCACTCCCTCTCTGGGCGCTGCTCACTGAGCCCGGCGACCAAAAGTGGCC 60

Db	1	TTTGCCCACTCCCTCTCTGTGCGCCTGTGCTGTGCTGTGGGGCTCGCGAACCAAGTCCGC	60
OY	61	CGACGCCCGGGCTTTTGCCCGGGCGGCTTCAGTGAACGACGACGCGCGACAGAGGGAGTG	120
Db	61	AGACGGCAGAGCTGTGCTGTGCGGCCCGACCGAGCGACGCGCGCAGAGGGGAGTG	120
OY	121	GCCAATCTCAATCATAGGGGT-----TCCTGAGGGGTGGAGTGTGA	163
Db	121	GGCAACTCCATCATAGGGGGTAAATCGCAGAGGCCCTCCACCGCTGCGGTGACGCTGA	180
OY	164	CGTGAATTACGTCANAGGGTTAAGGAGGTCCTGTATTTAAGGTCACGTGAGTG-TTTTGC	222
Db	181	CGTAATAATACGTACATAGG3--GAATGTGCTGTATATGTACTCATCGTAAGTCTTTTC	237
OY	223	GACATTTTGCACACCATGTGGTCAAGCTGGGTATTTAAGCCCGAGTGAACAACGAGGT	282
Db	238	GACATTTTGCACACCATGTGGCTATTAGGTTATATATGGCCGAGTGAACGACGAGAT	297
OY	283	CTCCATTTTGAAGCGGGAGTTTGAACCGCGACGCCCATGCGGGGTTTACGAGATTGT	342
Db	298	CTCCATTTTGAACCGGAAATTTGAACGACGACACCATGCGGGCTTCTACGAGATCGT	357
OY	343	GATTAAAGTCCCGACGACCTTGAACGACATCTGCGCGGCAATTTCTGACAGCTTTGTGA	402
Db	358	GATCAAGGTGCGACCGACCTGGAAGACACCTGCGGGCAATTTCTGATCTGTTGTGAG	417
OY	403	CTGGGTGCGCAGAAAGAAATGGAGATTCCGCGCAATTTCTGACATGATCTGAATCTGAT	462
Db	418	CTGGGTGCGCAGAAAGAAATGGAGATGCCCCGGAATTTGACATGATCTGAATCTGAT	477
OY	463	TGAGCAGGACCCCTGACCGTGGCCGAGAAAGCTGACGCGCATTTCTGTGTCACTGGCG	522
Db	478	TGAGCAGGACCCCTGACCGTGGCCGAGAAAGCTGACGCGCATTTCTGTGTCAATGGCG	537
OY	523	CCGCGTGAATGAAGCCCCCGGAGGCCCTCTTCTTTGTTCAAGTTGAGAAAGGGAGTCTTA	582
Db	538	CCGCGTGAATGAAGCCCCCGGAGGCCCTCTTCTTTGTTCAAGTTGAGAAAGGGAGTCTTA	597
OY	583	CTTCCACCTCCATATTTCTGTGAGAGACACGCGGGGTCAAATCCATGAGTCTGGCCGCTT	642
Db	598	CTTCCACCTCCATATTTCTGTGAGAGACACGCGGGGTCAAATCCATGAGTCTGGCCGCTT	657
OY	643	CCTGAGTCAGATTAGCGACAAAGCTGTGACAGCATCTCAACGCGGGGATCGAGCCGACCT	702
Db	658	CCTGAGTCAGATTAGCGACAAAGCTGTGACAGCATCTCAACGCGGGGATCGAGCCGACCT	717
OY	703	GCCCACTGTGTTCCGCGTGATCCAAAGACCGCTTAATGCGCGGAGGGGGACAAAGTGGT	762
Db	718	GCCCACTGTGTTCCGCGTGATCCAAAGACCGCTTAATGCGCGGAGGGGGACAAAGTGGT	777
OY	763	GGACGAGTGCATATCCCAACTCTCTGTGCCAAAGCTGACGCCGAGCTGCAGTGGGC	822
Db	778	GGACGAGTGCATATCCCAACTCTCTGTGCCAAAGCTGACGCCGAGCTGCAGTGGGC	837
OY	823	GTGACTTAATGAGAGAGTATTAATGAGCGCGTGTAAACCTGTGCCGAGCGCAAAACGCT	882
Db	838	GTGACTTAATGAGAGAGTATTAATGAGCGCGTGTAAACCTGTGCCGAGCGCAAAACGCT	897
OY	883	CGTGCGCAGACCACTGATCCACGTCAGCGCAACCCAGAGACGAACAAGAGATCTGAA	942
Db	898	CGTGCGCAGACCACTGATCCACGTCAGCGCAACCCAGAGACGAACAAGAGATCTGAA	957
OY	943	CCCCAATTCTGACGCGGCTGTCAATCCGGTCAAAAACCTCCGACGCTCATTTGAGACGTGT	1000
Db	958	CCCCAATTCTGACGCGGCTGTCAATCCGGTCAAAAACCTCCGCGGCTCATTTGAGACGTGT	1011
OY	1003	CGGGTGCATGAGACCGGGGCATCACTCCGAGAAAGCATGTGATCCAGAGAACAGAC	1062
Db	1018	CGGGTGCATGAGACCGGGGCATCACTCCGAGAAAGCATGTGATCCAGAGAACAGAC	1077
OY	1063	CTCGTATCATCTCTTTCAACCGCGGCTCCAACTCGCGGTGCCAGATCAAGGCGCTCTTGA	1122
Db	1078	CTCGTATCATCTCTTTCAACCGCGGCTCTTCAACTCGCGGTGCCAGATCAAGGCGCTCTTGA	1137



Qy 1123 CAATGCCGCGAAGATCATGCGCTGACCAAAATCCGCGCCGACTACCTTGATAGGCCCGC 1182  
| | | | |  
Db 1138 CAATGCCGCGAAGATCATGCGCTGACCAAAATCCGCGCCGACTACCTTGATAGGCCCGC 1197  
| | | | |  
Qy 1183 TCCGCCGCGCGACATTTAAACCAACCGCATTTTACCGCATCTTGAGCTGAAACGCTACGA 1242  
| | | | |  
Db 1198 TCCGCCGCGCGACATTTAAACCAACCGCATCTTACCGCATCTTGAGCTGAAACGCTACGA 1257  
| | | | |  
Qy 1243 CCGTCCGCTACCGCGCGCTCCGCTTTCTGCGCTGCGGCCCAAGAAAAGTTCCGAAAAACGCA 1302  
| | | | |  
Db 1258 ACTGCTCAACGCGCGCTCCGCTTTCTGCGCTGCGGCCCAAGAAAAGTTCCGAAAAACGCA 1317  
| | | | |  
Qy 1303 CACCATCTGCGCTGTTTGGGCGCGGCCACCAACGCGGCAAGCAACATCGCGGAAGCCATCGC 1362  
| | | | |  
Db 1318 CACCATCTGCGCTGTTTGGGCGCGGCCACCAACGCGGCAAGCAACATCGCGGAAGCCATCGC 1377  
| | | | |  
Qy 1363 CCACGCGCGTCCCTTTCTACCGGCTGCTCACTGACCAATGAGAACTTTCCCTTCAACGA 1422  
| | | | |  
Db 1378 CCACGCGCGTCCCTTTCTACCGGCTGCTCACTGACCAATGAGAACTTTCCCTTCAATGA 1437  
| | | | |  
Qy 1423 TTGGCTGCAACAAGATGATCTGGTGGAGGAGGCAAGATGACGGCCAAAGTCTGGA 1482  
| | | | |  
Db 1438 TTGGCTGCAACAAGATGATCTGGTGGAGGAGGCAAGATGACGGCCAAAGTCTGGA 1497  
| | | | |  
Qy 1483 GTCCGCGCAAGGCCATTTCTCGCGCGGAGCAAGTGGCGCTGACCAAAAGTCAAGTCTGC 1542  
| | | | |  
Db 1498 GTCCGCGCAAGGCGATTTCTCGCGCGGAGCAAGTGGCGCTGAGCAAAAGTCAAGTCTGC 1557  
| | | | |  
Qy 1543 CGCCCAAGTCCGATCCCAACCCCGCTGATGTCACCTCCACCAACCATGTCGCGCTGAT 1602  
| | | | |  
Db 1558 CGCCCAAGTCCGATCCCAACCCCGCTGATGTCACCTCCACCAACCATGTCGCGCTGAT 1617  
| | | | |  
Qy 1603 TGAAGGGAACAGCAACCACTTGAGCACAGAGCGCTGAGGACGGGATGTTCAATT 1662  
| | | | |  
Db 1618 TGAAGGGAACAGCAACCACTTGAGCACAGAGCGCTGAGGACGGGATGTTCAATT 1677  
| | | | |  
Qy 1663 TGAATCTCAACCCGCGCTGAGAGCATGTTTGGCAAGGTGACAAAGAGGAAGTCAAGA 1722  
| | | | |  
Db 1678 TGAATCTCAACCCGCGCTGAGAGCATGTTTGGCAAGGTGACAAAGAGGAAGTCAAGA 1737  
| | | | |  
Qy 1723 GTTCTTCCGCTGGGCGCAGAGTACGTGACCGAGGTGCGCATGATTTCTACGTAAGA 1782  
| | | | |  
Db 1738 GTTCTTCCGCTGGGCGCAGAGTACGTGACCGAGGTGCGCATGATTTCTACGTAAGA 1797  
| | | | |  
Qy 1783 GGGTGGAGCAACCAAGACACCGCGCCCGAGTGAACGGGATTAAGCGAGCCCAAGCGGGC 1842  
| | | | |  
Db 1798 GGGTGGAGCAACCAAGAGACCGCGCCCGAGTGAACGGGATTAAGCGAGCCCAAGCGGGC 1857  
| | | | |  
Qy 1843 CTGCCCCCTCAGTCCGCGATTCATTCGACGTCAAGACCGGAAAGAGCTCCGCTGATTC 1902  
| | | | |  
Db 1858 CTGCCCCCTCAGTCCGCGATTCATTCGACGTCAAGACCGGAAAGAGCTCCGCTGATTC 1917  
| | | | |  
Qy 1903 CGACAGGTAACCAAAACAATGTTCTGCTACCGCGGCACTGCTTCAAGTCTGTTCCCTG 1962  
| | | | |  
Db 1918 CGACAGGTAACCAAAACAATGTTCTGCTACCGCGGCACTGCTTCAAGTCTGTTCCCTG 1977  
| | | | |  
Qy 1963 CAAAACATGCGAGAGATGAATCAGATTTCAACTTTGCTTCAAGCAAGGAAACGAGGA 2022  
| | | | |  
Db 1978 CAAAACATGCGAGAGATGAATCAGATTTCAACTTTGCTTCAAGCAAGGAAACGAGGA 2037  
| | | | |  
Qy 2023 CTGTTTCAGAAATGTTTCCCGGCGGTGTCAGAAATCTCAACCGGTCTGACAGAAAGAGACTGA 2082  
| | | | |  
Db 2038 CTGTTTCAGAAATGTTTCCCGGCGGTGTCAGAAATCTCAACCGGTCTGACAGAAAGAGACTGA 2097  
| | | | |  
Qy 2083 TCGGAAACTCTGTGCAATTCATCATCTGTGGGCGGGCTCCGAGATTTGCTGCTCGGC 2142  
| | | | |  
Db 2098 TCGGAAACTCTGTGCAATTCATCATCTGTGGGCGGGCTCCGAGATTTGCTGCTCGGC 2157  
| | | | |  
Qy 2143 CTGCGATCTGGTCAAGCTGAGATCTGAGTGAATGTTTCTGAGCAATTAAGACTTAAC 2202  
| | | | |  
Db 2158 CTGCGATCTGGTCAAGCTGAGATCTGAGTGAATGTTTCTGAGCAATTAAGACTTAAC 2217  
| | | | |

Qy 2203 CAGGTATGCTGCCAGATGTTATCTTCCAGATTTGGCTCGAGGACCAACTCTCTGAGGGCA 2262  
| | | | |  
Db 2218 CAGGTATGCTGCCAGATGTTATCTTCCAGATTTGGCTCGAGGACCAACTCTCTGAGGGCA 2277  
| | | | |  
Qy 2263 TTCCGCACTGTGGGACTTTGAAACTCTGAGACCCCGAAACCCAAAGCCCAACAGCAAAAGC 2322  
| | | | |  
Db 2278 TTCCGCACTGTGGGACTTTGAAACTCTGAGACCCCGAAAGCCCAAGCCCAACAGCAAAAGC 2337  
| | | | |  
Qy 2323 AGGACAGCGGCGGGGCTCTGCTGCTTCTGACTTCAAGTACTCTGAGACCTTCAACGAGC 2382  
| | | | |  
Db 2338 AGGACAGCGGCGGGGCTCTGCTGCTTCTGACTTCAAGTACTCTGAGACCTTCAACGAGC 2397  
| | | | |  
Qy 2383 TCGACAAAGGGGAGACCCCGTCAACGCGCGGATGCAAGCGGCTCTGAGCAACGAGGCTT 2442  
| | | | |  
Db 2398 TCGACAAAGGGGAGACCCCGTCAACGCGCGGATGCAAGCGGCTCTGAGCAACGAGGCTT 2457  
| | | | |  
Qy 2443 ACGACCAAGCACTTAAGCGGGGTGACAAATCCGTAACCTGCGGTATTAACCAAGCCGACGCGC 2502  
| | | | |  
Db 2458 ACGACCAAGCACTTAAGCGGGGTGACAAATCCGTAACCTGCGGTATTAACCAAGCCGACGCGC 2517  
| | | | |  
Qy 2503 AGTTTCAGAGCGCTCTGCAAGAAATACGTCCTTTTGGGGGCAACCTCGGCGAGCAGTCT 2562  
| | | | |  
Db 2518 AGTTTCAGAGCGCTCTGCAAGAAATACGTCCTTTTGGGGGCAACCTCGGCGAGCAGTCT 2577  
| | | | |  
Qy 2563 TCCAGGCAAGAGAGGCTTCTCGAACCTTTTGTGCTGTTGAGAAAGTGTCTAAGACGG 2622  
| | | | |  
Db 2578 TCCAGGCAAGAGAGGCTTCTCGAACCTTCTCGGTCTGTTGAGAAAGGCGCTAAGACGG 2637  
| | | | |  
Qy 2623 CTCTCGGAAAGAAACGTCGCGGTAGAGATCGGCAAGAGCCGACCTCTCCGCGGCA 2682  
| | | | |  
Db 2638 CTCTCGGAAAGAAACGTCGCGGTAGAGATCGGCAAGAGCCGACCTCTCTCCGCGGCA 2697  
| | | | |  
Qy 2683 TTGSCAAGACAGGCGCAGCAGCCCGCTTAAAGAGACTCAATTTTGGCTCAGACTGCGACT 2742  
| | | | |  
Db 2698 TTGSCAAGACAGGCGCAGCAGCCCGCTTAAAGAGACTCAATTTTGGCTCAGACTGCGACT 2757  
| | | | |  
Qy 2743 CAGAGTCAAGTCCCGGACCCCAACACTCTCTGAGAACTCTCAAGAACCCCGCTGCTGTG 2802  
| | | | |  
Db 2758 CAGAGTCAAGTCCCGGACCCCAACACTCTCTGAGAACTCTCAAGAACCCCGCTGCTGTG 2817  
| | | | |  
Qy 2803 GACCTACTTAACATGCTTTCAGCGGCGTGGGCGCACCAATGGGAGCAATTAAGAGGCGCG 2862  
| | | | |  
Db 2818 GACCTACTTAACATGCTTTCAGCGGCGTGGGCGCACCAATGGGAGCAATTAAGAGGCGCG 2877  
| | | | |  
Qy 2863 ACGGAGTGGGTAATGCTCTCAGAAATTTGCAATTCGATTCACATGCTGGGCGACAGAG 2922  
| | | | |  
Db 2878 ACGGAGTGGGTAATGCTCTCAGAAATTTGCAATTCGATTCACATGCTGGGCGACAGAG 2937  
| | | | |  
Qy 2923 TCATCACCAACGACACCGGACATGGGCTTGGCCACTATTAACCACTCTACAGAGC 2982  
| | | | |  
Db 2938 TCATCACCAACGACACCGGACATGGGCTTGGCCACTATTAACCACTCTACAGAGC 2997  
| | | | |  
Qy 2983 AAATCTCAGTCTTCAACGGGGGCGAGCAACCAACCACTCTCGGCTACAGGACCC 3042  
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OY	3343	TAAAGCTCAACAATGGACAGCCAGGAGTGGAGCGCTCATCCTTTTAATGCTGGAAATAT	3402
Db	3358	TGAAGCTCAACAATGGACAGCCAGGCGGTGGAGCTTCACTCTTTTAATGCTGGAAATAT	341
OY	3403	TCCCATTCGCAAGTCTGTGAAGACGGGCAATTAATTTAACTTCAAGCTACCTTCCAGAGC	3462
Db	3418	TCCCTTCTCAAGTGTGTGAAGAGGGCAACAACTTTAACTTCAAGCTACCTTGGAGAG	3477
OY	3463	TGCTTTTCCACAGAGCTACGGCACAGCCAGAGCTGGACCGGCTGTGTGAATCTCTCA	3522
Db	3478	TGCTTTTCCACAGAGCTACGGCACAGCCAGAGCTGGACCGGCTGTGTGAATCTCTCA	3533
OY	3523	TCGACCAAGTACCTGTATTAACCTGAACAGAACTCAACATCAGTCGGAAAGTCCCAACA	3582
Db	3538	TCGACCAATACCTGTATTAACCTGAACAGAACTCAAAATCAGTCGGAAAGTCCCAACA	3597
OY	3583	AGGACTTGTGTGAAGCGGTGGGTCTCAAGCTGGAGATGTGTGTGAAGTCCCTCA	3642
Db	3598	AGGACTTGTGTGAAGCGGTGGGTCTCAAGCTGGAGATGTGTGTGAAGTCCCTCA	3657
OY	3643	TACCTGACCCCTGTATCCGGCAGACGCGCTTCTTAAACAAACAAACACAAACAACA	3702
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OY	3703	GCAACTTTAACTTGACCTGTGCTTCAAAATATACCTTAATGGGCTGAATCTATATCA	3762
Db	3718	GCAATTTTAACTTGACCTGTGCTTCAAAATATACCTTAATGGGCTGAATCTATATCA	3777
OY	3763	ACCTGGGACATGCTATGGGCTCACACAAAGACACAAAGACAAAGTCTTCCCATGAGAC	3822
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OY	3823	GTGTCTATATTTTGGAAAGAGAGCGCTGGAGCTTCAACACTGACATTTGACATGTCA	3882
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OY	3943	CTGTGGACGTCAATCTCCAGACAGACAGACCAAGCCCTGCGACCGGAGATGTGATTTA	4002
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OY	4003	TGGAGGCTTAACTTGGAAATGTGTGTGGCAAGACAGAGATTAATCTGAGAGGTCTATTT	4062
Db	4018	TGGAGGCTTAACTTGGGCAATGTGTGTGGCAAGATGAAGATGTATCTTGAAGGTCTCATTT	4077
OY	4063	GGGCGAAATTTCTCACACAGGATGACACTTTCACCCGTCTCTCTCAATGGGCGGCTTGG	4122
Db	4078	GGGCGAAATTTCTCACACAGATGACACTTTCACCCGTCTCTCTTAATGGGCGGCTTGG	4137
OY	4123	GACTTAAAGCACCCGCTCTCTCAAGTCTCTATCAAAACACGCTGTCTCTCGAATCTCTC	4182
Db	4138	GACTTAAAGCACCCGCTCTCTCAAGTCTCTATCAAAACACGCTGTCTCTCGAATCTCTC	4197
OY	4183	CGGCGAGATTTTCCGCTCAAAAGTTTGTCTATTCATCAACCCAGATTTCCACAGACAG	4242
Db	4198	CGGCGAGATTTTCAAGCTCAAAAGTTTGTCTATTCATCAACCCAGATTTCCACAGACAG	4257
OY	4243	TGAGCGTGAAGTGAATGGAGCTGACAGAAAGAAACAGCAAAAGCTGAATCCCGAG	4302
Db	4258	TGAGCGTGAAGTGAATGGAGCTGACAGAAAGAAACAGCAAAAGCTGAATCCCGAG	4317
OY	4303	TGCAATTAACAATCTTAATGAGAAATCTGCCAAGCTGAATTTCACTGTGAACAACATG	4362
Db	4318	TGCAATTAACAATCTTAATGAGAAATCTGCCAAGCTGAATTTCACTGTGAACAACATG	4377
OY	4363	GACTTAACTGAAGCTGCGCCCATTTGGACCCGTTAACCCTACCCGCTCCCTGTAAATGT	4422

Db	4378	GACCTTAACTGAGGCGCTCGCCCATTTGGGACACCCTGTACCTTAACCCGTCCTCCGTAAATTAC	4437
Qy	4423	GTGTTAAATCAATAAAACCGGTTAATTCTGTGTCAGTTGAACTTTGATCTCATGTCTTAATTA	4482
Db	4438	GGTTTAATCAATAAAACCGGTTGATTCGTTTCAGTTGAACCTTTGGCTCTGTCCTCTTA	4497
Qy	4483	TCTTATCTGTCATCAATGCAACCGGTTATGACATTTAACTGCTTAATTTGGCTTGGCGA--	4540
Db	4498	TCTTAATC-GGTTACCATGTTTATAGCTTACATTAACTGCTGTTGGTTCGCTTCCGATTA	4556
Qy	4541	-----ATACCCCTATGATGGAATTTGCCCACTCCCTCTATGCGCGC	4581
Db	4557	AAAGACTACGATCAATCGGGTTTACCCCTTATGATGGAATTTGCGCACTCCCTCTGCGCGC	4616
Qy	4582	TCGCTCGCTCGGTTGGGCGCGGCAAGACAGCTCTGCCGTCGCGGACCTTTGGTCGCA	4641
Db	4617	TCGCTCGCTCGGTTGGGCGCTCGGACCAAAAGTCCGCAAGACGAGACTCTGCTCTGCC	4678
Qy	4642	GGCCCCACCGAGCGAGCGGCGCATTAAGAGGAGTGGCCAA	4683
Db	4677	GGCCCCACCGAGCGAGCGGCGCATTAAGAGGAGTGGCCAA	4718
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DEFINITION	Sequence 1 from patent US 6759237.		
ACCESSION	AR562498		
VERSION	AR562498.1	GI:53976564	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 4718)		
TITLE	Wilson,J.M. and Xiao,W.		
JOURNAL	Adeno-associated virus serotype 1 nucleic acid sequences, vectors and host cells containing same		
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source	The Trustees of the University of Pennsylvania; Philadelphia, PA		
	Location/Qualifiers		
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	/organism="unknown"		
ORIGIN	/mol_type="genomic DNA"		
Query Match	90.8%; Score 4253.2; DB 2; Length 4718;		
Best Local Similarity	94.7%; Pred. No. 0;		
Matches 4471; Conservative	0; Mismatches 208; Indels 43; Gaps 5;		
Qy	1	TTGGGCACTCCCTCTCTGCGGCTCGCTCGCTCACTAGAGCCGGGCGACCAAGATCGCC	60
Db	1	TTGGCCAACTCCCTCTCTGCGGCTCGCTCGCTCGCTGAGGAGGCTCGCGACCAAGATCGCC	60
Qy	61	CGAGGCCCGGGCTTTGGCCCGGCGGCTCAATGAGCGGACGAGCGGCGGCAAGAGGAGTGT	120
Db	61	AGAGCGGAGAGCTCTGCTCTGCGCGGCGGCGGACGAGCGAGCGGCGGCAAGAGGAGTGT	120
Qy	121	GCCAACTCCATCACTAAGGAGT-----TCTTGAGGGGTGAGTCTGA	163
Db	121	GGCAACTCCATCACTAAGGAGTATCGGGAAGCGCTCCACGCTGCCGCGTCAACGCTGA	180
Qy	164	CGTGAATTAATGCTATAGGTTAAGGAGGTCTGTATTAAGAGTCAAGTGAATG-TTTTGC	222
Db	181	CGTAAATTAATGCTATAGG--GAGTGGTCTGTATTAAGTGTCACTGATGATGCTTTTGC	237
Qy	223	GACATTTTGCACACCAATGTGTCAAGCTGGGTTATTTAAGCCGAGTGAAGACCGAGGAT	282
Db	238	GACATTTTGCACACCAAGTGGCCATTTAAGGTATATATGGCCGAGTGAAGACGAGAT	297
Qy	283	CTCCATTTTGAAGCGGAGGTTTGAACGCGACGCGCATGCGGGGTTTTCAGGATGT	342
Db	298	CTCCATTTTGAACCGCGAAATTTGAACAGACGACGACATGCCGGGCTTTTACGAGATGT	357

QY	343	GATTTAAGSTCCCCACGCACTTTGACAGACATCTCCCGGCAATTTCTGACAGCTTTGTGAA	402
Db	358	GATCAAGGTGCGAGCGCACTTGACAGACACTGCGCGGCAATTTCTGACTGTGTGTAG	417
QY	403	CTGGGTGCGCAGAAAGAAATGGAGTTGCGCCAGATTCTCACTGATCTGAATCTGAT	462
Db	418	CTGGGTGCGCAGAAAGAAATGGAGTCTGCCCGGATTTCTGACATGATCTGAATCTGAT	477
QY	463	TGAGCAGGCACTCCCTGACCGTGTGCCGAGAGCTGCAAGCGCACTTCTGTGTCCACTGGCG	522
Db	478	TGAGCAGGCACTCCCTGACCGTGTGCCGAGAGCTGCAAGCTTCTGTGTCCAATGGCG	537
QY	523	CCGGGTGATTAAGGCCCCGAGAGGCCCTTCTTTGTTAGTTTCGAGAAAGGCGAGTCTTA	582
Db	538	CCGGGTGATTAAGGCCCCGAGAGGCCCTTCTTTGTTAGTTTCGAGAAAGGCGAGTCTTA	597
QY	583	CTTCCACTCTCATATTTCTGTGTGAGACCAAGGAGGTCAAAATCCATGTGTCTGGGCGCTT	642
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QY	643	CCTGAGTCAAGTTAAGCGCAAGAGCTGTGTGACCACTCAACCGCGGGAATCGAGCCGACT	702
Db	658	CCTGAGTCAAGTTAAGCGCAAGAGCTGTGTGACCACTCAACCGCGGGAATCGAGCCGACT	717
QY	703	GCCCAACTGTGTTCGGGTGACCAAGACCGCTAATGTGCGCCGAGGGGGGAAACAAGTGT	762
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QY	763	GAGCAGATGCTACATCTCCCAACTACCTCTCTGCCAAGACTAGCCCGGAGCTGTAGTGGGC	822
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Db	838	GTGACTCAACATGAGAGAGATATATTAAGGCGCGTATTAACTGTGCGCGAGCCCAACGCGT	897
QY	883	CGTGGCGCAAGACTTGACCTCAAGCTCAAGCCAGAGCAAGCAAGAGAAATCTGAA	942
Db	898	CGTGGCGCGAGACTTGACCTCAAGCTCAAGCCAGAGCAAGCAAGAGAAATCTGAA	957
QY	943	CCCCAATTTCTAGACGGCGCTGTATCTCGGTCGAAAACTCCGACGCTACATGAGAGCTGGT	1002
Db	958	CCCCAATTTCTAGACGGCGCTGTATCTCGGTCGAAAACTCCGACGCTACATGAGAGCTGGT	1017
QY	1003	CGGATGAGCTGTGTGACCGGAGGATCACTCCGAGAGAGAGTGTATCCAGAGAGACAGGC	1062
Db	1018	CGGATGAGCTGTGTGACCGGAGGATCACTCCGAGAGAGAGTGTATCCAGAGAGACAGGC	1077
QY	1063	CTTCGATCATTTCTTTCAAGCGCGCTCCAACTCCGCGGTCCCAAGATCAAGGCCGCTCTGGA	1122
Db	1078	CTTCGATCATTTCTTTCAAGCGCGCTTTCAACTCCGCGGTCCCAAGATCAAGGCCGCTCTGGA	1137
QY	1123	CAATGCGCGCAAGATCATGTGCGCTTACCAAAATCCGCGCCGACTCACTGTGTAGGCCCGC	1182
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QY	1183	TCCGCGCGCGCACTTAATAAACCAACCGCATTTTACCGCATCTGTGAGCTGAACGCTACGA	1242
Db	1198	TCCGCGCGCGCACTTAATAAACCAACCGCATTTTACCGCATCTGTGAGCTGAACGCTACGA	1257
QY	1243	CCGTGCTCAAGCGCGGCTCGCTTTCTGTGGGCTGGGGCCAGAAAAAGGTTGGAAAAACGCA	1302
Db	1258	ACCTGTCTTACCGCGGCTCGCTTTCTGTGGGCTGGGGCCAGAAAAAGGTTGGAAAAACGCA	1317
QY	1303	CACCATCTGTGCTTTGTGGGCGGGCCACCAACGGGCAAGACCAACATCGCGGAAGCATGCT	1362
Db	1318	CACCATCTGTGCTTTGTGGGCGGGCCACCAACGGGCAAGACCAACATCGCGGAAGCATGCT	1377
QY	1363	CCAGCGCGTGGCTTTCTAAGGTGTGTGCTCACTGTGACCAATGTGAAGACTTTCTCTTCAAG	1422
Db	1378	CCAGCGCGTGGCTTTCTAAGGTGTGTGCTCACTGTGACCAATGTGAAGACTTTCTCTTCAAG	1437
QY	1423	TTGCTCTGACAAGATGTGTGATCTGTGTGGAGGAGGCAAGATGACGGCCAGAGTCTGTGA	1482

Db	1438	TTGCGTCGCAAGAGTGTATCTGGTGGAGGAGGCGCAAGATACGGCCAGAGTCGTGGA	1497
Qy	1483	GTCCGCGCAAGGCGCATTTCTTGCGCGCGAGCAAGGTGCGCGTGGACCAAAAGTGCAGTCTGC	1542
Db	1498	GTCCGCGCAAGGCGCATTTCTTGCGCGCGAGCAAGGTGCGCGTGGACCAAAAGTGCAGTCTGC	1557
Qy	1543	CGCCCAAGATCCGATTCGCCACCCCGGTGATTCGTCACTCTCCACACCAACAATGTCGCCCGGAT	1602
Db	1558	CGCCCAAGATCCGATTCGCCACCCCGGTGATTCGTCACTCTCCACACCAACAATGTCGCCCGGAT	1617
Qy	1603	TGACCGGAAACACACACCCTTGAGAGCACGAGCCGTTGCAGAGCCGATGTTCAATT	1662
Db	1618	TGACCGGAAACACACACCCTTGAGAGCACGAGCCGTTGCAGAGCCGATGTTCAATT	1677
Qy	1663	TGAATCTCACCCGCGCTTGTGAGCATGATCTTTGGCAAGGTGACAAAGCAGAAATCAAAAG	1722
Db	1678	TGAATCTCACCCGCGCTTGTGAGCATATCTTTGGCAAGGTGACAAAGCAGAAATCAAAAG	1737
Qy	1723	GTTCCTTCGCGTGGGCGCAGGATTCACGTGACCGAGGTGGCGCATGAGTCTTACGTCAGAAA	1782
Db	1738	GTTCCTTCGCGTGGGCGCAGGATTCACGTGACCGAGGTGGCGCATGAGTCTTACGTCAGAAA	1797
Qy	1783	GGGTGAGGCGCAACACAGACCCGCGCCCGATGACGCGATTAAGAGCGAGCCACAGCGGGC	1842
Db	1798	GGGTGAGGCGCAACAAAGAACCGCGCCCGCATGACGCGATTAAGAGCGAGCCACAGCGGGC	1857
Qy	1843	CTGCCCTCAGTTCGGGATTCATCGACGTCAGCGGGAAGAGGCTCCGGTGGACCTTTGC	1902
Db	1858	CTGCCCTCAGTTCGGGATTCATCGACGTCAGCGGGAAGAGGCTCCGGTGGACCTTTGC	1917
Qy	1903	CGACAGGTACCAAAACAAATGTTCTGTGACGCGGGCATGCTTCAGATGCTGTTCCCTG	1962
Db	1918	CGACAGGTACCAAAACAAATGTTCTGTGACGCGGGCATGCTTCAGATGCTGTTCCCTG	1977
Qy	1963	CAAAACATCCGAGAGATGAATTCAGAAATTTCCAAATTTGCTTCAACGACGCGACCGAGAGA	2022
Db	1978	CAAGACATCCGAGAGATGAATTCAGAAATTTCCAAATTTGCTTCAACGACGCGACCGAGAGA	2037
Qy	2023	CTGTTTCAGAAATGTTTCCCGCGGTGCAGAAATCTCAACCGGTGTCAGAAAGAGAGCTA	2082
Db	2038	CTGTTTCAGAGTCTTCCCGCGGTGCAGAAATCTCAACCGGTGTCAGAAAGAGAGCTA	2097
Qy	2083	TCGGAACCTCTGTGCCATTCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCCTCGGC	2142
Db	2098	TCGGAACCTCTGTGCCATTCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCCTCGGC	2157
Qy	2143	CTGGCATCTGTGCACAGTGGATCTGGATACCTGTGTTCTGACCAATTAATGACTTAAAC	2202
Db	2158	CTGGCATCTGTGCACAGTGGATCTGGATACCTGTGTTCTGACCAATTAATGACTTAAAC	2217
Qy	2203	CAGGTATGGCTCGCGATGAGTTATCTTTCAGATTGGCTCGAGACAACTCTCTGAGGGCA	2262
Db	2218	CAGGTATGGCTCGCGATGAGTTATCTTTCAGATTGGCTCGAGACAACTCTCTGAGGGCA	2277
Qy	2263	TTCCGCGATGTGTGGGACTTGGAAACCTGGAGCCCGCGAAACCCAAAGCACAACCAAAAGC	2322
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Qy	2323	AGGACGACGGCGGGGTCTGTGTCTTCTGAGCTACCAAGTACTCTCGGACCTTCAACGAGAC	2382
Db	2338	AGGACGACGGCGGGGTCTGTGTCTTCTGAGCTACCAAGTACTCTCGGACCTTCAACGAGAC	2397
Qy	2383	TCGACAAAGGGGAGCCCGTCAACGCGCGGAGTACAGCGGCTCTTGAGACACAGAGGCTT	2442
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Qy	2443	ACGACCAAGAGCTCAAAAGCGGGTGAACAATCCGTAACCTGCGGTTAAACACAGCGGACGCG	2502
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LOCUS
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ACCESSION   AX753251
VERSION      AX753251.1 GI:3216108
KEYWORDS
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ORGANISM     Adeno-associated virus - 1
             Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
REFERENCE
AUTHORS      Geo, G., Wilson, J.M. and Alvira, M.
TITLE        A method of detecting and/or identifying adeno-associated virus
             (AVV) sequences and isolating novel sequences identified thereby
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SOURCE			
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AUTHORS		Xiao, W., Chirmule, N., Berta, S. C., McCullough, B., Gao, G. and Wilson, J. M.	
TITLE		Gene therapy vectors based on adeno-associated virus type 1	
JOURNAL		J. Virol. 73 (5), 3994-4003 (1999)	
PUBMED		10196295	
REFERENCE		2 (bases 1 to 4719)	
AUTHORS		Xiao, W. and Wilson, J. M.	
TITLE		Direct Submission	
JOURNAL		Submitted (05-MAY-1998) IHGT, University of Pennsylvania, 3601	

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CQ972062 4721 bp DNA linear PAT 05-JAN-2005  
LOCUS CQ972062 Sequence 7 from Patent WO2004108922.  
DEFINITION CQ972062  
ACCESSION CQ972062  
VERSION CQ972062.1 GI:57163375  
KEYWORDS  
SOURCE Adeno-associated virus  
ORGANISM Adeno-associated virus  
Virusess: ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;  
unclassified Dependovirus.  
REFERENCE  
1 Rader, D.J. and Wilson, J.M.  
AUTHORS Methods and compositions for lowering total cholesterol levels and  
TITLE Treatment of heart disease  
JOURNML Patent: WO 2004108922-A 7 16-DEC-2004;  
The Trustees of The University of Pennsylvania (US)  
FEATURES  
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VERSION  
KEYWORDS  
ORGANISM unidentified  
SOURCE unidentified  
unclassified sequences.

REFERENCE 1  
AUTHORS Wilson, J.M., Gao, G., Alvira, M.R. and Vandenbergh, L.H.  
TITLE Adeno-associated virus (aav) clades, sequences, vectors containing same, and uses therefor  
JOURNAL Patent: WO 2005033321-A 180 14-APR-2005;  
The Trustees of the University of Pennsylvania (US)  
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ORIGIN /note="adeno-associated virus serotype 7"

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 VERSION AX753246.1 GI:32166105  
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 ORGANISM Adeno-associated virus - 7  
 Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;  
 unclassified Dependovirus.  
 REFERENCE  
 1 Gao, G., Wilson, J.M. and Alvira, M.  
 AUTHORS A method of detecting and/or identifying adeno-associated virus  
 TITLE (AAV) sequences and isolating novel sequences identified thereby  
 JOURNAL Patent: EP 1310571-A.1 14-MAY-2003;  
 The Trustees of The University of Pennsylvania (US)  
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 Best Local Similarity 87.5%; Pred. No. 0;  
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 QY 61 CGAGCCCGGAGCTTTGCGCGGCGCTCAAGTACGAGCGAGCGCGAGAGGAGTG 120  
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 Db 61 AGAGCGAGAGCTCTGCTGCGGCGCCACCGAGCGAGGCGGCATAGAGGAGTG 120  
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 QY 121 GCCAACTTCATCACTAGGAGGTTCTTGAGG-----GCTGAGCTGTGAC 164  
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QY	4058	TATTTGGG	CCAAAATTCCTCA	CAGGAATGACATTTTCA	CCCGTCTCCTCAAGGGGCG	4117	
Db	4075	CATCTGGG	CCAAAGTTCCTCA	CAGGAATGACATTTTCA	CCCGTCTCCTTGAATGGGCG	4134	
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QY	4178	TCCTCCGG	CAGAGTTTGGGCTAC	AAAGTTTGTCTTATCTCA	CCAGATTTCCACAG	4237	
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QY	4478	TATTAATCT	TATCTGTGCA	CAATAGCAACCGGTTACATTA	ACTGCTTAGTGGGCTTCG	4537	
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[illegible]

Query Match	78.5%	Score 3678.4	DB 10	Length 4721
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QY	464	GAGCAGGACACCCCTGACCGGTGGCCGAGAGGCTGACGCGCATTTCTGTGTCACTGGCG	523	
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Db	538	CGCGGATGAAGGCCCGGAGGCCCTCTCTTTGTTCAAGTTGAGAAAGGCGAGACTAC	597	
QY	584	TTCCACCTCCATATTTGTGTGAGACCAACGCGGGGCTCAATTCATGTGCTGGGCGGCTTC	643	
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Db	1138	AATGCGGGCAAGATCATGCGGCTGACCAATTCGCGGCCGACT	ACCTGTGAGCCCGCTCG	1197
QY	1184	CGGCGCGCGACATTTAAAAACCAACGCGATTTTACGCGATCT	GTGAGACTGAA	1243
Db	1198	CTGCGCGCGGACATTTAAAAACCAACGCGATCTTACGCGAT	CTGAGACTGAA	1257
QY	1244	CTGCGCTACGCGGCTCCGCTCTTCTCGGCTGGGCCCAAAA	AGTTGCAAAA	1303
Db	1258	CTGCGCTACGCGGCTCCGCTCTTCTCGGCTGGGCCCAAAA	AGTTGCGGAAGCGCAAC	1317
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QY	1364	CACGCGGAGCCCTTTACGGGCTGGGCTCAACTGGACCAAT	TGAGAACTTTCCCTTCAACGAT	1423
Db	1378	CACGCGGAGCCCTTTACGGGCTGGGCTCAACTGGACCAAT	TGAGAACTTTCCCTTCAACGAT	1437
QY	1424	TGCGTCGACAAGATGTGATCTGTGTGGAGAGAGGCAAGATG	ACGGCCAAAGTCTGGAG	1483
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QY	1484	TCGCGCAAGGCCATTTCTGGCGGGACGAAGGTGGCCGTGG	ACAAAGTGCAGATCGTC	1543
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QY	1784	GGTGAGGCAACAAACAGACCCGCCCATGACGCGGATTA	AAAGGAGACCCCAAGCGGCG	1843
Db	1798	GCGGAGGCAACAAAGAACCCGCCCATGACGCGGATTA	AAAGGAGACCCCAAGCGGCG	1857
QY	1844	TGCGCTCAATCTGCGGATTCATGACGTCAGACGCGAAAG	AGCTTCGAGTCTTGGC	1903
Db	1858	TGCGCTCAATCTGCGGATTCATGACGTCAGACGCGAAAG	AGCTTCGAGTCTTGGC	1917
QY	1904	GACAGGTACAAAACAAATGTTCTGTGACGCGGGACATG	CTTCAATGCTGTTTCCCG	1963
Db	1918	GACAGGTACAAAACAAATGTTCTGTGACGCGGGACATG	CTTCAATGCTGTTTCCCG	1977
QY	1964	AAAAATGCGAGAGATGATCAGAAATTTCAACTTTCCTTAC	CCACGAGGACAGAAAC	2023

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Db	2038	TGTTTA	AGAGTGTTCCTCCCGGGGTTCAGAAATCTCAACCGGTCGTCAAAAABAACGTAT	2097
Oy	2084	CGAAAC	CTGTGGCCATTCATCATCTGCTGGGGGGGGCTCCCGAATTTGCTTGGCC	2143
Db	2098	CGAAAC	CTGTGGCGGATTCATCATCTGCTGGGGGGGGCCCGAATTTGCTTGGCC	2157
Oy	2144	TGCGAT	CTGTGTCACCTGTGATCTGGGAGACCTGTGTTCTGAGCAATTAATGACTTAAC	2203
Db	2158	TGCGAC	CTGTGTCACCTGTGACCTGGGACGACCTGCTTCTGAGCAATTAATGACTTAAC	2217
Oy	2204	AGATGAT	GAGCTGCGCATGTGATCTTCCAGATTTGGCTCGAGGACAACTCTCTGAGGGCAT	2263
Db	2218	AGGATAT	GAGCTGCGCATGTGATCTTCCAGATTTGGCTCGAGGACAACTCTCTGAGGGCAT	2277
Oy	2264	TCGGCAG	TGTGTGGGACTTTGAAACCTTGAGCCCGAAACCCAAAGCCAAACGACAAAAGCA	2323
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Oy	2324	GGACGA	CGGCTGGGGGTCTGTGCTTCTGTGCTACAAATGACTCTGGACCTTTCACCGACT	2383
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Oy	2384	CGACAG	GGGGGAGCCGTCACACGGGGGGGATGACGCGGGCTCTGAGCAGCAAGGCTTA	2443
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Db	2998	GCAAT	CTCCAGTCTTCAACGAGTATGACAAAGACAACTCACTTGGCTTCAAGAC	3057
Oy	3041	CCCT	TGGGGATTTTGAATTTCAACAGATTCACCTGCCATTTCTACCAAGTGACTGGCA	3100

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 ORGANISM  
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 unclassified Dependovirus.  
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 1  
 Gao,G., Wilson,J.M. and Alvirra,M.  
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 Db 123 GCTTTGGACATTTTGGACACCATGTGTCAATTTGAAGGTATTAATGAGTGA 182

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OY	335	GAGATTGTGATTAAGGTCCCGACACCTTGAACGAGCATCTGCGGGCATTTTCTACAGC	394
Db	243	GAGATTGTGATTCAGGTGCCGAGCCACTGTGACGAGCATCTGCCGGCATTTTCTACCT	302
OY	395	TTTGTGAACGTGGGTGGCCGAGAGGAATGGAGTTGGCCGACGATTTTGACATGGATCTG	454
Db	303	TTTGTGAACGTGGGTGGCCGAGAGGAATGGAGGTGTCGCCCGGATTTTGACATGGATCGG	362
OY	455	AATCTGATTGAGCAGAGGCAACCCCTGACCGTGGCCGAGAAAGTGTACCGGGCATTTCTGGCT	514
Db	363	AATCTGATTGAGCAGAGGCAACCCCTGACCGTGGCCGAGAAAGTGTACCGGGCATTTCTGGCT	422
OY	515	CAGTGGCCCGGTGAGTAAAGGCCCGGAGGCCCTCTTCTTTGTTCAAGTTGAGAAAGGCG	574
Db	423	CAATGGCCCGGTGAGTAAAGGCCCGGAGGCCCTCTTCTTTGTTCAAGTTGAGAAAGGCG	482
OY	575	GAGTCTTACCTTCACCTCCATATTTCTGGTGAAGACACAGGGGGTCAATTCATGGTGGTG	634
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OY	1055	GACCAGGCGCTGTACATCTCCTTCAACACGCGCTCACTCGCGGTCCGACATCAAGGCC	1114
Db	963	GACCAGGCGCTGTACATCTCCTTCAACACGCGCGCTCACTCGCGGTCCGACATCAAGGCC	1022
OY	1115	GCTCTGAGCAATGCCGGAGAGATCATGGCGCTGACCAATCCGCGCCGACTACCTGTGTA	1174
Db	1023	GCGCTGAGCAATGCCGGAGAGATCATGGCGCTGACCAATCCGCGCCGACTACCTGTGTA	1082
OY	1175	GGCCCGCGTCCGCCCGCGGACATTTAAACCAACCGCAATTTAACCGGATCCTGAGACTGAC	1234
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OY	1235	GGCTACGACCTCTGCTACGCGCGCTCCGTTCTTCTCGGCTGGGCCCAAAAAAGGTTCCGA	1294
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OY	1295	AAAGCGAACACCATCTGGCTGTTTGGGCGGGCACACAGGGCAGAACCAACATGCGGGA	1354
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OY	1415	TTCAACGATTTGCGTCGACAAGATGTGATCTGTGTGGAGGAGGAGCAATGACGGCCAA	1474
OY	1323	TTCAACGATTTGCGTCGACAAGATGTGATCTGTGTGGAGGAGGAGCAAGTGAAGCCCA	1382
OY	1475	GTGCTGAGATTCGCGCAAGGCCATTTCTGCGCGGAGCAAGGTGCGCGTGAACCAAGTGC	1534
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OY	1955	TTTCCCTCGCAAACTGTCGAGAGAAATGAAATTCGAATTCGAATTTGCTTCACGACGGG	2014
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OY	2075	AGGACGTATCGAAACTCTGTGCAATTCATCTGTGCGGCGGAGCTTCCGAGATTGCT	2134
OY	1983	AGGACGTATCGAAACTCTGTGCAATTCATCTGTGCGGCGGAGCTTCCGAGATTGCT	2042
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Db	2823	GGGCGACAGAGTCATACACACGACGACCCGAAACATGGGCAATTGCCACTTAACAACA	2882
Qy	2972	CCTCTAACAGCAATCTCCAGTCTTCAACGGGG---CGAGCAACGAAACCACTACTT	3028
Db	2883	CCTCTAACAGCAAACTCCAAATGGAAACATGGGAGGAAGACCAACGAAACACTACTT	2942
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Db	2943	TGGCTAACGACACCCCTGGGGGTATTTTGAATTCAAAGATTCACATGSCATTTCTACG	3002
Qy	3089	ACGTGACTGGCAGCGACTCATCAACAACAATTTGGGATTCGGGCCCAAGAGACTCAATT	3148
Db	3003	ACGTGACTGGCAGCGACTCATCAACAACAATTTGGGATTCGGGCCCAAGAGACTCAATT	3062
Qy	3149	CAAGCTCTTCAACATCCAAAGTCAAGAGAGTCAACGAAATATATGCGTCAAGACATATGC	3208
Db	3063	CAAGCTCTTCAACATCCAAAGTCAAGAGAGTTCACGAAACGAAGGACCAAGACCATATGC	3122
Qy	3209	TAAATAACTTACACAGCAGGTTCAAGTCTTGTGCACTCGAGTCAACGTTCCGTAAGT	3268
Db	3123	CAATAAACCCTTACACAGCAGGTTCAAGTCTTGTGCACTCGAGTCAACGTTCCGTAAGT	3182
Qy	3269	CCTCGGCTCTGGGACACAGGCGTGGCTCCCTCCGTTCCCGCGGACGTTTCAATGATTC	3328
Db	3183	CCTAGGCTCTGGGACCAAGAGTGGCTTCGCAACCGTTTCTCGACAGCTTTCATATGTTCC	3242
Qy	3389	GCAGTACGGCTTCAACGCTCAACATATGGCAGCGCAGGAGTGGGACGCTATCTTTTA	3388
Db	3243	TCAGTACGGCTTCAACGCTTCAACATATGGAAATGAAAGTCAACGTTTGAACGTTCTTTCTTA	3302
Qy	3389	CTGCTCGGAATATTTTCCATCGCAGATGCTGAGAACGGGCAATTAATTTTACGTA	3448
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Db	3363	CACCTTCAGAGCGGCTTTCACAGGAGCTAAGCGGACAGCGCAAGACCTCGAATCGACT	3422
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Db	3600	CCAAAATTAACAACAGCAACTTTGTGTGGACGGAGCTGTCTAAATTCAAGCTGAACGGAG	3659
Qy	3749	TGAATCTATATCAACCTGTGCACTGTATGCGCTTCACAAABAAGCAAAAGCAAGTT	3808
Db	3660	AGACTCGGTAAATGAATCTGTGGCGTGTGCAATGCAAAABAAGACAGAGCGCTT	3719
Qy	3809	CTTTCCCACTGACGGGTGCATGATTTTTTGGAAAGAGAGCGCGCGAGCTTCAACAATGCG	3868
Db	3720	CTTTTCCATCAAGTGGCGGTCTCATATTTTGGACACAAAGAGCGGGAACGATGAGTGA	3779
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Qy	3929	CGAAAGATTTTGGGACTGTGGCAGTCAATCTCCACAGACAGACACAGCCCTGGACCGG	3988
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Qy	4109	CATGGGCGGCTTTTGGACTTTAAGCACCGCGCTCTCAGATCTCTATCAAAAAACAGCCTGT	4168
Db	4020	GATGGGTGGAATTTGGAATGAAACACCCACCTCCACAGATTTCTATTTAAAAATACACAGT	4079
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KEYWORDS  
SOURCE Adeno-associated virus  
ORGANISM Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;  
REFERENCE 1  
AUTHORS Rader,D.J. and Wilson,J.M.  
TITLE Methods and compositions for lowering total cholesterol levels and  
JOURNAL treatment of heart disease  
The Trustees of The University of Pennsylvania (US)  
FEATURES  
source 1..4393  
/organism="Adeno-associated virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:272636"  
ORIGIN  
Query Match 72.0%; Score 3370.4; DB 2; Length 4393;  
Best Local Similarity 87.5%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 527; Indels 16; Gaps 9;  
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QY 216 G-TTTTGGACATTTTGGACACCATGTGTTCACGCTGGTATTTAACCCGAGTGAGCA 274  
Db 122 GCTTTTGGGCAATTTTGGACACCACTGGCCATTGAGTATATATGCGAGTGAGACG 181  
QY 275 CGCAGGCTCTCATTTTGAACGGGAGTTTGAACGCGCAGCCATCGCGGGTTTAC 334  
Db 182 AGCAGAGTCTCATTTTGAACGGGAGTTTGAACGAGCAGCAGCCATCGCGGGTTTAC 241  
QY 335 GAGATTGTGATTAAGTCCCGACGACCTTGAACGATCTGCCGCGATTCTGACAGC 394  
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Db 1082 CTGTTAGGCCCCGCTCCGCGCCGACGACATTAAACGCAATTACCGCATCTGGAG 1141  
QY 1229 CTGAACGCTACGACCTTGCCTACGCGGCTCGTCTTTCTCGGCTGGGCCAGAAAAAG 1288  
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QY	2009	CACGGGACCAAGAGACTGTTCAAGATGTTTCCCGGCGTGTCAGAATCTCAACCGGTGTC	2068
Db	1922	CACGGGGCTCAAGAGACTGCTCAGAGTGTTTCCCGCGGTGTCAGAATCTCAACCGGTGTC	1981
QY	2069	AGAAAGAGAGAGGTATCGGAAACTCTGATGACATTCATCTGATGGGGCGGGCTCCGAG	2128
Db	1982	AGAAAGAGAGAGGTATCGGAAACTCTGTGCAATTCATCTGTGTGGGGCGGGCTCCGAG	2041
QY	2129	ATTGCTTGCTCGGCTCGGATCTGGTTCACATGTGATTCGATGACTGTGTTTCTGACAA	2188
Db	2042	ATTGCTTGCTCGGCTCGGATCTGGTTCACATGTGATTCGATGACTGTGTTTCTGACAA	2101
QY	2189	TAAATGACTTAAACCAAGTATGCTGCTCCGATGTTATTTCTCAATTTGGCTCGAGACAA	2248
Db	2102	TAAATGACTTAAACCAAGTATGCTGCTCCGATGTTATTTCTCAATTTGGCTCGAGACAA	2161
QY	2249	CCTCTCTAGGGGCAATTGGGCAAGTGGTGGGCACTTGAAACTGTGAGCCCCGAAACCAAGC	2308
Db	2162	CCTCTCTAGGGGCAATTGGGCAAGTGGTGGGCGCTTGAAACTGTGAGCCCCGAAACCAAGC	2221
QY	2309	CAACGAGCAAAAGCAGAGCAGACGCGCCGGGCTGTGGTCTTCTGTGCTTCAAGTACTCTCG	2368
Db	2222	CAACGAGCAAAAGCAGAGCAGACGCGCCGGGCTGTGGTCTTCTGTGCTTCAAGTACTCTCG	2281
QY	2369	ACCTTTCACGGACTCGACAAAGGGGAGACCCGTCAACGCGCGGATGACGCGGCTTCGA	2428
Db	2282	ACCTTTCACGGACTCGACAAAGGGGAGACCCGTCAACGCGCGGATGACGCGGCTTCGA	2341
QY	2449	GCAGACAAAGGCTTACGACGACGAGCTCAAGCGGGTTCACATCCGTACTGGCGGTATTA	2488
Db	2342	GCAGACAAAGGCTTACGACGACGAGCTCAAGCGGGTTCACATCCGTACTGGCGGTATTA	2401
QY	2489	CCACGCCAGCCCGAGTTCAGAGAGCGTCTGCAAGAAATATAGTCTTTTGGGGCAACT	2548
Db	2402	CCACGCCAGCCCGAGTTCAGAGAGCGTCTGCAAGAAATATAGTCTTTTGGGGCAACT	2461
QY	2549	CGGGGAGACAGTCTTCACAGGCCCAAGAGAGGGTTCGAACTTTTGTGTTGAGA	2608
Db	2462	CGGGGAGACAGTCTTCACAGGCCCAAGAGAGGGTTCGAACTTTGTTGAGA	2521
QY	2609	AGGTGCTTAAGACGGTCTCTGGAAAGAAACGTCCGTATAGCANATGCCACA--AGAGCC	2665
Db	2522	AGGTGCTTAAGACGGTCTCTGGAAAGAAAGACCGGTATAGCANATGCCACCCGCGTTCGC	2581
QY	2666	AGACTCTCTCTCGGGCATTTGGCAAGACAGGCGAGAGGCCCTTAAGAAAGACTCAATTT	2725
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QY	2726	TGTTGAGACTGGCGACTCAAGATGATGATCCAGACCTCTCAACTCTCTCGGAGAACTTCGAGC	2785
Db	2642	TGTTGAGACTGGCGACTCAAGATGATGATCCAGACCTCTCAACTCTCTCGGAGAACTTCGAGC	2701
QY	2786	AAACCCCGCTGTGTGGGACCTTACTACAAATGGCTTCAGGCGGTGGCGGACCAATGGCAGA	2845
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QY	3023	CTACTTCGGCTTACAGCAACCCCTGGGGGTAATTTGATTTCAACAGATTCCATCGCATTT	3082
Db	2942	CTACTTCGGCTTACAGCAACCCCTGGGGGTAATTTGATTTCAACAGATTCCATCGCATTT	3001
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Db	3062	CAGCTTCAAGCTCTTCAACATCAAGTCAAGGAGGTCA	CGAAGATGAGGCA	CGAAC	3121
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Db	3122	CATCGCCAAATTA	CTCACACAGCACCATCCAGGTGTGTA	CGGACTCGAGTACAGCTGCGC	3181
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Db	3182	GTACGTCTCGGCTCTGCGACACAGGGGCGCTCGCTCGT	TTCCGGGGGAGCGTGTTCAT		3241
Oy	3383	GATTCGCGAGTACGGGCTACTTAACGCTCAACATGG	CAAGCCAGAGAGTGGAGCGCTCATC		3382
Db	3242	GATTCGCCAGTACGGGCTACTTAACACTCAACAGCGT	AGTCAAGCGGTGGAGCGCTCTC		3301
Oy	3383	CTTTTACTGCTCGAATAATTTCCATCGCAGATGCT	GAGAACGGGCATTAATCTTTA	CCTT	3442
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Oy	3443	CAGCTACACCTTCGAGGAGAGTCCCTTTCCACAG	CAGCTACCGGCACAGCAGCCTTGA		3502
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Db	3422	CCGGCTGATGAATCCCTCATGACACAGTACCTGTA	TACTGTAACAGAACTCACAAATCA		3481
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Db	3482	AGGAGGACAGGCAAAATACGACAGCTCTGGGCTT	CAGCCAGGTGGGCTTAATTAATGCGC		3541
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Oy	3683	AAAAACAGCAACAAACAGGAACTTTACCTGAGCTG	GTCTTCAAAATATTAACCTTAA		3742
Db	3602	AACCGGGCAAAACAAACATAGCACTTTGCTGAGCT	GCTGGGACCAATTAATCTTGA		3661
Oy	3743	TGGGCGTGAATCTATATCAACCTTGCGACTGCTA	TGAGCTTACCAAAAGACGACAAAGA		3802
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Oy	3803	CAAGTCTTTCCCATGAGGGGTGTCAATGTTTTTGA	AAAGAGAGGCGCGGAGCTTCA		3862
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Oy	3863	CAGTCGATTTGACAAATGTATGATCAACAGAGAA	AGAAATCAAGGCACTTAACCCGT		3922
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Oy	3983	GACCGAGATGTGCAATGTTATGGAGACCTTACCT	GGAATGTTGTGGCAAGACAGAGCT		4042
Db	3902	AATTGGAATCTCAACAGCACAGGGGCGCTTAC	CCGGTATGCTGCGCAAAACCGGAGCGT		3961
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Db	4262	CTTTGCTGTATATACGAAGGCGGTACTCTGGAACCCCGCCCAATTGGCAACCGGTACTCT	4321
Oy	4403	CACCCGTCCTCTGTAATATGTGTTTAATCAATTAACCGGTTAATATCGTCAAGTTGAAC	4462
Db	4322	CACCCGTAATCTGTATATGCTGCTGTTAATCAATTAACCGGTTAGTTTCGTTTCAAGTTGAAC	4381
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## RESULT 14

CS073594

LOCUS	CS073594	4393 bp	DNA	linear	PAT 05-MAY-2005
DEFINITION	Sequence 182 from Patent WO2005033321.				

ACCESSION CS073594

VERSION CS073594.1 GI:63090490

## KEYWORDS

**SOURCE** .....

ORGANISM unidentified

unclassified sequences.

REFERENCE 1  
WILSON, T. M. 1960. 27

## AUTHORS

ADENO-ASSOCIATED VIRUS (AAV) CLADES, SEQUENCES, VECTORS AND USES THEREFOR

Journal: WO 2005033333-A 193 14-PP-2005.  
Baton: and uses cerebral  
ballie, and uses cerebral

BOOKEND  
Parent: WO 2003033321-A 102 14-MPR-2003,  
The Trustees of the University of Pennsylvania

Location/Qualifiers

Source

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/organisms="unidentified"

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/moj type="unassigned DNA"

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/db xref="taxon:32644"
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/note="adeno-associated virus serotype 8"

## ORIGIN

Query Match	72.0%	Score 3370.4	DB 2	length 4393
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Best Local Similarity 87.5%; Pred. No. 0;

Matches 3785; Conservative 0; Mismatches 527; Indels 16; Gaps 9;

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QY	216	G-TTTTGGACATTTTGGGACACCATGTGTGCAGCTGGGTATTAAAGCCCGAATGACA	274
Db	122	GCTTTTGGGGCATTTTGGCACACACGCGGCATTGGATATATATGGCCGATGAGCG	181
QY	275	CGCAGGGCTCCATTTTGGAAAGCGGAGGTTGAAACGCGACGCGCATGCGGGGTTTAC	334
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QY	335	GAGATTGTGATTAAGTCCCGACGCACTTGACAGCATCTGCCCGCATTTCTGACGC	394
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DEFINITION Sequence 4 from Patent Epi310571.  
ACCESSION AX753249  
VERSION AX753249.1 GI:32166106  
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SOURCE Adeno-associated virus - 8  
ORGANISM Adeno-associated virus - 8  
Virusess; asDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;  
unclassified Dependovirus.

REFERENCE  
AUTHORS Gao, G., Wilson, J.M. and Alvira, M.  
TITLE A method of detecting and/or identifying adeno-associated virus  
JOURNALS (AAV) sequences and isolating novel sequences identified thereby  
The Trustees of The University of Pennsylvania (US)  
FEATURES  
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/mol\_type="unassigned DNA"

ORIGIN /db\_xref="taxon:202813"  
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 2	128.4	2.7	195	8	CO888893
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C 4	105.2	2.2	969	14	CO888893
C 5	102.4	2.2	917	14	CO888893
C 6	102.4	2.2	1165	14	CO888893
C 7	102.2	2.2	900	14	CO888893
C 8	101.6	2.2	835	14	CO888893
C 9	101.4	2.2	894	14	CO888893
C 10	101.2	2.2	895	14	CO888893
C 11	100.8	2.2	896	14	CO888893
C 12	100.6	2.1	919	14	CO888893
C 13	100.6	2.1	945	14	CO888893
C 14	100.4	2.1	937	14	CO888893
C 15	100.4	2.1	943	14	CO888893
C 16	100.2	2.1	920	14	CO888893
C 17	99.8	2.1	1032	14	CO888893
C 18	99.8	2.1	1051	14	CO888893
C 19	99.8	2.1	1057	14	CO888893

C 20	99.6	2.1	911	14	DU710661
C 21	99.4	2.1	882	14	DU710048
C 22	99.4	2.1	895	14	DU710511
C 23	99.4	2.1	916	14	DU710467
C 24	99.4	2.1	946	14	DU710802
C 25	99.4	2.1	961	14	DU710790
C 26	99.4	2.1	977	14	DU710516
C 27	99.4	2.1	1104	14	DU710637
C 28	99.2	2.1	958	14	DU710698
C 29	99	2.1	919	14	DU710988
C 30	99	2.1	937	14	DU710685
C 31	98.8	2.1	921	14	DU710471
C 32	98.8	2.1	938	14	DU710826
C 33	98.6	2.1	922	14	DU710448
C 34	98.6	2.1	980	14	DU710856
C 35	98.4	2.1	859	14	DU710005
C 36	98.4	2.1	859	14	DU710905
C 37	98.4	2.1	878	14	DU709966
C 38	98.4	2.1	888	14	DU710228
C 39	98.4	2.1	891	14	DU709911
C 40	98.4	2.1	898	14	DU710025
C 41	98.4	2.1	912	14	DU710452
C 42	98.4	2.1	912	14	DU710972
C 43	98.4	2.1	922	14	DU710037
C 44	98.4	2.1	922	14	DU710560
C 45	98.4	2.1	925	14	DU710832

#### ALIGNMENTS

RESULT 1  
CO892248/264 bp mRNA linear EST 01-SEP-2004  
LOCUS  
DEFINITION  
Bowgen.20573 normal cattle brain Bos taurus cDNA clone  
RZPDP1056M0360Q 5', mRNA sequence.  
CO892248

ACCESSION  
CO892248.1 GI:51822548

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Bos taurus (cattle)

REFERENCE  
Hemig, S., Janitz, M., Herwig, R. and Williams, J.  
Generation, annotation, evolutionary analysis and database  
integration of 14969 cattle EST clusters  
unpublished (2004)

JOURNAL  
COMMENT  
Contact: Hemig S  
Laboratory 123, dept. Lehrach  
Max-Planck-Institut fuer Molekulare Genetik  
Inhestr. 63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380  
Email: hemig@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting  
(ONFP) to reduce sequencing redundancy. According to the ONFP  
procedure, clones that display the same hybridisation matrix with a  
battery of 200 8mer oligonucleotides are grouped into clusters. One  
clone per ONFP cluster was selected for sequencing. cDNA clones and  
filters are distributed via Deutsches Ressourcenzentrum fuer  
Genomforschung GmbH (http://www.rzpd.de).

PCR Primers  
FORWARD: 5' CCCAGGCTTACACTTATCTCCGGCTCG 3' (M13RSP) 5'-seq  
BACKWARD: 5' GCTATACGCGACGCTGCAAGGGGATGTG 3' (M13FSP) 3'-seq  
Seq primer: 5'-CCGTCGGAATTCCTCCGGGT-3' (M13RSP).

#### FEATURES

source  
location/Qualifiers  
1..264  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="RZPDP1056M0360Q"

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/sex="female"
/tissue_type="brain tissue"
/dev_stage="adult brain"
/clone_lib="normal cattle brain"
/notes="Organ: Brain; Vector: pSport1, Site_1: NotI,
Site_2: SalI; Random primed and directionally cloned in
pSport1 vector using NotI
(5'-pGACTAGTTCTAGATCGCAGCGCCGCC (T)15-3' and SalI 5'-
TCGACCCAGCGGTCGCG-3' adapters (Gibco BRL) "
```

## ORIGIN

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Query Match 4.0%; Score 187.2; DB 8; Length 264;
Best Local Similarity 81.8%; Pred. No. 6.8e-39;
Matches 216; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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OY 4054 GTCCATTGTTGGGCGCAAAATTCCTCACAGGATGACACTTTCACCCGCTCTCTGCATGG 4113
DB 264 GTCCATTGTTGGGCGCAATGATTCACACTCGAGCAGCAATTTTCACCCCTCTCTGCATGG 205
OY 4114 GCGGCTTTGGAATTAAAGACCCGCTCTCTCAGATCCTCATCAAAAACAGCGCTGTTCTG 4173
DB 204 GGGGATTTGGGACTTAATACCTCTCTCCACAGATTTTATCAAGAAACAGCGGTTCTG 145
OY 4174 CGAATCTCCGCGCAGAGTTTTCGCTACAAAGTTTCTTCATTCATCAACCGATTTTCCA 4233
DB 144 CGAGTCTTTCGAGCAGCTTCAGTGGCGCAAGTTTGTTCATTCATCACAGTACTTCCA 85
OY 4234 CAGGACAGTGAAGCGGTGAGATGGAATGGGAGCTGCAGAAAGAAACAGCAACGCTTGA 4293
DB 84 CGGTCAGAGTCAAGCTGAGATTTGAGTGGAGCTGGGAGAAAGAAACAGCAACGCTTGA 25
OY 4294 ATCCGGAAGTGCAGTATACATCTA 4317
DB 24 ATCCGGAATTCAGTACACTTCCA 1
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RESULT 2  
CO888893/c 195 bp mRNA linear EST 01-SEP-2004  
LOCUS RZDPJ05600960Q 5', mRNA sequence.  
DEFINITION Bosgen 17218 normal cattle brain Bos taurus cDNA clone

ACCESSION CO888893  
VERSION CO888893.1 GI:51819178  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 195)  
Hemig,S., Janitz,M., Herwig,R. and Williams,J.  
Generation, annotation, evolutionary analysis and database  
integration of 14969 cattle EST clusters  
Unpublished (2004)

JOURNAL COMMENT  
Contact: Hennig S  
Laboratory 123, dept. Lehrach  
Max-Planck-Institut fuer Molekulare Genetik  
Inhestr.63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380  
Email: hennig@molgen.mpg.de  
The library was characterized by oligonucleotide fingerprinting  
(ONFP) to reduce sequencing redundancy. According to the ONFP  
procedure, clones that display the same hybridisation matrix with a  
battery of 200 8mer oligonucleotides are grouped into clusters. One  
clone per ONFP cluster was selected for sequencing. cDNA clones and  
filters are distributed via Deutsches Ressourcenzentrum fuer  
Genomforschung GmbH (<http://www.rzpd.de>).

PCR primers  
FORWARD: 5' CCCGAGGCTTACACTTATGCTTCGGCTCG 3' (M13SP) 5'-seq  
BACKWARD: 5' GCTATTACGACAGCTGGGAAAGGGGATGCG 3' (M13FSP) 3'-seq  
Seq primer: 5'-CCGATCCGGAATTCGGGT-3' (M13RSP).  
Location/Qualifiers

## FEATURES

## source

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1. 195
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="RZDPJ05600960Q"
/sex="female"
/tissue_type="brain tissue"
/dev_stage="adult brain"
/clone_lib="normal cattle brain"
/notes="Organ: brain; Vector: pSport1, Site_1: NotI,
Site_2: SalI; Random primed and directionally cloned in
pSport1 vector using NotI
(5'-pGACTAGTTCTAGATCGCAGCGCCGCC (T)15-3' and SalI 5'-
TCGACCCAGCGGTCGCG-3' adapters (Gibco BRL) "
```

## ORIGIN

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Query Match 2.7%; Score 128.4; DB 8; Length 195;
Best Local Similarity 78.9%; Pred. No. 5.9e-23;
Matches 153; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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OY 4224 CAGTATCCACAGGACAGTGAAGGAGATTTGAATGGAGGCTGCAGAAAGAAACAGC 4283
DB 194 CAGTATCCACAGGACAGTGAAGGAGATTTGAATGGAGGCTGCAGAAAGTAAACAGC 135
OY 4284 AAACGTCGAATCCCGAAGTGCAGTATATCATATCATATCAAAATCTGCCAAGTTGAT 4343
DB 134 AAACGTCGAATCCCGAATTCAGTACATTTCACTTCAACTACAAAGTCTGTTAATGTGAT 75
OY 4344 TTCACTGTGACAAACAATGCACTTATATCTGAGGCTTGGCCCATTTGGACCCGTTACTTC 4403
DB 74 TTTATATGTGACATTAATGAGCGTGTATTCAGAGCTTGGCCCATTTGGACACAGTACTTCG 15
OY 4404 ACCGTCCTCCCTGTA 4417
DB 14 ACTGTATATGTGTA 1
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RESULT 3  
DU710412/c 913 bp DNA linear GSS 15-NOV-2005  
LOCUS aav01.fpol0q008y1 Adeno-Associated Virus Vector Integration  
DEFINITION Junctions Homo sapiens genomic clone aav01.fpol0q008, genomic  
survey sequence.  
ACCESSION DU710412  
VERSION DU710412.1 GI:82414138  
KEYWORDS GSS.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 913)  
Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and  
Russell,D.W.  
Large-scale Analysis of Adeno-Associated Virus Vector Integration  
Sites

JOURNAL COMMENT  
Contact: Miller, D.G.  
Department of Pediatrics  
University of Washington  
HSP RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,  
USA  
Tel: 206 685 3882  
Fax: 206 221 5132  
Email: dgmiller@u.washington.edu  
AAV Vector:Chromosome Junction Sequences rescued as plasmids in  
bacteria. Files with names differing only by x1 or y1 contain  
sequence reads from either end of the same AAV provirus. 'y1'  
indicates the 'left' and 'x1' indicates the 'right' primer was used  
to initiate sequencing reactions.

Seq primer: left, 5'-GATAAGCTGTCAACATGAGATTC  
Class: Viral tagged.  
Location/Qualifiers

## FEATURES



Junctions"  
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction  
Sequences rescued as plasmids in bacteria. Files with  
names differing only by x1 or y1 contain sequence reads  
from either end of the same AAV vector provirus. 'y1'  
indicates the 'left' and 'x1' indicates the 'right' primer  
was used to initiate sequencing reactions."

## ORIGIN

Query Match 2.2%; Score 102.4; DB 14; Length 917;  
Best Local Similarity 90.8%; Pred. No. 1.1e-15;  
Matches 109; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 28 TCGCTCACTGAGCGCGCGCAAGGTGCGCCGAGCGCGGCTTTGCGCGGCGGCC 87  
Db 176 TTGCTCATCTCGGGTGTGTACCAAGGTGCGCCGAGCGCGGCTTTGCGCGGCGGCC 117  
Qy 88 TCAGTGAGCGAGCGAGCGCGAGAGAGAGGTGGCCAACTCCATCATAGGGGTTCTGTG 147  
Db 116 TCAGTGAGCGAGCGAGCGCGAGAGAGAGGTGGCCAACTCATCATAGGGGTTCTGTG 57

RESULT 6  
DUT10876/c 1165 bp DNA linear GSS 15-NOV-2005  
LOCUS aav01\_fp017q002y1 Adeno-Associated Virus Vector Integration  
DEFINITION Junctions Homo sapiens genomic clone aav01\_fp017q002, genomic  
survey sequence.

ACCESSION DUT10876  
VERSION DUT10876.1 GI:82414602  
KEYWORDS GSS.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

REFERENCE 1 (bases 1 to 1165)  
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and  
Russell,D.W.

TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration  
SITES Journal of Virology 79 (17), 11434-11442 (2005)

JOURNAL COMMENT  
Contact: Miller, D.G.  
Department of Pediatrics  
University of Washington  
HSB R3349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,  
USA  
Tel: 206 685 3882  
Fax: 206 221 5132

Email: dgmiller@u.washington.edu  
AAV Vector:Chromosome Junction Sequences rescued as plasmids in  
bacteria. Files with names differing only by x1 or y1 contain  
sequence reads from either end of the same AAV provirus. 'y1'  
indicates the 'left' and 'x1' indicates the 'right' primer was used  
to initiate sequencing reactions.  
Seq primer: left, 5'-GATTAAGCTGTCAACATGAGAAATTC  
Class: viral tagged.

## FEATURES

## source

1..1165  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="aav01\_fp017q002"  
/sex="male"  
/cell\_type="Human Primary Fibroblasts"  
/cell\_line="GM05387, Coriell Institute for Medical  
Research, Camden, NJ"  
/clone\_lib="Adeno-Associated Virus Vector Integration  
Junctions"  
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction  
Sequences rescued as plasmids in bacteria. Files with  
names differing only by x1 or y1 contain sequence reads  
from either end of the same AAV vector provirus. 'y1'

indicates the 'left' and 'x1' indicates the 'right' primer  
was used to initiate sequencing reactions."

## ORIGIN

Query Match 2.2%; Score 102.4; DB 14; Length 1165;  
Best Local Similarity 90.8%; Pred. No. 1.2e-15;  
Matches 109; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 28 TCGCTCACTGAGCGCGCGCAAGGTGCGCCGAGCGCGGCTTTGCGCGGCGGCC 87  
Db 226 TCACCACTAATCTTGCTGAGACCAAGGTGCGCCGAGCGCGGCTTTGCGCGGCGGCC 167  
Qy 88 TCAGTGAGCGAGCGAGCGCGAGAGAGAGGTGGCCAACTCCATCATAGGGGTTCTGTG 147  
Db 166 TCAGTGAGCGAGCGAGCGCGAGAGAGAGGTGGCCAACTCATCATAGGGGTTCTGTG 107

RESULT 7  
DUT10553/c 900 bp DNA linear GSS 15-NOV-2005  
LOCUS aav01\_fp011q043y1 Adeno-Associated Virus Vector Integration  
DEFINITION Junctions Homo sapiens genomic clone aav01\_fp011q043, genomic  
survey sequence.

ACCESSION DUT10553  
VERSION DUT10553.1 GI:82414279  
KEYWORDS GSS.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

REFERENCE 1 (bases 1 to 900)  
AUTHORS Russell,D.W., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and  
Russell,D.W.

TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration  
SITES Journal of Virology 79 (17), 11434-11442 (2005)  
JOURNAL COMMENT  
Contact: Miller, D.G.  
Department of Pediatrics  
University of Washington  
HSB R3349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,  
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Tel: 206 685 3882  
Fax: 206 221 5132

Email: dgmiller@u.washington.edu  
AAV Vector:Chromosome Junction Sequences rescued as plasmids in  
bacteria. Files with names differing only by x1 or y1 contain  
sequence reads from either end of the same AAV provirus. 'y1'  
indicates the 'left' and 'x1' indicates the 'right' primer was used  
to initiate sequencing reactions.  
Seq primer: left, 5'-GATTAAGCTGTCAACATGAGAAATTC  
Class: viral tagged.

## FEATURES

## source

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Research, Camden, NJ"  
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Junctions"  
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction  
Sequences rescued as plasmids in bacteria. Files with  
names differing only by x1 or y1 contain sequence reads  
from either end of the same AAV vector provirus. 'y1'  
indicates the 'left' and 'x1' indicates the 'right' primer  
was used to initiate sequencing reactions."

## ORIGIN

Query Match 2.2%; Score 102.2; DB 14; Length 900;



QY 105 GCGGAGAGGAGTGGCCAACTCCATCATAGGGGTTCTTG 147  
 Db 103 GCGGAGAGGAGTGGCCAACTCCATCATAGGGGTTCTTG 61  
 RESULT 10  
 LOCUS DU709924/c  
 DEFINITION aav01\_f0003q029y1 Adeno-Associated Virus Vector Integration  
 Functions Homo sapiens genomic clone aav01\_f0003q029, genomic  
 survey sequence.  
 ACCESSION DU709924 895 bp DNA linear GSS 15-NOV-2005  
 VERSION DU709924  
 KEYWORDS DU709924.1 GI:82413650  
 SOURCE GSS.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 895)  
 Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and  
 Russell,D.W.  
 Large-scale Analysis of Adeno-Associated Virus Vector Integration  
 Sites  
 Journal of Virology 79 (17), 11434-11442 (2005)  
 Contact: Miller, D.G.  
 Department of Pediatrics  
 University of Washington  
 HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,  
 USA  
 Tel: 206 685 3882  
 Fax: 206 221 5132  
 Email: dgmiller@u.washington.edu  
 AAV Vector:Chromosome Junction Sequences rescued as plasmids in  
 bacteria. Files with names differing only by x1 or y1 contain  
 sequence reads from either end of the same AAV provirus. 'y1'  
 indicates the 'left' and 'x1' indicates the 'right' primer was used  
 to initiate sequencing reactions.  
 Seq primer: left, 5'-GATTAAGCTGTCAAACTGAGAAATTC  
 Class: viral tagged.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="aav01\_f0003q029"  
 /sex="male"  
 /cell\_type="Human Primary Fibroblasts"  
 /cell\_line="GM05387, Coriell Institute for Medical  
 Research, Camden, NJ"  
 /clone\_lib="Adeno-Associated Virus Vector Integration  
 Junctions"  
 /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction  
 Sequences rescued as plasmids in bacteria. Files with  
 names differing only by x1 or y1 contain sequence reads  
 from either end of the same AAV vector provirus. 'y1'  
 indicates the 'left' and 'x1' indicates the 'right' primer  
 was used to initiate sequencing reactions."  
 ORIGIN  
 Query Match 2.2%; Score 101.2; DB 14; Length 895;  
 Best Local Similarity 93.0%; Pred. No. 2.3e-15;  
 Matches 106; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 34 ACTGAGCGCGGCGAACAAGTGCCTCCGAGCCCGGGCTTGGCCGGCGGCTCACTG 93  
 Db 170 ACGGGGTCTGACAGCAAGAGTGCCTCCGAGCCCGGGCTTGGCCGGCGGCTCACTG 111  
 QY 94 AGCGAGCGAGCGCGGAGAGGAGTGCCTCACTCATAGGGGTTCTTG 147  
 Db 110 AGCGAGCGAGCGCGGAGAGGAGTGCCTCACTCATAGGGGTTCTTG 57

RESULT 11  
 LOCUS DU709985/c  
 DEFINITION aav01\_f0003q079y1 Adeno-Associated Virus Vector Integration  
 Junctions Homo sapiens genomic clone aav01\_f0003q079, genomic  
 survey sequence.  
 ACCESSION DU709985 896 bp DNA linear GSS 15-NOV-2005  
 VERSION DU709985  
 KEYWORDS DU709985.1 GI:82413711  
 SOURCE GSS.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 896)  
 Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and  
 Russell,D.W.  
 Large-scale Analysis of Adeno-Associated Virus Vector Integration  
 Sites  
 Journal of Virology 79 (17), 11434-11442 (2005)  
 Contact: Miller, D.G.  
 Department of Pediatrics  
 University of Washington  
 HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,  
 USA  
 Tel: 206 685 3882  
 Fax: 206 221 5132  
 Email: dgmiller@u.washington.edu  
 AAV Vector:Chromosome Junction Sequences rescued as plasmids in  
 bacteria. Files with names differing only by x1 or y1 contain  
 sequence reads from either end of the same AAV provirus. 'y1'  
 indicates the 'left' and 'x1' indicates the 'right' primer was used  
 to initiate sequencing reactions.  
 Seq primer: left, 5'-GATTAAGCTGTCAAACTGAGAAATTC  
 Class: viral tagged.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="aav01\_f0003q079"  
 /sex="male"  
 /cell\_type="Human Primary Fibroblasts"  
 /cell\_line="GM05387, Coriell Institute for Medical  
 Research, Camden, NJ"  
 /clone\_lib="Adeno-Associated Virus Vector Integration  
 Junctions"  
 /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction  
 Sequences rescued as plasmids in bacteria. Files with  
 names differing only by x1 or y1 contain sequence reads  
 from either end of the same AAV vector provirus. 'y1'  
 indicates the 'left' and 'x1' indicates the 'right' primer  
 was used to initiate sequencing reactions."  
 ORIGIN  
 Query Match 2.2%; Score 100.8; DB 14; Length 896;  
 Best Local Similarity 93.8%; Pred. No. 3e-15; 7; Indels 0; Gaps 0;  
 Matches 105; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 36 TGAAGCCCGGCGAACAAGTGCCTCCGAGCCCGGGCTTGGCCGGCGGCTCACTGAG 95  
 Db 170 TGAAGCAAACTTACAAAGTGCCTCCGAGCCCGGGCTTGGCCGGCGGCTCACTGAG 111  
 QY 96 CGAGCGAGCGCGGAGAGGAGTGCCTCACTCATAGGGGTTCTTG 147  
 Db 110 CGAGCGAGCGCGGAGAGGAGTGCCTCACTCATAGGGGTTCTTG 59  
 RESULT 12  
 LOCUS DU710573/c  
 DEFINITION aav01\_f0011q064x1 Adeno-Associated Virus Vector Integration



Junctions Homo sapiens genomic clone aav01\_fp011q064, genomic survey sequence.

ACCESSION	DU710573
VERSION	DU710573.1
KEYWORDS	GSS.

SOURCE ORGANISM	Homo sapiens (human)
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100	100

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
1 (bases 1 to 919)  
Miller, D.G., Trobridge, G.D., Petek, L.M., Jacobs, M.A., Kaul, R. and Russell, D.W.

TITLE	JOURNAL
Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites	Journal of Virology 79 (17), 11434-11442 (2005)

COMMENT

Contact: Miller, D.G.  
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**AAV Vector:** Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions.  
**Seq primer:** right, 5'-ATCACGAGGCCCTTTCGTTTCAAG  
**Class:** Viral tagged.

FEATURES	Location/Qualifiers
source	1. .919

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/mol_type="genomic DNA"  
/db_xref="taxon:9606"  
/clone="aav01_fp01q064"  
sex="male"
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/cell_type="human Primary Fibroblasts"
/cell_line="GM03587, Coriell Institute for Medical
Research, Camden, NJ"
/clone_id="Adeno-Associated Virus Vector Integration
Junctions"
/note="Vector: AAV2-T0A; AAV Vector:Chromosome Junction
Sequences rescued as plasmids in bacteria. Files with
names differing only by x1 or y1 contain sequence reads
from either end of the same AAV vector provirus. 'y1'
indicates the 'left' and 'x1' indicates the 'right' primer
was used to initiate sequencing reactions."

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**ORIGIN**

Query Match 2.18; Score 100.6; DB 14; Length 919;

Best Local Similarity 96.3%; Pred. No. 3.4e-15;  
Matches 103; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 41 CCGGCGACCAAGSTCGCCCGACGCCCGGCTTTGCCCCGGGCGGCTCAGTATGCGAGC 100

Db 167 CCTCCGACCAAGSTCGCCCGACGCCCGGCTTTGCCCCGGGCGGCTCAGTATGCGAGC 108

Oy	101 GAGCGGCGAGAGGGAGTGGCCAACTTCATCA TAGGGGTTCCTGG	147
Db	107 GAGCGGCGAGAGGGAGTGGCCAACTTCATCA TAGGGGTTCCTTG	61

RESULT 13  
DU710776/c

LOCUS	945 bp	DNA	linear	GSS 15-NOV-2005
DEFINITION	DU710776			
	aaav01_fp014q045x1	Adeno-Associated Virus Vector	Integration	

Junctions Homo sapiens genomic clone aav01\_fp014q045, genomic survey sequence.

ACCESSION	DU710776	GI:82414502
VERSION	DU710776.1	
KEYWORDS	GSS.	

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
1 (bases 1 to 945)

AUTHORS	TITLE
Miller, D.G., Trobridge, G.D., Petek, L.M., Jacobs, M.A., Kaul, R. and Russell, D.W.	Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites

JOURNAL of Virology 79 (17), 11434-11442 (2005)  
COMMENT Contact: Miller, D.G.

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USA

Tel: 206 685 3882  
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AAV Vector: Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV provirus. 'y1'

indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions.  
 Seg primer: right, 5'-ATCAGGAGGCGCTTCTGTTCAAG  
 Class: viral tagged.

FEATURES	Location/Qualifiers
source	1. .945

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="aav01_fpo14q045"

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/sex="male"
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/cell_line="G05387, Coriell Institute for Medical
Research, Camden, NJ"
/clone_id="Adeno-Associated Virus Vector Integration
Junctions"
/notes="Vector: AAV2-T0A; AAV Vector:Chromosome Junction
Sequences rescued as plasmids in bacteria. Files with
names differing only by xl or y1 contain sequence reads
from either end of the same AAV vector provirus. 'y1'
indicates the 'left' and 'xl' indicates the 'right' primer
was used to initiate sequencing reactions."

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**ORIGIN**

Query Match 2.18; Score 100.6; DB 14; Length 945;

Best Local Similarity 96.3%; Pred. No. 3.5e-15;  
Matches 103; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 41 CCGGGGCGACCAAGTCCGCCGAGCCCGGGCTTTGCCCGGGCGGCTCAGTGGCGAGC 100

Db 167 CAGGTCACCAAGTCCGCCGAGCCCGGGCTTTGCCCGGGCGGCTCAGTGGCGAGC 108

Qy 101 GAGCGCCGAGAGGGAGTGGCCACTCCATCATTAGGGGTTCTCG 147  
|||  
Db 107 GAGCGCCGAGAGGGAGTGGCCACTCCATCATTAGGGGTTCTCG 61

RESULT 14  
DU710803/c

LOCUS	DU710803	937 bp	DNA	linear	GSS 15-NC
DEFINITION	aaov1_fp014q087x1 Adeno-Associated Virus Vector Integration				

Junctions Homo sapiens genomic clone aav01\_fp014q087, genomic survey sequence.

ACCESSION	DU710803
VERSION	DU710803.1
	GI:82414529

KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1 (bases 1 to 937)  
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.  
TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites  
JOURNAL Journal of Virology 79 (17), 11434-11442 (2005)  
COMMENT Contact: Miller, D.G.  
Department of Pediatrics  
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AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by 'xl' or 'yl' contain sequence reads from either end of the same AAV provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions.  
Seq primer: right, 5'-ATCAGGAGGCGCTTTCGTTCAAG  
Class: viral tagged.

FEATURES  
source  
Location/Qualifiers  
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/clone="aav01\_fp014q087"  
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/cell\_type="Human Primary Fibroblasts"  
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/clone\_1lb="Adeno-Associated Virus Vector Integration Junctions"  
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by 'xl' or 'yl' contain sequence reads from either end of the same AAV vector provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions."

ORIGIN  
Query Match 2.1%; Score 100.4; DB 14; Length 937;  
Best Local Similarity 90.7%; Pred. No. 3.9e-15;  
Matches 107; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 30 GCTCAGTGGCGCGGCGAGCAAGGTGCGCGGCGGCTTGGCGGGCGGCGCTC 89  
Db 178 CGAGCTTGGGCTCGAGCCCAAGGTGCGCGGCGGCTTGGCGGGCGGCTC 119  
Qy 90 AGTGAGCGAGCGCGCGCAGAGAGGAGTGCCCACTCATCACTAGGGGTTCTGG 147  
Db 118 AGTGAGCGAGCGCGCGCAGAGAGGAGTGCCCACTCATCACTAGGGGTTCTGG 61

RESULT 15  
DU710346 943 bp DNA linear GSS 15-NOV-2005  
DU710346/c aav01\_fp008q066y1 Adeno-Associated Virus Vector Integration Junctions Homo sapiens genomic clone aav01\_fp008q066, genomic survey sequence.  
ACCESSION DU710346  
VERSION DU710346.1 GI:82414072  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 943)  
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.  
TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites

JOURNAL Journal of Virology 79 (17), 11434-11442 (2005)  
COMMENT Contact: Miller, D.G.  
Department of Pediatrics  
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AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by 'xl' or 'yl' contain sequence reads from either end of the same AAV provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions.  
Seq primer: left, 5'-GATAGCTGTCAACATGAGATTTC  
Class: viral tagged.

FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/clone="aav01\_fp008q066"  
/sex="male"  
/cell\_type="Human Primary Fibroblasts"  
/cell\_line="GM05387, Coriell Institute for Medical Research, Camden, NJ"  
/clone\_1lb="Adeno-Associated Virus Vector Integration Junctions"  
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by 'xl' or 'yl' contain sequence reads from either end of the same AAV vector provirus. 'yl' indicates the 'left' and 'xl' indicates the 'right' primer was used to initiate sequencing reactions."

ORIGIN  
Query Match 2.1%; Score 100.4; DB 14; Length 943;  
Best Local Similarity 99.0%; Pred. No. 3.9e-15;  
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 46 CGACCAAGGTGCGCGGCGAGCGCGGCTTGGCGGGCGGCTTCAGTGAAGCGGCGG 105  
Db 158 CGACCAAGGTGCGCGGCGAGCGCGGCTTGGCGGGCGGCTTCAGTGAAGCGGCGG 99  
Qy 106 CGCAGAGGAGGTGGCCAACTCCATCACTAGGGGTTCTGG 147  
Db 98 CGCAGAGGAGGTGGCCAACTCCATCACTAGGGGTTCTGG 57

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